

Molecular biology and genetics / Biologie et génétique moléculaires

# Prospectives for applying molecular and genetic methodology to improve wheat cultivars in drought environments

Zhao Chang-Xing<sup>a,b,\*</sup>, Guo Ling-Yu<sup>a</sup>, Cheruth Abdul Jaleel<sup>c</sup>, Shao Hong-Bo<sup>d,e,f,\*</sup>,  
Yang Hong-Bing<sup>g</sup>

<sup>a</sup> College of Plant Science and Technology, Qingdao Agricultural University, Qingdao 266109, China

<sup>b</sup> State Key Laboratory of Urban and Regional Ecology Research Center for National Status, Research Center for Eco-Environmental Sciences, The Chinese Academy of Sciences, Beijing 100085, China

<sup>c</sup> Stress Physiology Laboratory, Department of Botany, Annamalai University, Annamalainagar 608002, Tamil Nadu, India

<sup>d</sup> Binzhou University, Binzhou 256603, China

<sup>e</sup> State Key Laboratory of Soil Erosion and Dryland Farming on the Loess Plateau, Institute of Soil and Water Conservation, Chinese Academy of Science, Yangling 712100, China

<sup>f</sup> Institute of Life Sciences, Qingdao University of Science & Technology, Zhengzhou Road 53, Qingdao 266042, China

<sup>g</sup> College of Life Sciences, Qingdao Agricultural University, Qingdao 266109, China

Received 3 May 2008; accepted after revision 27 May 2008

Presented by Philippe Morat

## Abstract

With the advent of molecular biotechnologies, new opportunities are available for plant physiologists to study the relationships between wheat traits and their genetic control. The functional determinations of all genes that participate in drought adaptation or tolerance reactions are expected to provide an integrated understanding of the biochemical and physiological basis of stress responses in wheat. However, despite all the recent technological breakthroughs, the overall contribution of genomics-assisted breeding to the release of drought-resilient wheat cultivars has so far been marginal. This paper critically analyses how biotechnological, genetic and information tools can contribute to accelerating the release of improved, drought-tolerant wheat cultivars. Armed with such information from established models, it will be possible to elucidate the physiological basis of drought tolerance and to select genotypes with an improved yield under water-limited conditions. **To cite this article:** C.-X. Zhao *et al.*, *C. R. Biologies 331 (2008)*.

© 2008 Académie des sciences. Published by Elsevier Masson SAS. All rights reserved.

**Keywords:** Wheat (*Triticum aestivum* L.); Drought environments; Comparative mapping; Segregating population; Genetic linkage maps; Genomics-assisted breeding

## 1. Introduction

Wheat (*Triticum aestivum* L.) production is adversely affected by drought in 50% of the area under production in the developing and 70% in the devel-

\* Corresponding authors.

E-mail addresses: [zhaochangxing@126.com](mailto:zhaochangxing@126.com) (C.-X. Zhao), [shaohongbochu@126.com](mailto:shaohongbochu@126.com) (H.-B. Shao).

oped countries [1]. As water resources are likely to decline in the coming decades [2], the areas devoted to wheat production will be increasingly threatened by water availability. Hence, improving wheat adaptation to drought will acquire a greater socioeconomic importance across the globe than it currently has.

As shortage of water is more limiting to crop production in arid regions than any other single factor, a better understanding and control of the mechanisms that enable a plant to adapt to low water potentials and maintain the processes involved in growth, development and production, has been an aim of breeding for drought resistance [3]. Therefore, the analysis of the physiological responses of various wheat genotypes to water stress was liable to lead to the development of more efficient selection criteria [4,5].

Whichever adaptation strategy is exerted in the wheat plant as a response to drought, it is paramount to elucidate the central element of control from the atomistic, reductionistic view. The dissection can be conducted at the translational, transcriptional or genetic levels for furthering the manipulation of the components of a genotypic response [6,7]. During the past three decades, 76 genetic and information tools have been developed (and adopted) to reveal basic features in the genetics and expression of different wheat species (Fig. 1). Some are presented as following.

## 2. Comparative mapping

Comparative maps allow transfer of information about genetic control of traits from species with small diploid genomes, such as rice (*Oryza sativa* L.), to species with more complex genomic structures (increased repetitive DNA, polyploidy) and less economic support [8,9]. Because of the size and complexity of the genomes, it may not be appropriate to sequence the entire genomes of wheat (*Triticum* spp.), rye (*Secale cereale* L.), oat (*Avena sativa* L.), or barley (*Hordeum vulgare* L.) [9,10]. However, alternative strategies involving identification of gene-rich regions of the Triticeae genome and comparison of the genome structure and genetic colinearity with rice, maize (*Zea mays* L.), sorghum (*Sorghum vulgare* L.), and other species provide Triticeae researchers with the knowledge and tools necessary for genetic parity with simpler genomes.

Crop species of the *Poaceae* display a remarkable level of genetic similarity despite their evolutionary divergence 65 million years ago [11]. Molecular markers have been used to develop comparative chromosome maps for several members of the *Gramineae* and these have been used to study genes of agronomic importance

across species [12,13]. Large segments of the genomes of maize, sorghum, rice, wheat, and barley conserve gene content and order [14–17], although the correspondence has been modified by duplications, inversions, and translocations. For the domesticated grasses, the conserved linkage blocks and their relationships with rice linkage groups provides the insight into the basic organization of the ancestral grass genome [18]. This allows the transfer of information from species with small diploid genomes, such as rice, to species with more complex genomic structures, such as that of wheat [16,19].

Despite the progress in comparative mapping, the application of this technology, especially for wheat, rye, oat, and barley will not be realized unless scientifically sound strategies for studying drought tolerance are devised that allow researchers to utilize genetic tools and information developed for model species [20]. This will require more detailed comparative genetic analysis from the DNA sequence of genes all the way to comparative analysis of QTL (quantitative trait locus).

## 3. Bulk segregant analysis

The usual method to locate and compare loci regulating quantitative traits (QTLs) requires a segregating population of plants with each one genotyped with molecular markers [21]. However, plants from such segregating populations can also be grouped according to phenotypic expression of a trait and tested for differences in allele frequency between the population bulks: bulk segregant analysis (BSA) [21,22]. The same probes used for making a genetic map (e.g., isozyme, RFLP, RAPD, etc.) can be used for BSA [23]. A molecular marker showing polymorphism between the parents of the population and which is closely linked to a major QTL regulating a particular trait will mainly cosegregate with that QTL, i.e. segregate according to the phenotype if the QTL has a large effect [21–24]. Thus, if plants are grouped according to the expression of the trait and extreme groups tested with that polymorphic marker, the frequency of the two marker alleles present within each of the two bulks should deviate significantly from the ratio of 1:1 expected for most populations [23]. As chromosomal locations of many molecular markers have now been determined in many species, the map location of closely-linked QTLs can therefore be deduced without having to genotype every individual in segregating populations [25].

This has been used successfully with composite populations of wheat to locate QTLs associated with yield under severe drought. An inbred line derived from one

Download English Version:

<https://daneshyari.com/en/article/2784584>

Download Persian Version:

<https://daneshyari.com/article/2784584>

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