

Available online at www.sciencedirect.com

ScienceDirect



Molecular genetic and genomic analysis of wheat milling and end-use traits in China: Progress and perspectives

Daowen Wang^{a,b,*}, Kunpu Zhang^{a,b}, Lingli Dong^a, Zhenying Dong^a, Yiwen Li^a, Abrar Hussain^{a,c}, Huijie Zhai^b

^aThe State Key Laboratory of Plant Cell and Chromosome Engineering, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing 100101, China

^bCollege of Agronomy, State Key Laboratory of Wheat and Maize Crop Science, Henan Agricultural University, Zhengzhou 450002, Henan, China

^cDepartment of Biosciences, COMSATS Institute of Information Technology, Sahiwal Campus, Pakistan

ARTICLE INFO

Article history:

Received 7 September 2017

Received in revised form

7 October 2017

Accepted 20 October 2017

Available online xxx

Keywords:

Genomics

Gluten protein

Grain hardness

Puroindoline

Wheat grain quality

ABSTRACT

Wheat is the most widely cultivated staple food crop, and multiple types of food derivatives are processed and consumed globally. Wheat grain quality (WGQ) is central to food processing and nutritional value, and is a decisive factor for consumer acceptance and commercial value of wheat cultivars. Hence, improvement in WGQ traits is top priority for both conventional and molecular wheat breeding. In this review we will focus on two important WGQ traits, grain milling and end-use, and will summarize recent progress in China. Chinese scientists have invested substantial effort in molecular genetic and genomic analysis of these traits and their effects on end-use properties. The insights and resources generated have contributed to the understanding and improvement of these traits. As high-quality genomics information and powerful genome engineering tools are becoming available for wheat, more fundamental breakthroughs in dissecting the molecular and genomic basis of WGQ are expected. China will strive to make further significant contributions to the study and improvement of WGQ in the genomics era.

© 2017 Crop Science Society of China and Institute of Crop Science, CAAS. Production and hosting by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Contents

1. Introduction	0
2. Grain hardness and milling traits	0
3. Gluten protein quality and end-use traits	0
3.1. HMW-GS proteins	0
3.2. LMW-GS proteins	0

* Corresponding author at: The State Key Laboratory of Plant Cell and Chromosome Engineering, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing 100101, China.

E-mail address: dwwang@genetics.ac.cn (D. Wang).

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

<https://doi.org/10.1016/j.cj.2017.10.001>

2214-5141 © 2017 Crop Science Society of China and Institute of Crop Science, CAAS. Production and hosting by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Please cite this article as: D. Wang, et al., Molecular genetic and genomic analysis of wheat milling and end-use traits in China: Progress and perspectives, *The Crop Journal* (2017), <https://doi.org/10.1016/j.cj.2017.10.001>

3.3. Gliadin proteins	0
3.4. Other proteins in the gluten complex	0
3.5. Transcriptional regulation of gluten gene expression	0
4. Toward establishing a mutagenetic platform for systematically studying WGQ related chromosomal loci and genes	0
5. Future perspectives and concluding remarks	0
Acknowledgments	0
References	0

1. Introduction

Wheat grain quality (WGQ) is largely determined by milling yield, end-use, flour color and nutritional properties. Genetically, WGQ is mainly the outcome of independent and interactive actions of a number of traits, including (but not limited to) grain hardness, gluten protein quality, flour color, starch quality, and contents of health-promoting substances. These traits are all controlled by polygenes and affected by agro-environmental factors. Consequently, WGQ varies from cultivar to cultivar, year to year and across ecological environments. Nevertheless, genetic factors are the main determinants [1]. A better understanding of the genetic, genomic and molecular bases of WGQ traits will enable more effective improvement of WGQ.

Although basic investigations of certain WGQ traits (e.g., gluten protein quality) have a long history, molecular genetic studies of these traits started in the 1990s when recombinant DNA technologies gained applications in plant biology and genetic research. Genomic research of WGQ traits began much later compared to similar studies in model plants such as *Arabidopsis thaliana* and rice. This is because the most widely cultivated crop, common wheat (*Triticum aestivum*, also called bread wheat), has a large and complex hexaploid genome (AABBDD, $2n = 6x = 42$, ~17 G) [2,3]. A draft reference genome sequence of common wheat was not available until 2014 [3]. In contrast, a high-quality reference genome sequence for rice was published in 2005 [4]. Difficulty in genetic transformation of common wheat also hampered molecular and genomic studies of agronomic traits including traits associated with WGQ. Reproducible and highly efficient *Agrobacterium*-mediated plant transformation became well established for rice in the 1990s [5], but only became available for some wheat genotypes in 2015 [6]. Despite these difficulties, substantial worldwide effort has been devoted to molecular genetic and genomic studies of WGQ traits [1,7]. In the following sections, we review recent progress made in China in molecular genetic and genomic analysis of grain milling and end-use traits of wheat. For each trait, a brief summary of current understanding is provided, and the progress made by Chinese researchers is outlined. Owing to limited space, achievements made in regard to wheat flour color, starch quality and nutritional traits are not included, but information relating to these aspects can be found in several recent articles [1,7-10].

2. Grain hardness and milling traits

The molecular genetic basis of wheat grain hardness (also referred as grain texture) was reviewed recently [11-16].

Although this trait is conditioned by multiple genes, *Puroindoline a* (*Pina*) and *Puroindoline b* (*Pinb*), located at the *Hardness* (*Ha*) locus on chromosome 5DS, are the major determinants of grain texture in common wheat. In general, the wild type (WT) alleles of *Pina* and *Pinb*, which encode two small and similar cysteine-rich proteins (~13 kDa, 68% similarity), confer soft kernel texture, but mutation of one or both genes leads to an increase in grain hardness. Both *Pina* and *Pinb* have multiple alleles in common wheat landraces and modern cultivars. The mutations are caused by either large deletions in the *Ha* locus, which results in the loss of *Pina* and/or *Pinb* genes, or SNPs in the coding regions, which create amino acid substitutions or truncations in the *Pina* or *Pinb* proteins. Detailed molecular and functional studies of these alleles are essential for not only systematically understanding the evolution and action of *Pina* and *Pinb* but also fine-tuning the kernel texture and milling quality of commercial varieties according to the end-use purpose.

A number of studies have been conducted in China to analyze allelic variations of *Pina* and *Pinb* [17-26]. These efforts have largely clarified the role of *Pina* and *Pinb* alleles and their combinations present in Chinese wheat landraces and commercial cultivars. The allelic diversities of *Pina* and *Pinb* are relatively high in Chinese wheat compared to those detected in the wheat populations from other countries (regions). For example, 13 allelic combinations of *Pina* and *Pinb* were found in 204 Chinese wheat landraces, whereas only three such combinations were detected in 104 wheat lines gathered from the International Maize and Wheat Improvement Center [26]. A number of *Pina* and *Pinb* alleles were first discovered in Chinese wheat lines, and some of them may have originated in China [26]. *Pinb-D1b* is the main allele detected in hard wheat varieties from the main wheat cultivation zone of China (i.e., the Yellow and Huai River Valley), followed by several other alleles, e.g., *Pinb-D1p*, *Pina-D1b*, and *Pina-D1r* [17-19,22,24-26]. Chen et al. [26] provided a comprehensive summary of the *Pina* and *Pinb* alleles detected so far in common wheat, along with the molecular changes in variant alleles, and their effects on grain hardness.

Chinese researchers have also investigated *Pina* and *Pinb* orthologs in related Triticeae grasses. For example, two new alleles of *Sina* and *Sinb*, the orthologs of *Pina* and *Pinb* in rye (*Secale cereale*, RR, $2n = 2x = 14$), were identified [27]. *Dina* and *Dinb*, the orthologs of *Pina* and *Pinb* in *Haynaldia villosa* (VV, $2n = 2x = 14$), were described [28]. The latter study is particularly interesting because the chromosomal fragment carrying *Dina* and *Dinb* was transferred to the genome of a soft kernel common wheat cultivar, leading to a further reduction of kernel softness. This is valuable for developing environmentally stable

Download English Version:

<https://daneshyari.com/en/article/8408793>

Download Persian Version:

<https://daneshyari.com/article/8408793>

[Daneshyari.com](https://daneshyari.com)