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▶ 前沿资讯

1. 新疆棉花品种又添俩“新丁”

简介: 新疆棉花品种又添俩“新丁”：“新农大3号棉”和“新农大4号棉”。3月29日，新疆农业大学传出这一喜讯。“新农大3号棉”和“新农大4号棉”是新疆农业大学农学院教授陈全家团队培育出的棉花新品种。他们将长绒棉的优秀基因“嫁接”到陆地棉上，成功改良了陆地棉的纤维品质。两个新品种在沙湾县的试验示范表明，与当地常种的品种“新陆早36”相比，棉花产量分别增加了17.9%和20.2%，马克隆值分别达4.7和4.3，衣分分别为43.7%和46.6%，纤维长度分别达到33毫米和32毫米，具有长绒棉优良纤维的品质。

来源: 中国生物技术信息网

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全文链接:

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

2. 美农业部确认不监管基因编辑作物

简介: 美国农业部28日发表声明，表示不会对使用一些新技术育种的农作物进行监管，其中包括基因编辑技术。美农业部长桑尼·珀杜在声明中说，根据农业部生物法规，只要这些新技术没有利用植物害虫，农业部现在不会、也没有计划对使用这些新技术培育的农作物进行监管。珀杜说，基因编辑等新技术扩大了植物育种工具库，它们可以更快、更精准地培育出农作物新性状，可能在育种方面节约数年甚至数十年时间。“植物育种创新前景广阔，新技术有助于农作物增强抗旱、抗病虫害的能力，还可增加营养价值。”珀杜说。与通常所说的转基因作物需要转入外源遗传物质有所不同的是，基因编辑育种使用CRISPR-Cas9或锌指核酸酶（ZFN）等技术对植物基因进行编辑，可设计出¹不含外源DNA（脱氧核糖核酸）的植物。美国现行法律规定，只有由细菌等植物病原体或其DNA构建的转基因作物被认定为“管制作物”，最新声明再次明确了基因编辑作物不会受到监管。

来源: 基因农业网

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全文链接:

<http://www.agrogene.cn/info-4832.shtml>

▶ 学术文献

1. Syngenta releases results of its 2017 Good Growth Plan (先正达公布2017年“绿色增长计划”实施成果)

简介: 近日，先正达公布2017年“绿色增长计划”报告。先正达在实施“绿色增长计划”过程中使用了更高效、更安全，更可持续的技术和产品，大大提高了作物的产量，在该计划执行的第4年展现出不错的成果。“绿色增长计划”涵盖了促进农业生产和乡村社区可持续发展的6项承诺，旨在2020年以前实现这些目标。为此，农民与先正达田间专家合作，分享技能，在41个国家超过1400座农场的22种作物中试验新的解决方案。

相比2014年，试验农场在2017年每公顷平均增产10.9%，增产量比对照农场高出50%。小型试验农场生产力的提高尤为明显，涨幅为21.6%，比对照农场高5.1%。大部分的农场在2017年更高效地使用了农药、肥料等投入，提高了每公顷的产量。每生产1公斤作物所使用的农药量，相比2014年下降了14.2%，是对照农场减少量的近3倍。在试验农场中对温室气体的分析表明，相比2014年，每单位产量造成的温室气体排放量减少了14%。

来源: AgroNews

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全文链接:

<http://news.agropages.com/News/NewsDetail—25831.htm>

2. Ribosomal RNA Biogenesis and its Response to Chilling Stress in *Oryza sativa* L. (水稻核糖体RNA生物合成及其对低温胁迫的响应)

简介: Ribosome biogenesis is crucial for plant growth and environmental acclimation. Processing of ribosomal RNAs (rRNAs) is an essential step in ribosome biogenesis and begins with transcription of the rDNA. The resulting pre-rRNA transcript undergoes systematic processing, where multiple endonucleolytic and exonucleolytic cleavages remove the external and internal transcribed spacers (ETS and ITS). The processing sites and pathways for pre-rRNA processing have been deciphered in *Saccharomyces cerevisiae* and, to some extent, in *Xenopus*, mammalian cells, and *Arabidopsis thaliana*. However, the processing sites and pathways remain largely unknown in crops, particularly in monocots such as rice (*Oryza sativa* L.), one of the most important food resources in the world. Here, we identified the rRNA precursors produced during rRNA biogenesis and the critical endonucleolytic cleavage sites in the transcribed spacer regions of pre-rRNAs in rice. We further found that two pre-rRNA processing pathways, distinguished by the order of 5' ETS removal and ITS1 cleavage, co-exist in vivo. Moreover, exposing rice to chilling stress resulted in the inhibition of rRNA biogenesis mainly at the pre-rRNA processing level, suggesting that these energy-intensive processes may be reduced to increase acclimation and survival at lower temperatures. Overall, our study identified the pre-rRNA processing pathway in rice and showed that ribosome biogenesis is quickly inhibited by low temperatures, which may shed light on the link between ribosome biogenesis and environmental acclimation in crop plants.

来源: Plant Physiology期刊

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全文链接:

<http://agri.ckcest.cn/ass/df4a6770-4771-4226-80cd-4e7dfc1490bb.pdf>

3. TGW3, a Major QTL that Negatively Modulates Grain Length and Weight in Rice (TGW3是负调控水稻谷粒长度和重量的一个关键QTL位点)

简介: Grain length (size) and weight is an essential component trait of crop yield. To date, several QTLs for the trait have been identified. GS3 encodes a putative transmembrane protein and functions as a negative regulator, and its larger-grain allele contains a nonsense

mutation causing a 178-aa truncation (Fan et al., 2006). GL3.1/qGL3 acts also as a negative regulator encoding a putative protein phosphatase (Qi et al., 2012; Zhang et al., 2012). Another negative regulator is TGW6 that hydrolyzes indole-3-acetic acid (IAA)-glucose into IAA and glucose (Ishimaru et al., 2013). In contrast, GW6a is a positive regulator that encodes a novel histone H4 acetyltransferase (Song et al., 2015). Copy number variations at the GL7/GW7 locus cause elevated expression of GL7 and thus an increase in grain length (Wang et al., 2015a; Wang et al., 2015b). GL2/GS2 encodes a plant-specific transcription factor OsGRF4, and its larger-grain allele harbors a mutation perturbing the cleavage by miR396c that has elevated GL2/GS2 expression (Hu et al., 2015; Che et al., 2016). GLW7 encodes the plant-specific transcription factor OsSPL13, and its higher expression is associated with larger grains (Si et al., 2016). These findings greatly enhanced our knowledge of grain length and weight regulation; however, there still exists gaps to integrate these factors into genetic network(s). Here we report a thorough dissection of QTL compositions of a super large grain, and characterization of a novel QTL qTGW3 that regulates grain length and weight in rice.

来源: Molecular Plant期刊

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全文链接:

<http://agri.ckcest.cn/ass/8e3e7fb1-446e-488f-8506-3214a52a2605.pdf>