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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;顾亮亮

联系电话：010-82109850

邮箱：agri@ckcest.cn

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▶ 前沿资讯

1. 巴斯夫创新杀菌剂Belanty®获澳大利亚登记 预计2020年上市 (BASF receives approval to introduce innovative new fungicide Belanty® to Australian farmers)

简介: The Australian Pesticides and Veterinary Medicines Authority (APVMA) has approved the use of Belanty®; an innovative new fungicide from BASF that provides fast-acting and long-lasting disease control for a broad range of crops and disease combinations. Belanty will be officially launched in 2020. "Belanty fungicide is the result of years of research and expertise. It was designed to meet the highest level of regulatory standards while helping growers manage their toughest disease challenges, including resistant plant pathogens," said Gavin Jackson, Head of BASF Agricultural Solutions in Australia and New Zealand. Belanty has a unique isopropanol link that can flex to control a broad spectrum of fungal diseases and DMI-resistant strains. In trials, it has shown exceptional biological performance against several economically significant diseases, including powdery mildew in grapes and black spot in apples. Belanty fungicide offers growers unique benefits when compared to other DMI fungicides - including much lower residues than alternative triazoles and already approved maximum residue limits for EU export. Belanty also provides plants with immediate and powerful disease protection via quick absorption, as well as longer residual activity due to its excellent rain-fastness and low water solubility. In addition, Belanty fungicide can be applied after infection which helps stop the disease from progressing before symptoms develop, therefore improving yield quality. Belanty is powered by BASF's new active ingredient, Revysol®; which is expected to become BASF's new global blockbuster fungicide with a targeted peak sales potential above €1 billion around the world. Besides Australia, BASF has received registrations in the EU, the Americas, and South Korea with further registrations in Asia Pacific anticipated soon, covering over 40 crops. The active ingredient will be available in customized formulations to enable farmers worldwide to better protect their crops under various growing conditions.

来源: AgroNews期刊

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全文链接:

<http://news.agropages.com/News/NewsDetail---31051.htm>

2. 我国科学家实现小鼠个体水平的靶向遗传筛选

简介: 近年来, CRISPR-Cas9技术介导的突变筛选在小鼠和人细胞中已被广泛应用, 而实现高效的小鼠个体水平遗传筛选对哺乳动物功能基因组研究具有重要意义。中国科学院分子细胞科学卓越创新中心(生物化学与细胞生物学研究所)李劲松和邹卫国研究团队合作应用孤雄单倍体胚胎干细胞(“人造精子细胞”)介导的半克隆技术, 结合CRISPR-Cas9介导的基因编辑技术, 成功实现了小鼠骨发育相关基因的个体水平遗传筛选, 并揭示Irx5基因作为骨发育过程中重要调控因子, 通过抑制PPAR γ 分子促进成骨分化并抑制成脂分化, 为小鼠发育过程中关键基因功能研究开辟了新的途径。李劲松研究员告诉《中国科学报》记者, 科研人员基于体外成骨分化过程高通量测序分析数

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据，筛选了72个潜在骨发育相关基因，建立了一个携带216个向导RNA（sgRNA）的单倍体干细胞库（即“人造精子细胞库”），其中的每个“人造精子”一般都携带一个针对不同基因的“sgRNA导航器”，精确定位到靶基因上并对其进行基因编辑。李劲松解释道，“我们将这些携带修饰基因的‘人造精子’逐一注射入小鼠MII期卵母细胞，一个月不到，就获得了400多只携带不同突变基因的半克隆小鼠。”邹卫国研究员说：“我们在这些小鼠出生后，就开始对其进行骨骼整体染色分析，依据骨骼大小、钙化、颅顶骨、长骨、椎骨形态等指标对每只小鼠进行评分。与此同时，我们利用每只小鼠携带的‘sgRNA导航器’对骨发育异常的小鼠所携带的‘靶基因’的测序分析，最终确定其是否存在基因突变。”“我们从72个候选基因中筛选出了4个参与骨发育调控的关键基因。”邹卫国进一步介绍说，“在这4个关键基因中，基因Zic1和Clec11a被其他研究证实参与骨发育调控，而基因Rln1和Irx5在小鼠骨发育过程中的功能尚不明确。为了验证它们在小鼠骨骼发育中的调控机制，我们构建了基因Rln1和基因Irx5敲除的小鼠模型来验证这两个基因在骨发育过程中的作用，发现敲除了Rln1基因的小鼠在出生时骨骼较小，而成年后差异不显著；敲除基因Irx5的小鼠在出生时和成年后骨骼较小和骨量下降特征均很显著，同时伴随着骨髓中脂肪形成增加的特征。进一步的分子机制研究表明，IRX5通过抑制PPAR γ 通路的激活，促进成骨分化同时抑制脂肪生成。”“这项研究的理论价值在于首次实现了小鼠个体水平骨发育靶向遗传筛选。”谈及对于未来的临床应用价值，邹卫国表示，“我们希望我们的基础研究能为临床服务，为骨质疏松症的药物研发和临床应用等提供理论支撑。”

来源：科学网

发布日期:2019-07-07

全文链接:

<http://news.sciencenet.cn/htmlnews/2019/7/428146.shtm>

3. Federal office for the environment approves GM barley field trial in Switzerland (瑞士批准转基因大麦田间实验)

简介：the Environment (FOEN) of Switzerland has given permission to the University of Zurich to conduct field trials of genetically modified (GM) barley under strict conditions on June 12, 2019. The FOEN approved the application and set out the measures that the university had to take to prevent GM material from spreading outside the experimental area. These requirements are comparable to those made in previous trials conducted in Switzerland. The field trial has been restricted to five cultivation periods from spring 2019 to autumn 2023 and will be carried out on a protected site at the Reckenholz (ZH) site of the Swiss Federal Research Station Agroscope. The barley that will be tested has been modified with the wheat resistance gene Lr34. The researchers want to find out whether the gene can also protect corn and barley. The crop will be exposed to barley leaf rust and powdery mildew fungi to test resistance. The field trials will also test whether the genetic modifications have any effect on crop development and yield.

来源：AgroNews

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<http://news.agropages.com/News/NewsDetail---31038.htm>

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4. 我国科研人员持续攻关 适宜低纬度种植的大豆材料诞生

简介: 近日, 中国农科院作物科学研究所植物转基因技术研究中心、大豆育种技术创新与新品种选育创新团队, 利用CRISPR/Cas9基因组编辑技术定点敲除大豆开花调控关键基因GmFT2a和GmFT5a, 创制出更适合低纬度地区种植的突变体材料。据介绍, 大豆对光周期反应敏感, 绝大多数品种只有在日照长度缩短到一定程度后, 才能从营养生长转入生殖生长, 进而开花结荚。大豆的这种光周期反应特性, 造成大豆品种北移种植时, 因生长季节日照加长, 往往表现为晚花晚熟、生长期延长, 甚至不能开花或正常成熟; 南移种植时, 则因生长季节日照缩短, 一般表现为过早开花、生长期缩短, 产量降低甚至不能正常生长。已有研究表明, GmFT2a和GmFT5a基因是大豆的重要开花促进因子。该研究通过构建GmFT2a和GmFT5a基因的过表达植株, 并利用CRISPR/Cas9基因组编辑技术对GmFT2a和GmFT5a进行定点敲除, 结合杂交手段, 创制出单基因和双基因突变体材料。该研究表明, GmFT5a基因是主要的开花促进基因, 是使大豆能够适应长日照环境的关键基因。研究还发现, 创制的双基因突变体在短日照条件下平均57.4天开花, 比野生型晚花约31.3天, 株高和节数较野生型显著提高, 单株荚数和粒数也显著增加, 这为适合低纬度地区种植的大豆品种改良提供了新的基础材料。

来源: 中工网

发布日期: 2019-07-05

全文链接:

http://media.worker.cn/sites/media/grrb/2019_07/05/GR0603.htm

5. 优质强筋小麦新品种中麦578实打实收创佳绩

简介: 近日, 为了进一步确认中麦578的产量表现, 河南、安徽、江苏、河北、山东等省陆续举行了中麦578实打实收活动。活动表明, 中麦578在各地实打实收活动中大面积产量接近高产品种, 既优质强筋又高产稳产的特性符合产业的需求, 受到企业的高度认可。其中, 河南焦作地区沁阳市百亩方平均亩产730.1公斤, 高产攻关田亩产785.2公斤; 新乡市新乡县千亩方平均亩产625.8公斤; 阜阳市颍上县和济南市章丘区高产攻关平均亩产分别为745.6和718.5公斤; 河北省邢台市金沙河农作物种植专业合作社种植的860亩平均亩产600.1公斤, 与当地高产品种持平, 较优质主栽品种平均增产9%。安徽、上海、河北相关公司分别就中麦578优质麦收购意向签订了订单协议。中麦578由中国农业科学院作物科学研究所和棉花研究所合作, 历时20年选育而成, 已经通过河南省品种审定, 并正在参加黄淮南片生产试验和黄淮北片第2年区域试验, 有望于2019和2020年底分别通过相应区域国家审定。根据多年多点试验和大面积展示示范, 该品种表现高产早熟抗倒伏、抗病抗逆适应性广、优质强筋且品质稳定等突出特点。区域试验中比对照平均增产3%左右, 大面积示范与周麦18和济麦22产量持平; 比对照平均早熟2天, 为玉米早播奠定基础, 有利于全年丰收; 抗倒伏, 籽粒常年千粒重50克以上, 外观商品性好。兼抗条锈、叶锈和白粉病, 赤霉病中等偏轻, 较耐穗发芽, 灌浆速率快, 耐高温, 抗冬季冻害和春季低温。该品种平均蛋白质含量14.7%, 吸水率60%, 稳定时间18分钟, 延展性163毫米; 面包体积1000毫升、评分90分, 面包品质达到进口优质加麦水平。

来源: 中国农业科学院

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<http://www.caas.net.cn/xwzx/kyjz/297607.html>

学术文献

1. A stigmatic gene confers interspecies incompatibility in the Brassicaceae (柱头的基因赋予十字花科的种间不相容性)

简介: Pre-zygotic interspecies incompatibility in angiosperms is a malefemale relationship that inhibits the formation of hybrids between two species. Here, we report on the identification of STIGMATIC PRIVACY 1 (SPRI1), an interspecies barrier gene in *Arabidopsis thaliana*. We show that the rejection activity of this stigma-specific plasma membrane protein is effective against distantly related Brassicaceae pollen tubes and is independent of self-incompatibility. Point-mutation experiments and functional tests of synthesized hypothetical ancestral forms of SPRI1 suggest evolutionary decay of SPRI1-controlled interspecies incompatibility in self-compatible *A. thaliana*. Hetero-pollination experiments indicate that SPRI1 ensures intraspecific fertilization in the pistil when pollen from other species are present. Our study supports the idea that SPRI1 functions as a barrier mechanism that permits entrance of pollen with an intrinsic signal from self species.

来源: Nature Plants 期刊

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全文链接:

http://agri.ckcest.cn/file1/M00/00/01/Csgk0V0muYiADZypAB_GbZz_t_g436.pdf

2. An EDS1-SAG101 Complex is Essential for TNL-mediated Immunity in *Nicotiana benthamiana* (烟草EDS1-SAG101复合体参与TNL介导的免疫反应)

简介: Heterodimeric complexes containing the lipase-like protein ENHANCED DISEASE SUSCEPTIBILITY1 (EDS1) are regarded as central regulators of plant innate immunity. In this context, a complex of EDS1 with PHYTOALEXIN DEFICIENT4 (PAD4) is required for basal resistance and signaling downstream of immune receptors containing an N-terminal Toll-interleukin-1 receptor-like domain (TNLs) in *Arabidopsis thaliana*. Here we analyze EDS1 functions in the model Solanaceous plant *Nicotiana benthamiana* (Nb). Stable Nb mutants deficient in EDS1 complexes are not impaired in basal resistance, a finding which contradicts a general role for EDS1 in immunity. In Nb, PAD4 demonstrated no detectable immune functions, but TNL-mediated resistance responses required EDS1 complexes incorporating a SENESCENCE ASSOCIATED GENE101 (SAG101) isoform. Intriguingly, SAG101 is restricted to those genomes also encoding TNL receptors, and we propose it may be required for TNL-mediated immune signaling in most plants, except the Brassicaceae. Transient complementation in Nb was used for accelerated mutational analyses while avoiding complex biotic interactions. We identify a large surface essential for EDS1-SAG101 immune functions, which extends from the N-terminal lipase domains to the C-terminal EP domains and might mediate interaction partner recruitment. Further, this work demonstrates the

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value of genetic resources in Nb, which will facilitate elucidation of EDS1 functions.

来源: The plant cell期刊

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/88/Csgk0F0kft2AJVzsAml3cW19MII002.pdf>

3. CRD1, an Xpo1 domain protein, regulates miRNA accumulation and crown root development in rice (一种Xpo1结构域蛋白CRD1可调节水稻中miRNA的积累和冠根发育)

简介: Crown root is the main component of the fibrous root system in cereal crops, but the molecular mechanism underlying crown root development is still unclear. Here, we isolated the crown root defect 1 (crd1) mutant from ethyl methane sulfonate (EMS)-mutated mutant library, which significantly inhibited crown root development. The CRD1 was identified through genome resequencing and complementation analysis, which encodes an Xpo1 domain protein: the rice ortholog of Arabidopsis HASTY (HST) and human exportin-5 (XPO5). CRD1 is ubiquitously expressed, with the highest expression levels in the crown root primordium at the stem base. CRD1 is a nucleocytoplasmic protein. The crd1 mutant contains significantly reduced miRNA levels in the cytoplasm and nucleus, suggesting that CRD1 is essential for maintaining normal miRNA levels in plant cells. The altered crown root phenotype of crd1 was simulated by target mimicry of miR156, suggesting that this defect is due to the disruption of miR156 regulatory pathways. Our analysis of CRD1, the HST ortholog identified in monocots, expands our understanding of the molecular mechanisms underlying miRNA level and crown root development.

来源: Plant Journal期刊

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全文链接:

<http://agri.ckcest.cn/file1/M00/00/00/Csgk0V0kexWAatZuAAuotMyc7Bo878.pdf>