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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. 先正达拟在荷兰投资1500万欧元 兴建一座蔬菜种子“回交工厂”

简介: 正达将投资1500万欧元在荷兰的恩克赫伊森(Enkhuizen)兴建一个新的研发设施蔬菜种子回交工厂。在这个新设施中,蔬菜作物将在适当的条件下通过回交获得重要的性状,如抗病性。在这个回交工厂,回交的过程将更加自动化,所需时间进一步缩短,使高品质的蔬菜种子能够更快的进入市场。去年先正达在当地还投资了2100万欧元,用于建立新的蔬菜种子研发技术中心,该中心预计将在今年年底投入使用。先正达Enkhuizen分公司的总裁Peter Acda表示:“通过这项投资,我们在Enkhuizen的研发机构将达到世界一流的水平。这将帮助我们更好地向我们的种植者提供新的产品。先正达在蔬菜种子创新上历史悠久,我们一直致力于为消费者提供高品质、口感优秀的新鲜蔬菜。”

来源: 基因农业网

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全文链接:

<http://www.agrogene.cn/info-4404.shtml>

2. 草甘膦在欧盟“涉险过关”可继续使用五年

简介: 中新社布鲁塞尔11月27日电,备受争议的除草剂草甘膦11月27日在欧盟“涉险过关”,其使用期限被延长5年。当日欧盟负责农药安全审批的委员会举行投票,表决结果为18国赞成,9国反对,1国弃权,最终批准将下月15日到期的草甘膦使用期限延长5年。作为上世纪70年代由化工巨头孟山都公司研发的除草剂,草甘膦(商品名为农达、年年春等)多年来畅销全球,年销售额现居农药之首,但2015年世卫组织下属的国际癌症研究机构声称“草甘膦可能致癌”,自此便争议不断。11月27日表决前,欧盟各成员国已争吵数月。英国、荷兰等国支持按惯例将草甘膦的使用期限延长10年,法国、意大利等国则坚决反对,要求缩短草甘膦使用期限直至逐出欧盟农药市场。据路透社等媒体报道,草甘膦最终在欧盟过关,得益于德国在最后关头投出赞成票,令支持草甘膦的成员国数量超过16国,代表的欧盟总人口超过65%,达到欧盟投票表决“双重多数”要求。

来源: 基因农业网

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全文链接:

<http://www.agrogene.cn/info-4522.shtml>

▶ 学术文献

1. 'Two-floret spikelet' as a novel resource has the potential to increase rice yield (“多花小穗” 水稻品种可以作为新的资源来提高水稻的产量)

简介: Yield in rice (*Oryza sativa*) is determined by three major components: panicle number per plant, grain weight and grain/spikelet number per panicle (Zhou et al., 2015). Grain number per panicle is one of the main targets and mainly results from the number of spikelets.

Traditionally, rice breeders have focused on the improvement of spikelet number per panicle and rarely focused on the number of florets because a normal rice spikelet has one fertile floret and produces one seed. In grass, the spikelet comprises one to 40 florets depending on the species and shows determinacy or indeterminacy. In rice (*O. sativa*) with a determinate spikelet, the spikelet meristems produced the fixed floral meristems, resulting in the formation of one floret. In wheat (*Triticum aestivum*) with an indeterminate spikelet, the spikelet meristems produced the variable floral meristems, resulting in the formation of more florets. How to further increase rice yield? If the number of florets in a spikelet could be increased, it may be a new method for rice high production. In our study, we characterized two allelic mutants with two florets within a single spikelet, double floret1-1(df1-1) and df1-2. We next focused on the df1-1 mutant to investigate the regulation of floret number in rice, and this provided a new perspective for increasing grain number per panicle and yield.

来源: Plant Biotechnology Journal 期刊

发布日期: 2017-11-07

全文链接:

<http://agri.ckcest.cn/ass/d3ddc648-e837-4434-9e0a-b5012633fabf.pdf>

2 . Echinochloa crus-galli genome analysis provides insight into its adaptation and invasiveness as a weed (稗属稻田稗草的基因组分析为杂草的适应性和入侵性提供了见解)

简介: Barnyardgrass (*Echinochloa crus-galli*) is a pernicious weed in agricultural fields worldwide. The molecular mechanisms underlying its success in the absence of human intervention are presently unknown. Here we report a draft genome sequence of the hexaploid species *E. crus-galli*, i.e., a 1.27Gb assembly representing 90.7% of the predicted genome size. An extremely large repertoire of genes encoding cytochrome P450 monooxygenases and glutathione S-transferases associated with detoxification are found. Two gene clusters involved in the biosynthesis of an allelochemical 2,4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one (DIMBOA) and a phytoalexin momilactone A are found in the *E. crus-galli* genome, respectively. The allelochemical DIMBOA gene cluster is activated in response to co-cultivation with rice, while the phytoalexin momilactone A gene cluster specifically to infection by pathogenic *Pyricularia oryzae*. Our results provide a new understanding of the molecular mechanisms underlying the extreme adaptation of the weed.

来源: Nature 期刊

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全文链接:

<http://agri.ckcest.cn/ass/76f272cc-79f8-471e-88cd-c573d853fdcf.pdf>

3 . The Aegilops tauschii genome reveals multiple impacts of transposons (粗山羊草基因组解释了转座子的多重影响)

简介: Wheat is an important global crop with an extremely large and complex genome that contains more transposable elements (TEs) than any other known crop species. Here, we

generated a chromosome-scale, high-quality reference genome of *Aegilops tauschii*, the donor of the wheat D genome, in which 92.5% sequences have been anchored to chromosomes. Using this assembly, we accurately characterized genic loci, gene expression, pseudogenes, methylation, recombination ratios, microRNAs and especially TEs on chromosomes. In addition to the discovery of a wave of very recent gene duplications, we detected that TEs occurred in about half of the genes, and found that such genes are expressed at lower levels than those without TEs, presumably because of their elevated methylation levels. We mapped all wheat molecular markers and constructed a high-resolution integrated genetic map corresponding to genome sequences, thereby placing previously detected agronomically important genes/quantitative trait loci (QTLs) on the *Ae. tauschii* genome for the first time.

来源: Nature期刊

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<http://agri.ckcest.cn/ass/ab6daaa9-4180-47b1-ab19-e2e6aac26708.pdf>