Crop Science Society of China

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Wheat functional genomics research in China: a decade of development☆,☆☆

1. Introduction

In the past decade we witnessed a revolutionary development of wheat genomics and functional genomics, thanks to the development of next generation sequencing (NSG) technology. Wheat, as one of the most important crops in China and the world and with a huge, repetitive, and polyploid genome, was unconquerable in the past and is now catching up with other crops due to the availability of an increasing number of resources and platforms.

Wheat researchers in China have worked unostentatiously during the last decade after The National High Technology Research and Development Program of China first set up the wheat functional genomics program in 2005. Since then many papers on wheat were published in a wide range of international journals demonstrating significant progress in wheat functional genomics.

At such an exciting moment it is timely to publish a special issue of The Crop Journal on wheat functional genomics to showcase the achievements of Chinese wheat researchers to the world crop community. Here, we compiled nine review papers and one research article. The aim of this special issue is to overview major progress in wheat functional genomics, especially in China. We also predict the future direction of wheat functional genomics research. We must acknowledge the landmark contributions of the international wheat research community, without which it would have been much harder for Chinese researchers to reach their goals. The publication of this special issue is therefore to acquaint our colleagues both within and outside China with the work conducted by Chinese wheat scientists and to promote further international collaborations in wheat functional genomics research. The following is a brief introduction to these review articles. Moreover, a number of important achievements in wheat functional genomics studies that are not included in this issue are also highlighted.

2. Pioneering work in wheat genome sequencing and analysis

Jia et al. [1] highlight currently available tools and methodologies for wheat functional genomics research that were developed in the era of NGS technology. These range from the concerted international effort in generating multiple reference genomes to novel strategies to attain genome-wide genetic variation; from mutant population generation to NGS-supported gene cloning and functional characterization. These resources provide the necessary foundation for wheat research by bridging the gap between genotype and phenotype and greatly support genomics-assisted selection and breeding of elite varieties. Shi and Ling [2] then provide a comprehensive overview on the development of wheat genome sequencing that occurred in the last five years. Diploid donor species, such as *Triticum urartu*, the AA genome donor and *Aegilops tauschii*, the DD genome donor, were first sequenced by two groups led by Chinese Scientists [3,4], accompanied by the simultaneous acquisition of a shotgun-derived draft sequence of common wheat variety Chinese Spring [5]. Over the next few years, a series of wheat genome sequences were published by the International Wheat Genome Sequencing Consortium (IWGSC) [6,7]. The recent publication of a high quality wild emmer genome [8] permits further improvement of both the diploid and hexaploid wheat genome sequences. The availability of three levels of wheat genome sequences provides a long needed stepping-stone to conduct functional genomics researches in wheat.

☆ Peer review under responsibility of Crop Science Society of China and Institute of Crop Science, CAAS.

☆☆ **Cover:** The new era of wheat functional genomics research in China. In the middle of the picture the sun rising into the blue sky and lighting up the wheat field in the foreground implies the new era. On the left the ancient Chinese pictograms depict two cereal plants attended by a human being, representing wheat production in China. On the right a DNA double helix emerges from the wheat field, representing genomics and functional genomics research on wheat. (Credit: Qianning Wang, 9 years old, Elementary School of the Chinese Academy of Agricultural Sciences).

https://doi.org/10.1016/j.cj.2018.01.001

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3. A leap in transformation efficiency for wheat genome editing

One of the key developments for wheat functional genomics is the breakthrough in wheat plant transformation. The mysterious and patented technology that was developed by the Japanese Tobacco Institute has been transferred to other counties such as China, providing critical support for functional characterization of wheat genes. Wang et al. [9] review recent progress in wheat transformation that greatly expedited the application of genome editing technology in this important crop. Together with other platforms, such as exon sequenced TILLING libraries [10], the functions of a large number of genes responsible for important agronomic traits will be identified in the foreseeable future. Together with recent progress in plant genome editing technology, these authors discuss possibilities to further increase transformation efficiency and to generate publicly acceptable, biotechnologically engineered wheat varieties.

4. Understanding molecular mechanisms of wheat response to heat and salt stresses

Environmental changes are major factors affecting wheat yield. In this special issue, two review articles report recent studies on heat tolerance and salt tolerance in wheat. With increasing global warming, the weather has become less predictable, especially during the grain development and ripening period when hot, dry winds may cause significant yield losses. Ni et al. [11] review recent progress in understanding the molecular mechanisms of heat tolerance and related genetic improvement in wheat. They introduce recent works in identification of heat-tolerance QTL on different chromosomes and heat responsive genes/proteins using genome-wide analysis. Hormones, especially ABA and ethylene, and epigenetics are new factors and mechanisms involved in regulation of heat tolerance in wheat [11]. On the other hand, saline land represents a large area that can be utilized for agriculture using salt tolerant crops. Study of the molecular mechanisms of salt tolerance in wheat should greatly help in breeding salt tolerant wheat varieties that can be grown on large areas of saline coastal land in China as well as many other locations in the world. Wang and Xia [12] overview current understanding of the major physiological processes associated with salt tolerance and the genes controlling them. They particularly focus on high-affinity potassium transporter (HKT) genes in enhancing salt tolerance in wheat. They also report studies to link maintenance of reactive oxygen species (ROS) homeostasis and salt tolerance through comprehensive studies on a wheat introgression line. The authors summarize the most recent progress in omics investigations, and new research strategies to uncover the mechanisms underlying salt tolerance [12].

5. Continuous effort to understand mechanisms underlying disease resistance

The arms race between crops and pathogens is an ongoing subject in biology. Fusarium head blight (FHB) or scab caused by *Fusarium graminearum* is a major threat to wheat production in China and elsewhere. This special issue features a review from Dr. Zhengqiang Ma's laboratory at Nanjing Agricultural University where there has been a long and arduous effort covering almost twenty years to understand Fusarium head blight resistance in Chinese wheat landrace Wangshuibai. They present results on resistance QTL identification, candidate functional gene discovery, and marker-assisted improvement of FHB resistant varieties. Although one gene effective in FHB resistance has been cloned [13], the underlying molecular mechanism of resistance to this devastating disease is still controversial and far from being fully understood [14].

6. An emerging genomics era for biotrophic pathogens in wheat

Obligate biotrophic fungi such as those that cause rust and powdery mildew diseases are major biotic constraints on wheat production in China as well as the world. The team led by Professor Zhengshen Kang at Northwest Agriculture and Forestry University is one of the leading groups in pathogenomics studies of wheat biotrophic fungi in the world. Here, Tang et al. [15] review recent progress in the application of next generation sequencing technology to achieve the genome sequences of wheat pathogens. The authors summarize recent genomics advances in understanding the biology and pathogenesis of biotrophic fungal pathogens attacking wheat both in China and in the world. Genomics advances in all three major rust pathogens — *Puccinia striiformis* f. sp. *tritici* (*Pst*), *Puccinia graminis* f. sp. *tritici* (*Pgt*), and *Puccinia triticina* (*Pt*) that cause stripe rust, stem rust and leaf rust, respectively, and *Blumeria graminis* f. sp. *tritici* (*Bgt*) that causes powdery mildew are introduced particularly in regard to their genome sequencing, avirulence gene cloning, effector discovery, and pathogenomics. New insights in biotrophic adaptation, pathogenicity mechanisms, and population dynamics of these fungi should assist in development of new strategies for breeding wheat varieties with durable resistance. Such knowledge is essential for wheat variety deployment in regard to year-to-year dynamics of wheat pathogen populations and hence better field management and yield.

7. Extensive genetic and genomics analyses of wheat grain qualities

Grain quality is central to food processing and nutritional value of wheat-based food products. It is a decisive factor for consumer acceptance and commercial value of wheat cultivars. Wang et al. [16] review recent progress in understanding molecular genetics and genomics mechanisms of wheat grain quality, particularly in regard to milling and end-use traits. The authors review multiple pubications by Chinese scientists to understand the relationships between grain hardness and milling traits and between gluten protein quality and end-use traits, especially the roles of the HMW-GS proteins, LMW-GS proteins, and gliadins, as well as the transcriptional

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