



2023年第26期总274期

小麦遗传育种专题

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▶ 前沿资讯

1 . Multi-modal deep learning improves grain yield prediction in wheat breeding by fusing genomics and phenomics (多模态深度学习通过融合基因组学和表型组学来提高小麦育种中的产量预测)

简介: Motivation: Developing new crop varieties with superior performance is highly important to ensure robust and sustainable global food security. The speed of variety development is limited by long field cycles and advanced generation selections in plant breeding programs. While methods to predict yield from genotype or phenotype data have been proposed, improved performance and integrated models are needed. Results: We propose a machine learning model that leverages both genotype and phenotype measurements by fusing genetic variants with multiple data sources collected by unmanned aerial systems. We use a deep multiple instance learning framework with an attention mechanism that sheds light on the importance given to each input during prediction, enhancing interpretability. Our model reaches 0.754 ± 0.024 Pearson correlation coefficient when predicting yield in similar environmental conditions; a 34.8% improvement over the genotype-only linear baseline (0.559 ± 0.050). We further predict yield on new lines in an unseen environment using only genotypes, obtaining a prediction accuracy of 0.386 ± 0.010 , a 13.5% improvement over the linear baseline. Our multi-modal deep learning architecture efficiently accounts for plant health and environment, distilling the genetic contribution and providing excellent predictions. Yield prediction algorithms leveraging phenotypic observations during training therefore promise to improve breeding programs, ultimately speeding up delivery of improved varieties. Availability and implementation: Available at <https://github.com/BorgwardtLab/PheGeMIL> (code) and <https://doi.org/doi:10.5061/dryad.kpr4xh5p> (data).

来源: PubMed Central

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<http://agri.ckcest.cn/file1/M00/03/5B/Csgk0Yj12x-AJ9SsAEzkyBLrLes177.pdf>

2 . Genome-wide association mapping in elite winter wheat breeding for yield improvement (优质冬小麦育种增产的全基因组关联图谱研究)

简介: Increased grain yield (GY) is the primary breeding target of wheat breeders. We performed the genome-wide association study (GWAS) on 168 elite winter wheat lines from an ongoing breeding program to identify the main determinants of grain yield. Sequencing of Diversity Array Technology fragments (DARtseq) resulted in 19,350 single-nucleotide polymorphism (SNP) and presence-absence variation (PAV) markers. We identified 15 main genomic regions located in ten wheat chromosomes (1B, 2B, 2D, 3A, 3D, 5A, 5B, 6A, 6B, and 7B) that explained from 7.9 to 20.3% of the variation in grain yield and 13.3% of the yield stability. Loci identified in the reduced gene pool are important for wheat improvement

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using marker-assisted selection. We found marker-trait associations between three genes involved in starch biosynthesis and grain yield. Two starch synthase genes (TraesCS2B03G1238800 and TraesCS2D03G1048800) and a sucrose synthase gene (TraesCS3D03G0024300) were found in regions of QGy.rut-2B.2, QGy.rut-2D.1, and QGy.rut-3D, respectively. These loci and other significantly associated SNP markers found in this study can be used for pyramiding favorable alleles in high-yielding varieties or to improve the accuracy of prediction in genomic selection.

来源: SPRINGER LINK

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➤ 学术文献

1 . Multimodal deep learning methods enhance genomic prediction of wheat breeding (多模态深度学习方法增强了小麦育种的基因组预测)

简介: While several statistical machine learning methods have been developed and studied for assessing the genomic prediction (GP) accuracy of unobserved phenotypes in plant breeding research, few methods have linked genomics and phenomics (imaging). Deep learning (DL) neural networks have been developed to increase the GP accuracy of unobserved phenotypes while simultaneously accounting for the complexity of genotype-environment interaction (GE); however, unlike conventional GP models, DL has not been investigated for when genomics is linked with phenomics. In this study we used 2 wheat data sets (DS1 and DS2) to compare a novel DL method with conventional GP models. Models fitted for DS1 were GBLUP, gradient boosting machine (GBM), support vector regression (SVR) and the DL method. Results indicated that for 1 year, DL provided better GP accuracy than results obtained by the other models. However, GP accuracy obtained for other years indicated that the GBLUP model was slightly superior to the DL. DS2 is comprised only of genomic data from wheat lines tested for 3 years, 2 environments (drought and irrigated) and 2-4 traits. DS2 results showed that when predicting the irrigated environment with the drought environment, DL had higher accuracy than the GBLUP model in all analyzed traits and years. When predicting drought environment with information on the irrigated environment, the DL model and GBLUP model had similar accuracy. The DL method used in this study is novel and presents a strong degree of generalization as several modules can potentially be incorporated and concatenated to produce an output for a multi-input data structure.

来源: PubMed Central

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<http://agri.ckcest.cn/file1/M00/03/5B/Csgk0Yj13m0Aan7DAAh4g-OCEak497.pdf>

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➤ 相关专利

1. 一种小麦种子育种装置

简介：本实用新型公开了一种小麦种子育种装置，涉及小麦育种技术领域，包括培育箱和喷淋单元；培育箱侧面开设有通槽，通槽内转动连接转轴，所述转轴连接门板，所述培育箱上设置有温控单元、监控单元和PLC控制器，PLC控制器的输入端电连接外部电源的输出端；喷淋单元包含有支撑板、电机、螺杆、滑块、集液板、喷头、输液管、潜水泵、营养液盒和滤盒，所述营养液盒设置在培育箱内，营养液盒的侧面开设有滑槽，滑槽内滑动连接滤盒，营养液盒内设置有培养漏板和潜水泵，所述潜水泵连接输液管的一端，该装置能够对小麦种子均匀喷洒营养液，避免对营养液造成浪费，且培育人员能够实时对小麦种子的状态进行查看。

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<http://agri.ckcest.cn/file1/M00/03/5B/Csgk0Yj11dWAZCILAAjU4dH2Mps642.pdf>

2. 一种小麦的育种装置

简介：本实用新型公开一种小麦的育种装置，涉及育种技术领域。该小麦的育种装置，包括底座，所述底座的上表面设置有电机，所述底座的上表面设置有固定条，所述育种机构设置在固定条的上表面。该小麦的育种装置，通过设置承载条，当需要对小麦进行育苗时，首先通过在承载条的内部设置有若干个隔板，以隔出若干个育种槽，以便于育苗，而在承载条的下表面固定有强力磁铁，通过强力磁铁设置在铁板的顶部，且当铁板和强力磁铁相吸时，可将承载条固定在固定条的内部，该装置便于对小麦进行育苗。

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