

Advances in Crop Molecular Breeding and Genetics

Wanning Liu, Guan Li, Jiezheng Ying  and Zhiyong Li * 

State Key Laboratory of Rice Biology and Breeding, China National Rice Research Institute, Hangzhou 311400, China; dearliuwanning@126.com (W.L.); liguan@caas.cn (G.L.); yingjiezheng@caas.cn (J.Y.)

* Correspondence: lizhiyong@caas.cn

Selecting crop varieties with high and stable yields, as well as improving quality and economic benefits, has become a long-term topic while facing the continuous increasing population and the adverse effects of environmental changes. Crop breeding is an important way to ensure human food security all over the world. Over recent decades, the process of crop breeding has greatly accelerated due to the application of modern molecular biology technologies and the basis of plant genetics. However, scientists and crop breeders still have a long way to go. Recently, some researchers have improved rice yields or quality by controlling grain size [1], some have optimized crop growth by increasing nitrogen use efficiency [2], and some aim to make crops more resilient to cold, salt, and drought to ensure high yields [3–5]. These understandings of the molecular basis for improved product quality, nutrient utilization, and adaptation to stress highlight the need for higher crop yields.

This issue focuses on the latest fundamental discoveries in crop genetics, germplasm resources, crop adaptation to climate change, and their potential applications. These findings will play an important role in regulating important developmental processes, finding beneficial agronomic traits, and achieving high yields. This issue has published five articles on the topic “Crop Molecular Breeding and Genetics”. Different technologies were used to explore the relevant genes of important traits that affect crop yield and quality, such as whole genome analysis, phylogenetic analysis, multi-omics technology, and molecular marker assistance technology. There are also different perspectives, including molecular mechanisms related to seed germination, grain development, rice quality, heat stress, and carotenoid regulation. It helps to understand the regulatory mechanisms of important agronomic traits and provides gene resources for crop genetic improvement.

Maize (*Zea mays* L.) is an important source of food, feed, and industrial raw materials. Currently, global maize production has exceeded that of rice and wheat [6]. Healthy seed germination is important for improving the yield and quality of maize, but the molecular mechanisms regulating maize seed germination are still unclear. Generally, gibberellin (GA) is considered a phytohormone which has the function of releasing seed dormancy and promoting seed germination [7]. A recent study by Han et al. investigated the molecular mechanism of GA-induced maize seed germination, using multi-omics analysis, including transcriptome, miRNA, and degradome sequencing. Multiple items were found to be closely related to the seed germination process. A newly discovered lipid metabolism-related gene *ZmSLP* has a negative regulatory effect on maize germination. Over-expression of this gene in *Arabidopsis* can lead to seed lipid metabolism disorders and inhibit seed germination and seedling growth. This study provided valuable information for molecular research on maize seed germination.

In high plants, HD-Zip transcription factors play an important role in plant growth and tolerance to environmental stress [8]. So far, the HD-Zip gene has been extensively and systematically studied in *Arabidopsis thaliana*, *Manihot esculenta*, and *Zea mays* [9–11]. Yin et al. analyzed the function of HD-Zip gene family related to heat stress and carotenoid accumulation in three genomes of Brassicaceae plants, *B. rapa*, *B. oleracea*, and *B. napus*.



Citation: Liu, W.; Li, G.; Ying, J.; Li, Z. Advances in Crop Molecular Breeding and Genetics. *Agronomy* **2023**, *13*, 2311. <https://doi.org/10.3390/agronomy13092311>

Received: 14 August 2023

Accepted: 30 August 2023

Published: 1 September 2023



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They identified 93, 96, and 184 HD-Zip genes, respectively. They found that the expression level of *BraA09g011460.3C* was up-regulated after heat stress treatment, and significantly decreased in varieties with high carotenoid content, indicating that it has the potential for heat tolerance and regulating the level of carotenoid. This study provides important gene resources for the follow-up breeding of Chinese cabbage.

The NLR (nucleotide-binding site leucine-rich repeat receptor) gene family is large and diverse, and can activate ETI (effector-triggered immunity) in response to pathogen effectors and subsequently mediate immune signaling [12,13]. The unique composition of the NLR gene family in papaya (*Carica papaya* L.) has attracted researchers to study its characteristics, evolution, and function.

Papaya is a special plant with fewer genes than most flowering plant genomes, and the lack of disease resistance genes was reconfirmed in the latest genome release [14]. Wu et al. identified 59 NLR genes from the improved papaya genome via a customized RGAugury. They conducted a comprehensive analysis, including structural composition, sequence diversity, chromosome distribution, and phylogenetic analysis. The NLR family members were identified and classified more accurately than previous research on papaya NLR. Wu et al. showed that the NLR family of papaya is a simplified set of NLRs in typical Eudicots, making papaya a suitable plant model for studying basic disease resistance genes. This study provides a new perspective for the evolution of the NLR gene in papaya, which will help us better understand the complex and diverse disease resistance genes in Eudicots, and provides a basis for disease resistance breeding of crops.

Among various traits related to rice yield, grain filling is considered a limiting factor affecting rice yield and quality, and some reports support a close relationship between grain filling and starch metabolism in plants [15,16]. We still require further research to solve the problem of high yields and high grain-filling ratio in cultivated rice varieties using modern molecular biology technologies [17,18]. The new research findings reported by Lee et al. revealed several QTLs related to rice grain filling. They used a doubled haploid (DH) population along with Kompetitive allele-specific PCR (KASP) markers and Fluidigm markers to achieve this. Notably, *qFG3*, *qFG5-1*, and *qFG5-2* were significant in grain filling. The newly discovered *qFG3* has been detected in both early and normal cultivation environment and is considered a stable QTL that can serve as a useful gene source for breeding. *qFG3* carries genes related to cell division, elongation and differentiation, photosynthesis, and starch synthesis. This study provides target QTL regions for future breeding work, including fine mapping and functional characterization of candidate genes during rice filling.

In recent decades, the yield of rice has increased significantly, basically meeting the demand. However, there is a contradiction between high yield and high quality in crops generally. With the gradual improvement of people's living standard and consumption level, improving the quality of rice has become more and more important [19]. Gong et al. reviewed the genes that had beneficial effects on rice quality and their applications in breeding practices from four aspects: milling quality, appearance quality, edible and cooking quality, and nutritional quality. Significant progress has been made in the study of rice quality functional genomics, with the cloning of many important genes related to the regulation of rice quality traits. However, rice quality is composed of multiple traits, and there are always interactions between different quality traits and environmental factors. The application of new technologies such as GWAS, genetically modified organisms, and gene editing can accelerate the improvement of rice quality. Gong et al. also believe that different populations show diverse taste preferences under different environmental conditions. Therefore, developing fragrant rice varieties, strengthening the breeding of high-quality conventional indica rice, and developing functional rice with special nutritional value or specific needs of specific populations are important directions for future rice breeding. This review further deepens our understanding of rice quality regulation and breeding applications.

In summary, the studies presented in “Crop Molecular Breeding and Genetics” will help to improve the understanding of important traits and their molecular mechanisms and help to develop effective and efficient trait improvement strategies. The research of Han et al. revealed a new mechanism for regulating seed germination in maize. Wu et al. provided a new perspective for the evolution of the NLR gene in papaya and a basis for disease resistance breeding of crops. Lee et al. revealed several QTLs related to rice grain filling and provided a new target region for downstream breeding. Gong et al. reviewed excellent genes that affect rice quality and their applications in breeding. They will be beneficial for future work on genomic selection, QTL mapping, marker-assisted selection, gene editing, and breeding design in crops. It is expected that crop molecular breeding will have a broader development, from laboratory research to field selection, and new varieties with ideal traits will be cultivated using comprehensive methods.

Funding: This research was funded by grants from the National Natural Science Foundation of China (32201805), China Postdoctoral Science Foundation (2023T160701), and Zhejiang Provincial Natural Science Foundation of China (LQ21C130003).

Conflicts of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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