小麦遗传育种专题

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1．Identification of wheat seedling varieties based on MssiapNet（基于MssiapNet的小麦幼苗品种鉴定）

简介：Introduction: In the actual planting of wheat, there are often shortages of seedlings and broken seedlings on long ridges in the field, thus affecting grain yield and indirectly causing economic losses. Variety identification of wheat seedlings using physical methods timeliness and is unsuitable for universal dissemination. Recognition of wheat seedling varieties using deep learning models has high timeliness and accuracy, but fewer researchers exist. Therefore, in this paper, a lightweight wheat seedling variety recognition model, MssiapNet, is proposed.Methods: The model is based on the MobileVit-XS and increases the model's sensitivity to subtle differences between different varieties by introducing the scSE attention mechanism in the MV2 module, so the recognition accuracy is improved. In addition, this paper proposes the IAP module to fuse the identified feature information. Subsequently, training was performed on a self-constructed real dataset, which included 29,020 photographs of wheat seedlings of 29 varieties.Results: The recognition accuracy of this model is 96.85%, which is higher than the other nine mainstream classification models. Although it is only 0.06 higher than the Resnet34 model, the number of parameters is only 1/3 of that. The number of parameters required for MssiapNet is 29.70MB, and the single image Execution time and the single image Delay time are 0.16s and 0.05s. The MssiapNet was visualized, and the heat map showed that the model was superior for wheat seedling variety identification compared with MobileVit-XS.Discussion: The proposed model has a good recognition effect on wheat seedling varieties and uses a few parameters with fast inference speed, which makes it easy to be subsequently deployed on mobile terminals for practical performance testing.

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http://agri.nais.net.cn/file1/M00/03/64/CsgkOWWo2iCAcPDcAHY3fiR7iAY867.pdf

2．Effects of elevated atmospheric [CO_2] on grain starch characteristics in different specialized wheat（大气[CO_2]升高对不同小麦籽粒淀粉特性的影响）

简介：The increasing atmospheric [CO_2] poses great challenges to wheat production. Currently, the response of starch characteristics in different specialized wheat cultivars to elevated [CO_2], as well as the underlying physiological and molecular mechanisms remains unclear. Therefore, an experiment was conducted with open-top chambers to study the effects of ambient [CO_2] [a(CO_2)] and elevated [CO_2] [e(CO_2)] on photosynthetic performance, yield and starch characteristics of bread wheat (Zhengmai 369, ZM369) and biscuit wheat (Yangmai 15, YM15) from 2020 to 2022. The results demonstrated a significant improvement in photosynthetic performance, yield, amylose and amylopectin content, volume ratio of large granules under e[CO2]. Moreover, e[CO2] upregulated the

gene expression and enzyme activities of GBSS (Granule-bound starch synthase) and SSS (Soluble starch synthase), increased starch pasting viscosity, gelatinization enthalpy and crystallinity. Compared to YM15, ZM369 exhibited a higher upregulation of GBSSI, greater increase in amylose content and volume ratio of large granules, as well as higher gelatinization enthalpy and crystallinity. However, ZM369 showed a lower increase in amylopectin content and a lower upregulation of SSSI and SSSII. Correlation analysis revealed amylose and amylopectin content had a positive correlation with GBSS and SSS, respectively, a significant positively correlation among the amylose and amylopectin content, starch granule volume, and pasting properties. In conclusion, these changes may enhance the utilization value of biscuit wheat but exhibit an opposite effect on bread wheat. The results provide a basis for selecting suitable wheat cultivars and ensuring food security under future climate change conditions.

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3．Detection of consensus genomic regions and candidate genes for quality traits in barley using QTL meta-analysis（利用QTL分析检测大麦品质性状的基因组区域和候选基因）

简介：Improving barley grain quality is a major goal in barley breeding. In this study, a total of 35 papers focusing on quantitative trait loci (QTLs) mapping for barley quality traits published since 2000 were collected. Among the 454 QTLs identified in these studies, 349 of them were mapped onto high-density consensus maps, which were used for QTL meta-analysis. Through QTL meta-analysis, the initial QTLs were integrated into 41 meta-QTLs (MQTLs) with an average confidence interval (CI) of 1. 66 cM, which is 88.9% narrower than that of the initial QTLs. Among the 41 identified MQTLs, 25 were subsequently validated in publications using genome-wide association study (GWAS). From these 25 validated MQTLs, ten breeder's MQTLs were selected. Synteny analysis comparing barley and wheat MQTLs revealed orthologous relationships between eight breeder's MQTLs and 45 wheat MQTLs. Additionally, 17 barley homologs associated with rice quality traits were identified within the regions of the breeder's MQTLs through comparative analysis. The findings of this study provide valuable insights for molecular marker-assisted breeding and the identification of candidate genes related to quality traits in barley.

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4．Genomic prediction reveals unexplored variation in grain protein and lysine content across a vast winter wheat genebank collection（基因组预测揭示了大量冬小麦基因库收集的谷物蛋白和赖氨酸含量的

变异)

简介：Globally, wheat (Triticum aestivum L.) is a major source of proteins in human nutrition despite its unbalanced amino acid composition. The low lysine content in the protein fraction of wheat can lead to protein-energy-malnutrition prominently in developing countries. A promising strategy to overcome this problem is to breed varieties which combine high protein content with high lysine content. Nevertheless, this requires the incorporation of yet undefined donor genotypes into pre-breeding programs. Genebank collections are suspected to harbor the needed genetic diversity. In the 1970s, a large-scale screening of protein traits was conducted for the wheat genebank collection in Gatersleben; however, this data has been poorly mined so far. In the present study, a large historical dataset on protein content and lysine content of 4,971 accessions was curated, strictly corrected for outliers as well as for unreplicated data and consolidated as the corresponding adjusted entry means. Four genomic prediction approaches were compared based on the ability to accurately predict the traits of interest. High-quality phenotypic data of 558 accessions was leveraged by engaging the best performing prediction model, namely EG-BLUP. Finally, this publication incorporates predicted phenotypes of 7,651 accessions of the winter wheat collection. Five accessions were proposed as donor genotypes due to the combination of outstanding high protein content as well as lysine content. Further investigation of the passport data suggested an association of the adjusted lysine content with the elevation of the collecting site. This publicly available information can facilitate future pre-breeding activities.

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http://agri.nais.net.cn/file1/M00/10/36/Csgk0GWo1_KAK8BrACE8-pNUApY935.pdf

➤ 学术文献

1．Genetic improvement of photosynthetic nitrogen use efficiency of winter wheat in the Yangtze River Basin of China（长江流域冬小麦光合氮利用效率的遗传改良）

简介：Improving the photosynthetic capacity of crops is key to achieving synergism between high crop yield and nitrogen (N) efficiency, and it is also an important target for future cultivar breeding and cultivation management. Although photosynthetic N use efficiency (PNUE) is commonly used to determine the N economy of leaves, it is unclear whether the PNUE of wheat has improved through genetic engineering of wheat cultivars. Our results suggest that lower Rubisco activation is a major reason for the lower PNUE of modern wheat cultivars, and improving Rca content and activity in the future could enhance Pn and PNUE while improving the N utilization of leaves to enhance crop yield and N efficiency of wheat under current or lower leaf N conditions.

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