小麦遗传育种专题

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前沿资讯

1．SCGNet: efficient sparsely connected group convolution network for wheat grains classification（SCGNet：用于小麦籽粒分类的高效稀疏连通群卷积网络）

简介：Specifically, our proposed model incorporates several modules that enhance information exchange and feature multiplexing between group convolutions. This mechanism enables the network to gather feature information from each subgroup of the previous layer, facilitating effective utilization of upper-layer features. Additionally, we introduce sparsity in channel connections between groups to further reduce computational complexity without compromising accuracy. Furthermore, we design a novel classification output layer based on 3-D convolution, replacing the traditional maximum pooling layer and fully connected layer in conventional convolutional neural networks (CNNs). This modification results in more efficient classification output generation.

来源：Frontiers

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全文链接：

http://agri.nais.net.cn/file1/M00/10/35/Csgk0GW0K7yAUOBRAGI4ELRhVxQ959.pdf

2．Phytochemical profile and anti-inflammatory activity of the hull of γ-irradiated wheat mutant lines (Triticum aestivum L.)（γ辐照小麦突变系(Triticum aestivum L.)的植物化学特征及抗炎活性）

简介：Wheat (Triticum aestivum Linn.; Poaceae) is the second most cultivated food crop among all global cereal crop production. The high carbohydrate content of its grains provides energy, multiple nutrients, and dietary fiber. After threshing, a substantial amount of wheat hull is produced, which serves as the non-food component of wheat. For the valorization of these by-products as a new resource from which functional components can be extracted, the hull from the seeds of cultivated wheat mutant lines bred after γ-irradiation were collected. Untargeted metabolite analysis of the hull of the original cultivar (a crossbreeding cultivar., Woori-mil × D-7) and its 983 mutant lines were conducted using ultra-performance liquid chromatographyelectrospray ionization quadrupole time-of-flight mass spectrometry technique. A total of 55 molecules were tentatively identified, including 21 compounds found in the Triticum species for the first time and 13 compounds not previously described. Among them, seven flavonolignans with a diastereomeric structure, isolated as a single compound from the hull of T. aestivum in our previous study, were used as the standards in the metabolite analysis. The differences in their collision cross-section values were shown to contribute to the clear distinction between tricine-lignan stereoisomers. To select functionally active agents with anti-inflammatory activity among the identified compounds, the wheat hull samples were evaluated for their inhibitory effect on nitric oxide production in lipopolysaccharide-stimulated RAW 264.7 cells. As a result of multivariate analysis based on

the results of chemical and biological profiles of the wheat hull samples, 10 metabolites were identified as key markers, contributing to the distinction between active and inactive mutant lines. Considering that one of the four key markers attributed to anti-inflammatory activity has been identified to be a flavonolignan, the wheat hull could be a valuable source of diverse tricin-lignan type compounds and used as a natural health-promoting product in food supplements.

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http://agri.nais.net.cn/file1/M00/10/35/Csgk0GWOKR2AADZ3AEeS1HBfCec533.pdf

3．A lightweight network for improving wheat ears detection and counting based on YOLOv5s（利用YOLOv5s改进小麦穗检测计数的轻量级网络）

简介：This study proposes a lightweight method for detecting and counting wheat ears based on YOLOv5s. It utilizes the ShuffleNetV2 lightweight convolutional neural network to optimize the YOLOv5s model by reducing the number of parameters and simplifying the complexity of the calculation processes. In addition, a lightweight upsampling operator content-aware reassembly of features is introduced in the feature pyramid structure to eliminate the impact of the lightweight process on the model detection performance. This approach aims to improve the spatial resolution of the feature images, enhance the effectiveness of the perceptual field, and reduce information loss. Finally, by introducing the dynamic target detection head, the shape of the detection head and the feature extraction strategy can be dynamically adjusted, and the detection accuracy can be improved when encountering wheat ears with large-scale changes, diverse shapes, or significant orientation variations.

来源：Frontiers

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http://agri.nais.net.cn/file1/M00/03/63/Csgk0WWOKgqAJDEcAD_tJgJKJzI936.pdf

学术文献

1．CRISPR/Cas9 genome editing in wheat: enhancing quality and productivity for global food security—a review（小麦CRISPR/Cas9基因组编辑：提高全球粮食安全质量和生产力）

简介：Wheat (Triticum aestivum L.) is an important cereal crop that is grown all over the world for food and industrial purposes. Wheat is essential to the human diet due to its rich content of necessary amino acids, minerals, vitamins, and calories. Various wheat breeding techniques have been utilized to improve its quality, productivity, and resistance to biotic and abiotic stress impairing production. However, these techniques are expensive,

demanding, and time-consuming. Additionally, these techniques need multiple generations to provide the desired results, and the improved traits could be lost over time. To overcome these challenges, researchers have developed various genome editing tools to improve the quality and quantity of cereal crops, including wheat. Genome editing technologies evolve quickly. Nowadays, single or multiple mutations can be enabled and targeted at specific loci in the plant genome, allowing controlled removal of undesirable features or insertion of advantageous ones. Clustered, regularly interspaced short palindromic repeat (CRISPR)/CRISPR-associated protein (Cas) is a powerful genome editing tool that can be effectively used for precise genome editing of wheat and other crops. This review aims to provide a comprehensive understanding of this technology's potential applications to enhance wheat's quality and productivity. It will first explore the function of CRISPR/Cas9 in preserving the adaptive immunity of prokaryotic organisms, followed by a discussion of its current applications in wheat breeding.

来源：Springer Link

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http://agri.nais.net.cn/file1/M00/03/63/CsgkOWWOLemAV-f5ABPMnttE7WU062.pdf

2．Genetic diversity analysis in wheat cultivars using SCoT and ISSR markers, chloroplast DNA barcoding and grain SEM（利用SCoT和ISSR标记、叶绿体DNA条形码和籽粒扫描电镜分析小麦品种遗传多样性）

简介：Background Wheat is a major cereal that can narrow the gap between the increasing human population and food production. In this connection, assessing genetic diversity and conserving wheat genetic resources for future exploitation is very important for breeding new cultivars that may withstand the expected climate change. The current study evaluates the genetic diversity in selected wheat cultivars using ISSR and SCoT markers, the rbcL and matK chloroplast DNA barcoding, and grain surface sculpture characteristics. We anticipate that these objectives may prioritize using the selected cultivars to improve wheat production. The selected collection of cultivars may lead to the identification of cultivars adapted to a broad spectrum of climatic environments.

来源：BMC

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