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农业生物技术专题

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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

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前沿资讯

1. 陶氏杜邦正式合并 全球最大化工公司诞生

简介：陶氏杜邦9月1日宣布，陶氏化学公司（陶氏）与杜邦公司（杜邦）于2017年8月31日成功完成对等合并。合并后的实体为一家控股公司，名称为“陶氏杜邦”，公司拥有三大业务部门：农业、材料科学、特种产品，分拆将于18个月内开始陶氏杜邦执行董事长利伟诚（Andrew Liveris）表示：“我们两家公司的历史广为人知，而今天正是这一历史的一个重要里程碑。我们完成了这项转型历程中的合并，并将进一步分拆为三家行业领先的、独立的上市公司，对此我们倍感振奋。我们两家公司集合于一起的悠久历史传承与优势极为引人注目，而这一合并的真正价值在于按计划成立三大行业巨擘，它们将各自定义自己所在的市场、推动增长、为所有的利益相关方创造价值。我们的团队已经紧密合作一年多时间，致力于制定整合规划，从今天起，我们将积极着手实施这些规划，努力尽快完成分拆。

来源：基因农业网

发布日期：2017-09-04

全文链接：

<http://www.agrogene.cn/info-4342.shtml>

2. 巴西Microquimica上市大豆种子解决方案 结合两款接种剂

简介：近日，巴西Microquimica公司上市了一种大豆种子解决方案，结合了两款接种剂AzzoFix（活性成分：固氮螺菌）和Atmo（慢生根瘤菌），以及一种生物保护剂SynFlex。该解决方案已获得巴西农业、畜牧业和供应部（MAPA）登记批准，用于大豆种子处理。Microquimica技术总监Roberto Berwanger Batista表示，这些产品的结合带来了更好的生物固氮和生物保护效果，可用于种子的预处理。

来源：基因农业网

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<http://www.agrogene.cn/info-4343.shtml>

学术文献

1. A Broad-Spectrum Inhibitor of CRISPR-Cas9 (CRISPR-Cas9的广谱抑制剂)

简介：CRISPR-Cas9 proteins function within bacterial immune systems to target and destroy invasive DNA and have been harnessed as a robust technology for genome editing. Small bacteriophage-encoded anti-CRISPR proteins (Acrs) can inactivate Cas9, providing an efficient off switch for Cas9-based applications. Here, we show that two Acrs, AcrIIC1 and AcrIIC3, inhibit Cas9 by distinct strategies. AcrIIC1 is a broad-spectrum Cas9 inhibitor that prevents DNA cutting by multiple divergent Cas9 orthologs through direct binding to the conserved HNH catalytic domain of Cas9. A crystal structure of an AcrIIC1-Cas9 HNH domain complex shows how AcrIIC1 traps Cas9 in a DNA-bound but catalytically inactive

state. By contrast, AcrIIC3 blocks activity of a single Cas9 ortholog and induces Cas9 dimerization while preventing binding to the target DNA. These two orthogonal mechanisms allow for separate control of Cas9 target binding and cleavage and suggest applications to allow DNA binding while preventing DNA cutting by Cas9.

来源: Cell期刊

发布日期:2017-08-24

全文链接:

<http://agri.ckcest.cn/ass/NK007-20170911004.pdf>

2. LATERAL FLORET 1 induced the three-florets spikelet in rice (水稻小穗侧生小花的发育调控机制)

简介: The spikelet is a unique inflorescence structure in grass. The molecular mechanisms behind the development and evolution of the spikelet are far from clear. In this study, a dominant rice mutant, lateral florets 1 (lf1), was characterized. In the lf1 spikelet, lateral floral meristems were promoted unexpectedly and could generally blossom into relatively normal florets. LF1 encoded a class III homeodomain-leucine zipper (HD-ZIP III) protein, and the site of mutation in lf1 was located in a putative miRNA165/166 target sequence. Ectopic expression of both LF1 and the meristem maintenance gene OSH1 was detected in the axil of the sterile lemma primordia of the lf1 spikelet. Furthermore, the promoter of OSH1 could be bound directly by LF1 protein. Collectively, these results indicate that the mutation of LF1 induces ectopic expression of OSH1, which results in the initiation of lateral meristems to generate lateral florets in the axil of the sterile lemma. This study thus offers strong evidence in support of the “three-florets spikelet” hypothesis in rice.

来源: 美国科学院院报

发布日期:2017-08-04

全文链接:

<http://agri.ckcest.cn/ass/NK007-20170911003.pdf>

3. Genome-wide association studies dissect the genetic networks underlying agronomical traits in (全基因组关联研究分析了大豆中农艺性状的遗传网络)

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. 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 Faploci, as well as 16 undefined associated loci, have pleiotropic effects on different traits.

来源: Genome Biology期刊

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全文链接:

<http://agri.ckcest.cn/ass/NK007-20170911005.pdf>