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杂交水稻专题

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▶ 前沿资讯

1. 端粒到端粒的无缺失染色体组装技术新路线

简介: 近日, 南京农业大学农学院甘祥超教授与其原德国马克斯·普朗克植物育种研究所团队在《Nature Communications》上发表题为“GALA: a computational framework for de novo chromosome-by-chromosome assembly with long reads”的研究论文, 并发布了相应的开源软件GALA (<http://github.com/ganlab/gala>), 为利用三代测序实现端粒到端粒的无缺失染色体组装提供了一条全新的技术路线。植物和动物基因组中通常包含多条染色体, 比如水稻有12对染色体, 而我们人类有23对染色体。现有的染色体分离技术虽然可用实现染色体的物理分离, 但是该技术依赖昂贵仪器, 需要大量人力物力, 难以大规模应用于基因组测序。对当前的整个基因组混合测序的数据, 现有的基因组组装算法都是“先组装、后染色体分离”的流程。本研究针对现有的测序技术中多条染色体混合、数据互相串扰的瓶颈问题, 首创了“先分离, 后组装”的技术路线。利用多层统计网络模型, 研发了将无参考序列组装复杂的流程模块化技术, 首次实现了三代测序中Pacbio、Nanopore数据的集成组装, 和多种异质性数据如参考基因组、遗传图谱以及Hi-C数据的灵活利用, 并开发了算法GALA。首先利用多层统计网络模型实现对预组装和原始数据编码, 并利用计算机图论经典算法对数据纠错。然后利用统计网络对原始测序数据实现染色体级别的分离, 该网络模型同时也可以Hi-C、Bionano、近亲或者同物种参考基因组信息辅助数据分离。利用GALA这种先数据分离, 然后组装的策略, 我们可以实现线虫、水稻基因组端粒到端粒的无缺失组装。对更复杂的人类基因组, 仅利用Nanopore测序数据, 也能实现多条染色体的无缺失组装, 进一步分析表明, 部分染色体中的缺失是源自数据自身的缺失造成的。

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2. 水稻田土壤重金属污染风险评估及精准修复方面取得新进展

简介: 近日, 华中农业大学资源与环境学院土壤化学与环境团队在在水稻田土壤重金属污染风险评估及精准修复方面取得新进展, 相关成果分别发表于环境类期刊Journal of Hazardous Materials和Ecotoxicology and Environmental Safety上。水稻作为中国主要粮食作物, 吸收了土壤中Cd等重金属, 使其面临较严重的粮食安全问题。水稻往往易吸收土壤中生物有效态Cd, 而土壤pH值和多种金属离子共存对Cd形态分布有显著影响。鉴于水稻土高异质性和复杂性, 尚缺乏Cd与其它金属的交互作用对水稻毒性的影响、应用于区域尺度水稻土Cd生物有效性及其关联的水稻食品安全等预测研究。基于此, 华中农业大学土壤化学与环境团队耦合多表面模型(MSM)和地理信息系统(GIS)技术实现县域尺度水稻-土壤系统中生物有效性Cd预测, 进一步构建了一套基于水稻食品安全的pH调控图(图1), 从而实现县域尺度石灰材料修复土壤Cd污染的精准施用技术。基于三种分析场景, 本研究量化了pH对Cd生物有效性的影响贡献, 显示有87.51% Cd生物有效变异解释率, 并结合pH提升建议值和石灰材料施用量计算器, 绘制了Cd污染修复石灰材料精确施用量地图, 对研究区域水稻土Cd污染风险评估提出了有效措施。该研究结果可为重金属污染土壤修复提供精准修复策略, 也可作为评估水稻土重金属环境风险的

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重要工具。此外，土壤化学与环境团队结合浓度相加(CA)模型、独立作用(IA)模型和多元回归树分析(MRT)，建立了镉、铅复合污染对水稻毒害的定量分析体系(图2)。研究表明Pb-Cd间的交互作用均能减弱Pb和Cd的毒性，其中Cd对Pb毒性的抑制作用显著；Pb-Cd复合浓度相近时，Pb和Cd相互作用对水稻根系伸长具有显著的拮抗作用；在低Pb浓度($Cd > 0.0195$, $Pb < 0.015$ mg/L)，对水稻根系有协同作用；高浓度Pb ($Cd < 0.225$, $Pb \geq 1.25$ mg/L)，Pb对水稻根系的毒性主要为Pb。该研究首次提出了评价不同剂量水平下重金属相互作用行为的系统方法，可为制定农田重金属复合污染控制标准提供方法参考。

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➤ 学术文献

1. Insights Into the Genetics of the Zhonghua 11 Resistance to *Meloidogyne graminicola* and Its Molecular Determinism in Rice (中华11号水稻抗麦根结线虫基因及其分子决定因素的研究)

简介：Meloidogyne graminicola is a widely spread nematode pest of rice that reduces crop yield up to 20% on average in Asia, with devastating consequences for local and global rice production. Due to the ban on many chemical nematicides and the recent changes in water management practices in rice agriculture, an even greater impact of M. graminicola can be expected in the future, stressing the demand for the development of new sustainable nematode management solutions. Recently, a source of resistance to M. graminicola was identified in the Oryza sativa japonica rice variety Zhonghua 11 (Zh11). In the present study, we examine the genetics of the Zh11 resistance to M. graminicola and provide new insights into its cellular and molecular mechanisms. The segregation of the resistance in F-2 hybrid populations indicated that two dominant genes may be contributing to the resistance. The incompatible interaction of M. graminicola in Zh11 was distinguished by a lack of swelling of the root tips normally observed in compatible interactions. At the cellular level, the incompatible interaction was characterised by a rapid accumulation of reactive oxygen species in the vicinity of the nematodes, accompanied by extensive necrosis of neighbouring cells. The expression profiles of several genes involved in plant immunity were analysed at the early stages of infection during compatible (susceptible plant) and incompatible (resistant plant) interactions. Notably, the expression of OsAtg4 and OsAtg7, significantly increased in roots of resistant plants in parallel with the cell death response, suggesting that autophagy is activated and may contribute to the resistance-mediated hypersensitive response. Similarly, transcriptional regulation of genes involved in hormonal pathways in Zh11 indicated that salicylate signalling may be important in the resistance response towards M. graminicola. Finally, the nature of the resistance to M. graminicola and the potential exploitation of the Zh11 resistance for breeding are discussed.

来源：FRONTIERS IN PLANT SCIENCE

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2. Grain yield performance of hybrid rice in relation to inbred cultivars in long-term multi-environment tests in India (印度长期多环境试验中杂交水稻与近交品种的产量表现)

简介: We analyzed the yield data of 2,070 rice hybrid F-1 genotypes with inbred local cultivars (ILCv) evaluated over 32 yr (from 1988 to 2019) in 2,376 multi-environment experiments executed at 102 locations in the irrigated ecosystem across India. The genetic gain or loss in yield of hybrid F-1 genotypes estimated over the test duration was nonsignificant. The differences were highly significant between the means of group of F-1 hybrid genotypes with yields higher than ILCvs in 985 experiments and the group of F-1 hybrid genotypes with yields lower than ILCvs in 962 experiments. Hybrids produced 10% more yield (728-2,588 kg ha⁻¹) than ILCvs in 672 experiments at several locations. Our analyses have established that grain yields of 7.0-7.9 Mg ha⁻¹, were harvested in hybrid F-1 genotypes with early- (110-120 d), mid-early- (121-130 d), and medium- (131-140 d) maturity duration, and in those with medium slender grains (130 +/- 5 d) at many locations in 374 out of the 985 experiments. A higher level of rice (*Oryza sativa* L.) productivity per day (62-63 kg ha⁻¹) was recorded with the early-maturing and mid-early-maturing hybrid genotypes. Both the hybrid F-1 genotypes and ILCvs produced grain yields (≥ 10 Mg ha⁻¹) similar to values that were recorded previously with commercial inbred cultivars since 1968 at many locations. The attainable grain yield records of ILCvs were not broken by the yields of hybrid F-1 genotypes. Hence the doubt arises whether there was any overestimation of hybrid genotypes or an underestimation of inbred yields. Therefore, any genetic gain or loss for grain yields in new genotypes developed in experiments can be estimated only when ILCvs produce their attainable yield recorded previously. There is scope for breeders to limit test locations to represent specific target areas to avoid data loss.

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3. Uncovering the Novel QTLs and Candidate Genes of Salt Tolerance in Rice with Linkage Mapping, RTM-GWAS, and RNA-seq (用连锁图谱、RTM-GWAS和RNA-seq揭示水稻耐盐性的新QTL和候选基因)

简介: Salinity is a major abiotic stress that limits plant growth and crop productivity. Indica rice and japonica rice show significant differences in tolerance to abiotic stress, and it is considered a feasible method to breed progeny with stronger tolerance to abiotic stress by crossing indica and japonica rice. We herein developed a high-generation recombinant inbred lines (RILs) from Luohui 9 (indica) X RPY geng (japonica). Based on the high-density bin

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map of this RILs population, salt tolerance QTLs controlling final survival rates were analyzed by linkage mapping and RTM-GWAS methods. A total of seven QTLs were identified on chromosome 3, 4, 5, 6, and 8. qST-3.1, qST-5.1, qST-6.1, and qST-6.2 were novel salt tolerance QTLs in this study and their function were functionally verified by comparative analysis of parental genotype RILs. The gene aggregation result of these four new QTLs emphasized that the combination of the four QTL synergistic genotypes can significantly improve the salt stress tolerance of rice. By comparing the transcriptomes of the root tissues of the parents' seedlings, at 3 days and 7 days after salt treatment, we then achieved fine mapping of QTLs based on differentially expressed genes (DEGs) identification and DEGs annotations, namely, LOC_Os06g01250 in qST-6.1, LOC_Os06g37300 in qST-6.2, LOC_Os05g14880 in qST-5.1. The homologous genes of these candidate genes were involved in abiotic stress tolerance in different plants. These results indicated that LOC_Os05g14880, LOC_Os06g01250, and LOC_Os06g37300 were the candidate genes of qST-5.1, qST-6.1, and qST-6.2. Our finding provided novel salt tolerance-related QTLs, candidate genes, and several RILs with better tolerance, which will facilitate breeding for improved salt tolerance of rice varieties and promote the exploration tolerance mechanisms of rice salt stress.

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