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农业生物技术专题

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▶ 前沿资讯

1. 我国科研团队率先完成菊花基因组测序

简介: 12月7日, 中国中医科学院中药研究所和安利植物研发中心宣布, 由该联合团队发起的菊花全基因组计划取得重大进展, 利用纳米孔测序技术突破复杂基因组测序, 该团队在世界首次完成了菊属植物菊花的全基因组测序, 并完成了重要的药用菊花品种——杭白菊的全长转录组遗传信息发掘。相关研究成果和基因组数据已于12月7日在中国中医科学院中药研究所官网及安利植物研发中心学术研究网站公布, 并向全世界研究菊花的学术团队和非盈利组织免费开放。

来源: 科学网

发布日期:2017-12-08

全文链接:

<http://news.sciencenet.cn/htmlnews/2017/12/396607.shtm>

2. 巴斯夫成立水稻知识中心帮助亚太区农户提高产量、减少排放

简介: 2017年12月5日, 巴斯夫全新水稻知识中心今日在其菲律宾拉古纳省海湾市农业研究站落成启用。它将汇聚巴斯夫在全球水稻种植领域的专业知识, 为农户提供更好的农艺和技术支持, 帮助他们可持续地提高水稻产量, 致力于收集和共享全球水稻种植的最佳实践, 与国际水稻研究所(IRRI)展开科研合作, 以加快耐除草剂杂交直播稻等新技术的采用, 直播稻的用水量和温室气体排放量更少。巴斯夫作物保护部亚太区高级副总裁古达福表示: “水稻是全球半数以上人口的主食; 如何满足人口对水稻日益增长的需求, 同时尽量减少对环境的影响, 是水稻种植户面临的一大严峻挑战。新成立的巴斯夫水稻知识中心将使我们能与种植者分享最新技术和最佳实践, 以推动水稻种植技术的进一步创新。”

来源: 基因农业网

发布日期:2017-12-06

全文链接:

<http://www.agrogene.cn/info-4541.shtml>

▶ 学术文献

1. Phytochrome-interacting factors directly suppress MIR156 expression to enhance shade-avoidance syndrome in Arabidopsis (光敏色素作用因子直接抑制MIR156的表达来增强拟南芥的庇荫反应)

简介: Plants have evolved a repertoire of strategies collectively termed the shade-avoidance syndrome to avoid shade from canopy and compete for light with their neighbors. However, the signaling mechanism governing the adaptive changes of adult plant architecture to shade is not well understood. Here, we show that in Arabidopsis, compared with the wild type, several PHYTOCHROME-INTERACTING FACTORS (PIFS) overexpressors all display constitutive shade-avoidance syndrome under normal high red to far-red light ratio conditions but are less sensitive to the simulated shade, whereas the MIR156 overexpressors exhibit an

opposite phenotype. The simulated shade induces rapid accumulation of PIF proteins, reduced expression of multiple MIR156 genes, and concomitant elevated expression of the SQUAMOSA-PROMOTER BINDING PROTEIN-LIKE (SPL) family genes. Moreover, in vivo and in vitro assays indicate that PIFs bind to the promoters of several MIR156 genes directly and repress their expression. Our results establish a direct functional link between the phytochrome-PIFs and miR156-SPL regulatory modules in mediating shade-avoidance syndrome.

来源: Nature Communications 期刊

发布日期: 2017-08-24

全文链接:

<http://agri.ckcest.cn/ass/cb6b0dde-b10d-4727-b2cb-ae94e0709783.pdf>

2. Long-term balancing selection contributes to adaptation in Arabidopsis and its relatives (长期的平衡选择研究为拟南芥及其近缘属的适应性提供了贡献)

简介: Background In contrast to positive selection, which reduces genetic variation by fixing beneficial alleles, balancing selection maintains genetic variation within a population or species and plays crucial roles in adaptation in diverse organisms. However, which genes, genome-wide, are under balancing selection and the extent to which these genes are involved in adaptation are largely unknown. We performed a genome-wide scan for genes under balancing selection across two plant species, *Arabidopsis thaliana* and its relative *Capsella rubella*, which diverged about 8 million generations ago. Among hundreds of genes with shared coding-region polymorphisms, we find evidence for long-term balancing selection in five genes: AT1G35220, AT2G16570, AT4G29360, AT5G38460, and AT5G44000. These genes are involved in the response to biotic and abiotic stress and other fundamental biochemical processes. More intriguingly, for these genes, we detected significant ecological diversification between the two haplotype groups, suggesting that balancing selection has been very important for adaptation. Our results indicate that beyond the well-known S-locus genes and resistance genes, many loci are under balancing selection. These genes are mostly correlated with resistance to stress or other fundamental functions and likely play a more important role in adaptation to diverse habitats than previously thought.

来源: Genome Biology 期刊

发布日期: 2017-11-15

全文链接:

<http://agri.ckcest.cn/ass/f4de07b0-3dda-4eb0-95af-003469f3cd2a.pdf>

3. cGMP is involved in Zn tolerance through the modulation of auxin redistribution in root tips (cGMP是通过调节根尖生长素的积累来调节锌的耐受性)

简介: Excess zinc (Zn) inhibits primary root (PR) growth but induces lateral root (LR) formation. Both auxin and cGMP play a role in controlling root growth in plants. However, whether and how their interaction is involved in Zn-regulated root development remain

unclear. Here, we reported that excess Zn leads to auxin accumulation in root tips, as indicated by DR5:GUS expression. Further study showed that excess Zn represses PIN4:GFP abundance in root tips and that PR elongation and LR formation in the *pin4* mutant is insensitive to excess Zn. Excess Zn also elevates cyclic guanosine monophosphate (cGMP) production in seedlings. Supplementation with the exogenous cGMP donor 8-bromoguanosine 3',5'-cyclic guanosine monophosphate (8-Br-cGMP) increased PR elongation and LR formation in Zn-treated seedlings, whereas the guanylate cyclase (GC) inhibitor LY83583 decreased these processes. Additional physiological and genetic analyses indicated that PIN4 is involved in cGMP-modulated root development in Zn-treated seedlings. Taken together, these results indicate that Zn-regulated cGMP production plays an important role in modulating root development by maintaining PIN4 abundance in excess Zn-treated roots and subsequent adaptation to Zn toxicity.

来源: Environmental and Experimental Botany 期刊

发布日期: 2017-10-30

全文链接:

<http://agri.ckcest.cn/ass/a7ff2e6d-275b-446e-9d56-a619069a8d82.pdf>