



2023年第41期总289期

小麦遗传育种专题

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➤ 前沿资讯

1 . Wheat powdery mildew resistance: from gene identification to immunity deployment (小麦白粉病抗性: 从基因鉴定到免疫部)

简介: Powdery mildew is one of the most devastating diseases on wheat and is caused by the obligate biotrophic phytopathogen *Blumeria graminis* f. sp. *tritici* (Bgt). Due to the complexity of the large genome of wheat and its close relatives, the identification of powdery mildew resistance genes had been hampered for a long time until recent progress in large-scale sequencing, genomics, and rapid gene isolation techniques. Here, we describe and summarize the current advances in wheat powdery mildew resistance, emphasizing the most recent discoveries about the identification of genes conferring powdery mildew resistance and the similarity, diversity and molecular function of those genes. Multilayered resistance to powdery mildew in wheat could be used for counteracting Bgt, including durable, broad spectrum but partial resistance, as well as race-specific and mostly complete resistance mediated by nucleotide-binding and leucine rich repeat domain (NLR) proteins. In addition to the above mentioned layers, manipulation of susceptibility (S) and negative regulator genes may represent another layer that can be used for durable and broad-spectrum resistance in wheat. We propose that it is promising to develop effective and durable strategies to combat powdery mildew in wheat by simultaneous deployment of multilayered immunity.

来源: Frontiers

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<http://agri.nais.net.cn/file1/M00/03/5F/Csgk0Y1npXCAEDZGAA0m13eJF4E919.pdf>

➤ 学术文献

1 . Plant Breeding to Mitigate Climate Change—Present Status and Opportunities with an Assessment of Winter Wheat Cultivation in Northern Europe as an Example (植物育种减缓气候变化的现状与机遇——以北欧冬小麦种植评估为例)

简介: Crop yield has been a major target of plant breeding, although resistance and quality have also been important. The current climate change is calling for breeding actions to mitigate greenhouse gas (GHG) emissions. The present review focuses on opportunities from plant breeding to mitigate climate change while simultaneously securing yield and food requirements, as exemplified by winter wheat cultivation in Northern Europe. Therefore, we review the history of traditional plant breeding, the impact of climate change on crops and implications for plant breeding, opportunities to use plant breeding as a tool to mitigate climate change, and then we assess the estimated mitigation effects from plant breeding and discuss their impact on climate effects. Nitrogen uptake efficiency (NUpE) was indicated as the character with the highest potential to contribute to climate change

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mitigation, with positive effects also from increased straw length and stubble heights, while increased total biomass yield (root or above-ground) showed less effect. In addition to contributing to climate change mitigation, NUpE might increase profitability for growers and decrease nitrogen leakage from agricultural fields. An increase in NUpE by 15% through plant breeding has the potential to result in reduced GHG emissions corresponding to 30% of the fossil fuel use in agriculture in Sweden.

来源: MDPI

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<http://agri.nais.net.cn/file1/M00/10/31/Csgk0GURNRyAejDsABD8LDu6-SQ489.pdf>

2 . Variability and interrelation of the main breeding traits of the winter soft wheat quality (冬软小麦品质主要育种性状的变异及相互关系)

简介: Wheat bread rightfully belongs to the greatest inventions of mankind. The concept of wheat quality is very capacious and includes a wide range of characteristics: physical, chemical, rheological and consumer, which are in complex relationships with each other. The main purpose of soft wheat is the manufacture of bakery products. In this regard, the actual task of science is the creation and introduction into production of new varieties with high baking properties. The purpose of the research is to study the variability and relationships of quality traits; identification of the best varieties for use in the breeding process. It was found that the most strongly varying features were the specific work of deformation of the dough (11.7%) and the coefficient of the ratio of dough elasticity to extensibility (23.5%). The results of a correlation analysis on the conjugation of the characteristics of the quality of grain, flour and baking properties are presented. The quality of bread significantly depended on the volumetric yield of bread ($r=0.9118$) and the specific work of dough deformation ($r=0.5119$). A significant positive, strong relationship was found between the content of protein and gluten in the grain ($r=0.8471$). New varieties and lines of winter soft wheat of intensive type, distinguished by a complex of studied traits: the new variety Privolye, lines 1518/18 and 1401/19, are recommended to be used in the breeding process aimed at improving the quality of winter soft wheat grain.

来源: E3S

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<http://agri.nais.net.cn/file1/M00/10/31/Csgk0GURKnKAavF6ACAf8BiHubs177.pdf>

3 . Genetic Variation and Heritability of Sensory and Artisan Bread Traits in a Set of SRW Wheat Breeding Lines (一组SRW小麦选品系感官和手工面包性状的遗传变异和遗传力)

简介: Focus on local food production and supply chains has heightened in recent years, as evidenced and amplified by the COVID-19 pandemic. This study aimed to assess the suitability of soft red winter (SRW) wheat breeding lines for local artisan bakers interested

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in locally sourced, strong gluten wheat for bread. Seventy-six genotyped SRW wheat breeding lines were milled into whole wheat flour and baked into small loaves. Bread aroma, flavor, and texture were evaluated by a sensory panel, and bread quality traits, including sedimentation volume, dough extensibility, and loaf volume, were measured to estimate heritability. SE-HPLC was performed on white flour, and breeding lines were characterized for different protein fraction ratios. Heritability of loaf volume was moderately high ($h^2 = 0.68$), while heritability of sedimentation volume, a much easier trait to measure, was slightly lower ($h^2 = 0.55$). Certain protein fraction ratios strongly related to loaf volume had high heritability ($h^2 = 0.7$). Even though only a moderate heritability estimate of dough extensibility was found in our study, high positive correlations were found between this parameter and sedimentation volume ($r = 0.6$) and loaf volume ($r = 0.53$). This low-input and highly repeatable parameter could be useful to estimate dough functionality characteristics. Flavor and texture heritability estimates ranged from 0.16 to 0.37, and the heritability estimate of aroma was not significantly different from zero. However, the sensorial characteristics were significantly correlated with each other, suggesting that we might be able to select indirectly for aroma by selecting for flavor or texture characteristics. From a genome-wide association study (GWAS), we identified six SNPs (single nucleotide polymorphisms) associated with loaf volume that could be useful in breeding for this trait. Producing high-quality strong gluten flour in our high rainfall environment is a challenge, but it provides local growers and end users with a value-added opportunity.

来源: MDPI

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http://agri.nais.net.cn/file1/M00/03/5F/Csgk0Y1n38yAX_amACe6pxWowC0630.pdf

4 . Identification of a pleiotropic QTL cluster for Fusarium head blight resistance, spikelet compactness, grain number per spike and thousand-grain weight in common wheat (普通小麦抗赤霉病、小穗密实度、穗粒数和千粒重多效性QTL群体的鉴定)

简介: Simultaneously improving Fusarium head blight (FHB) resistance and grain yield is challenging in wheat breeding. The correlations between spikelet compactness (SC), grain number per spike (GNS), thousand-grain weight (TGW) and FHB resistance remains unclear in common wheat. Identification of major quantitative trait loci (QTL) conferring FHB resistance and yield components, and development of breeder-friendly markers for the QTL are prerequisites for marker-assisted selection (MAS). Here, a recombinant inbred line (RIL) population derived from a cross between a resistant cultivar Yangmai 12 (YM12) and a susceptible cultivar Yanzhan 1 (YZ1) was used to map QTL for FHB resistance and yield components. A total of 22 QTL were identified; among these, six are likely to be new for corresponding traits. A QTL cluster (Qclu.yas-2D) for FHB type II resistance, SC, GNS, and TGW was detected on chromosome 2D. Breeder-friendly kompetitive allele-specific PCR (KASP) markers flanking the interval of Qclu.yas-2D were developed and validated in a diverse panel of 166 wheat cultivars and advanced lines. The YM12 alleles of Qclu.yas-2D

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significantly increased FHB resistance, SC, and GNS but decreased TGW in the validation population. The KASP markers developed for Qclu.yas-2D have great potential for breeding high-yielding wheat cultivars with enhanced FHB resistance.

来源: ScienceDirect

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