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➤ 前沿资讯

1. 首款植物纤维基地膜投产 可明显减少农药使用

简介：农药虽然可以很好的防治病虫害、帮助农作物增产增收，但过量的使用农药也会对环境造成极大的危害。近日有消息称，首款植物纤维基地膜已正式在五常二河乡投产，此项技术可明显减少农药使用。今年，五常二河乡有机水稻种植基地插秧工序比往年多了一道——农户先在水田里铺上一层棕色地膜，然后才透过地膜插秧。这层地膜功能可不小：抑制杂草生长、保墒，重要的是两个月后秧苗长起来，它可自行降解，完全解决了传统塑料地膜使用后产生白色污染的难题。据悉，这些可降解地膜由几十公里外的黑龙江乐农农业科技发展公司生产，全部以秸秆为原料加工而成，是全球首款以植物为原料的可降解环保地膜。目前企业已计划在俄罗斯、加拿大和美国申请专利，为下一步开拓国外市场做准备。

来源：基因农业网

发布日期：2017-06-05

全文链接：

<http://www.agrogene.cn/info-4119.shtml>

➤ 学术文献

1. A receptor-like protein acts as a specificity switch for the regulation of stomatal development (受体蛋白像一个特殊的开关来调控气孔的发育)

简介：Stomata are microscopic openings that allow for the exchange of gases between plants and the environment. In Arabidopsis, stomatal patterning is specified by the ERECTA family (ERf) receptor kinases (RKs), the receptor-like protein (RLP) TOO MANY MOUTHS (TMM), and EPIDERMAL PATTERNING FACTOR (EPF) peptides. Here we show that TMM and ER or ER-LIKE1 (ERL1) form constitutive complexes, which recognize EPF1 and EPF2, but the single ERfs do not. TMM interaction with ERL1 creates a binding pocket for recognition of EPF1 and EPF2, indicating that the constitutive TMM-ERf complexes function as the receptors of EPF1 and EPF2. EPFL9 competes with EPF1 and EPF2 for binding to the ERf-TMM complex. EPFL4 and EPFL6, however, are recognized by the single ERfs without the requirement of TMM. In contrast to EPF1,2, the interaction of EPFL4,6 with an ERf is greatly reduced in the presence of TMM. Taken together, our data demonstrate that TMM dictates the specificity of ERfs for the perception of different EPFs, thus functioning as a specificity switch for the regulation of the activities of ERfs.

来源：Genes & Development 期刊

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全文链接：

<http://agri.ckceest.cn/ass/NK007-20170612003.pdf>

2. CRISPR/Cas9-mediated targeted mutagenesis of GmFT2a delays

flowering time in soybean (利用crispr/cas9技术修饰目标突变基因GmFT2a来延长大豆的开花时间)

简介: Flowering is an indication of the transition from vegetative growth to reproductive growth and has considerable effects on the life cycle of soybean (*Glycine max*). In this study, we employed the CRISPR/Cas9 system to specifically induce targeted mutagenesis of GmFT2a, an integrator in the photoperiod flowering pathway in soybean. The soybean cultivar Jack was transformed with three sgRNA/Cas9 vectors targeting different sites of endogenous GmFT2a via *Agrobacterium tumefaciens*-mediated transformation. Site-directed mutations were observed at all targeted sites by DNA sequencing analysis. T1 generation soybean plants homozygous for null alleles of GmFT2a frameshift mutated by a 1-bp insertion or short deletion exhibited late flowering under natural conditions (summer) in Beijing, China (N39°58', E116°20'). We also found that the targeted mutagenesis was stably heritable in the following T2 generation, and the homozygous GmFT2a mutants exhibited late flowering under both long-day and short-day conditions. We identified some “transgene-clean” soybean plants that were homozygous for null alleles of endogenous GmFT2a and without any transgenic element from the T1 and T2 generations. These “transgene-clean” mutants of GmFT2a may provide materials for more in-depth research of GmFT2a functions and the molecular mechanism of photoperiod responses in soybean. They will also contribute to soybean breeding and regional introduction.

来源: Plant Biotechnology Journal

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<http://agri.ckcest.cn/ass/NK007-20170612002.pdf>

3. A Pheromone Antagonist Regulates Optimal Mating Time in the Moth *Helicoverpa armigera* (信息素的拮抗作用可以调控棉铃虫的交配时间)

简介: Many insect species use multi-component sex pheromones to discriminate among potential mating partners. In moths, pheromone blends tend to be dominated by one or two major components, but behavioral responses are frequently optimized by the inclusion of less abundant minor components. An increasing number of studies have shown that female insects use these chemicals to convey their mating availability to males, who can assess the maturity of females and thus decide when to mate. However, little is known about the biological mechanisms that enable males to assess female reproductive status. In this study, we found that females of *Helicoverpa armigera* avoid nonoptimal mating by inhibiting males with pheromone antagonist *cis*-11-Hexadecenol (Z11-16:OH). We also show that this antagonist-mediated optimization of mating time ensures maximum fecundity. To further investigate molecular aspects of this phenomenon, we used the CRISPR/Cas9 system to knock out odorant receptor 16 (OR16), the only pheromone receptor tuned to Z11-16:OH. In mutant males, electrophysiological and behavioral responses to Z11-16:OH were abolished. Inability to detect Z11-16:OH prompted the males to mate with immature females, which resulted in significantly reduced viability of eggs. In conclusion, our study demonstrates that the sensitivity of OR16 to Z11-16:OH regulates optimal mating time and thus ensures maximum fecundity. These results may suggest novel strategies to disrupt pest insect mating.

来源: Current Biology 期刊

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全文链接:

<http://agri.ckcest.cn/ass/NK007-20170612001.pdf>

4. Genomic variation associated with local adaptation of weedy rice during de-domestication (杂草稻通过基因组变异去驯化并适应环境)

简介: De-domestication is a unique evolutionary process by which domesticated crops are converted into 'wild predecessor like' forms. Weedy rice (*Oryza sativa f. spontanea*) is an excellent model to dissect the molecular processes underlying de-domestication. Here, we analyse the genomes of 155 weedy and 76 locally cultivated rice accessions from four representative regions in China that were sequenced to an average $18.2 \times$ coverage. Phylogenetic and demographic analyses indicate that Chinese weedy rice was de-domesticated independently from cultivated rice and experienced a strong genetic bottleneck. Although evolving from multiple origins, critical genes underlying convergent evolution of different weedy types can be found. Allele frequency analyses suggest that standing variations and new mutations contribute differently to *to japonica* and *indica* weedy rice. We identify a Mb-scale genomic region present in weedy rice but not cultivated rice genomes that shows evidence of balancing selection, thereby suggesting that there might be more complexity inherent to the process of de-domestication.

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<http://agri.ckcest.cn/ass/NK007-20170612004.pdf>