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农业生物技术专题

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▶ 前沿资讯

1. 全球转基因种植面积再创历史新高

简介: 1996年,全球转基因作物种植面积仅有170万公顷。在短短的21年商业化进程当中,转基因作物在全球迅速开疆拓土,2016年全球种植总面积达到1.851亿公顷,实现了110倍的增长。2017年5月4日,国际农业生物技术应用服务组织(ISAAA)在京发布了《2016年全球生物技术/转基因作物商业化发展态势》报告,再次强调了转基因作物为发展中国家和发达国家的农民带来的长期收益,以及近期获得批准并被商业化的新品种为消费者带来的诸多好处。

来源: 生物技术信息网

发布日期: 2017-06-12

全文链接:

<http://www.biotech.org.cn/information/147215>

2. 中国化工完成对全球第一大农药、第三大种子巨头先正达的收购

简介: 中国化工集团公司(ChemChina,下称“中国化工”)6月8日宣布,对全球第一大农药公司瑞士先正达(Syngenta)的收购已完成交割。截至目前,中国化工拥有先正达94.7%的股份,下一步将推动先正达股票从瑞士交易所退市、美国存托凭证从纽约交易所退市。先正达是全球第一大农药、第三大种子农化高科技公司,有259年历史,拥有农药、种子、草坪和园艺三大业务板块。2016年,先正达销售收入约900亿元(人民币,下同),净利润84亿元。其中,农药和种子分别占全球市场份额的20%和8%。公开资料显示,中国化工是在原化工部所属企业基础上组建的国有企业。中国化工2015年财务报表显示,其总资产为3725亿元。中国化工2015年的营业收入为414.1亿美元,在2016年财富世界500强排行榜中列234位。2016年2月3日,中国化工与先正达签署收购协议,彼时股权对价为430亿美元。

来源: 基因农业网

发布日期: 2017-06-09

全文链接:

<http://www.agrogene.cn/info-4133.shtml>

▶ 学术文献

1. Higher yields and lower methane emissions with new rice cultivars (新水稻品种更加高产, 甲烷排放量更低)

简介: Breeding high-yielding rice cultivars through increasing biomass is a key strategy to meet rising global food demands. Yet, increasing rice growth can stimulate methane (CH₄) emissions, exacerbating global climate change, as rice cultivation is a major source of this powerful greenhouse gas. Here, we show in a series of experiments that high-yielding rice cultivars actually reduce CH₄ emissions from typical paddy soils. Averaged across 33 rice cultivars, a biomass increase of 10% resulted in a 10.3% decrease in CH₄ emissions in a soil with a high carbon (C) content. Compared to a low-yielding cultivar, a high-yielding cultivar

significantly increased root porosity and the abundance of methane-consuming microorganisms, suggesting that the larger and more porous root systems of high-yielding cultivars facilitated CH₄ oxidation by promoting O₂ transport to soils. Our results were further supported by a meta-analysis, showing that high-yielding rice cultivars strongly decrease CH₄ emissions from paddy soils with high organic C contents. Based on our results, increasing rice biomass by 10% could reduce annual CH₄ emissions from Chinese rice agriculture by 7.1%. Our findings suggest that modern rice breeding strategies for high-yielding cultivars can substantially mitigate paddy CH₄ emission in China and other rice growing regions.

来源: Global Change Biology 期刊

发布日期: 2017-06-01

全文链接:

<http://agri.ckcest.cn/ass/NK007-20170619003.pdf>

2. Plants transfer lipids to sustain colonization by mutualistic mycorrhizal and parasitic fungi (植物转移脂肪酸来维持共生的菌根真菌的寄生)

简介: Arbuscular mycorrhizal (AM) fungi facilitate plant uptake of mineral nutrients and draw organic nutrients from the plant. Organic nutrients are thought to be supplied primarily in the form of sugars. Here we show that the AM fungus *Rhizophagus irregularis* is a fatty acid auxotroph and that fatty acids synthesized in the host plants are transferred to the fungus to sustain mycorrhizal colonization. The transfer is dependent on RAM2 (REQUIRED FOR ARBUSCULAR MYCORRHIZATION 2) and the ATP binding cassette transporter-mediated plant lipid export pathway. We further show that plant fatty acids can be transferred to the pathogenic fungus *Golovinomyces cichoracearum* and are required for colonization by pathogens. We suggest that the mutualistic mycorrhizal and pathogenic fungi similarly recruit the fatty acid biosynthesis program to facilitate host invasion.

来源: Science

发布日期: 2017-06-08

全文链接:

<http://agri.ckcest.cn/ass/NK007-20170619002.pdf>

3. The Ectopic Overexpression of the Cotton Ve1 and Ve2-Homolog Sequences Leads to Resistance Response to Verticillium Wilt in Arabidopsis (棉花Ve1和Ve2同族序列的异常过度表达可以导致拟南芥对黄萎病的拒表达)

简介: *Verticillium* wilt, caused by the *Verticillium dahliae* phytopathogen, is a devastating disease affecting many economically important crops. A receptor-like protein (RLP) gene, *Ve1*, has been reported to confer resistance to *V. dahliae* in tomato plants, but few genes have been found to be involved in cotton *Verticillium* wilt resistance. Here, we cloned two RLP gene homologs, *Gossypium barbadense* resistance gene to *Verticillium dahliae* 1 (*GbaVd1*) and *GbaVd2*, from the *Verticillium* wilt-resistant cultivar *G. barbadense* cv.

Hai7124. *GbaVd1* and *GbaVd2* display sequence divergence, but both encode typical RLPs. Virus-induced gene silencing of *GbaVd1* or *GbaVd2* compromised the resistance of cotton to *V. dahliae*, and both genes conferred *Verticillium* wilt resistance after interfamily transfer into *Arabidopsis*. Microarray analysis revealed that *GbaVd1* and *GbaVd2* participate in *Verticillium* wilt resistance in *Arabidopsis* through activation of defense responses, including the endocytosis process, signaling factors, transcription factors and reinforcement of the cell wall, as demonstrated by lignification in *Arabidopsis* transgenic plants. In addition, microarray analysis showed that *GbaVd1* and *GbaVd2* differentially mediate resistance signaling and activation of defense responses after overexpression in *Arabidopsis*. Thus, *GbaVd1* and *GbaVd2* encode RLPs and act as disease resistance genes that mediate the defense response against *V. dahliae* in cotton.

来源: Frontiers in Plant Science期刊

发布日期:2017-05-29

全文链接:

<http://agri.ckcest.cn/ass/NK007-20170619001.pdf>