



Available online at www.sciencedirect.com

ScienceDirect



RESEARCH ARTICLE

Genetic characteristics of a wheat founder parent and a widely planted cultivar derived from the same cross



CHANG Li-fang^{*}, LI Hui-hui^{*}, WU Xiao-yang, LU Yu-qing, ZHANG Jin-peng, YANG Xin-ming, LI Xiu-quan, LIU Wei-hua, LI Li-hui

National Key Facility for Gene Resources and Genetic Improvement/Key Laboratory of Crop Germplasm Utilization, Ministry of Agriculture/Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing 100081, P.R.China

Abstract

Founder parents have contributed significantly to the improvement of wheat breeding and production. In order to investigate the genetic characteristics of founder parents and widely planted cultivars, Mazhamai (M), Biyumai (B) and six sibling lines (BM1–6) derived from the cross M×B were phenotyped for eight yield-related traits over multiple years and locations and genotyped using the wheat 90K single nucleotide polymorphism (SNP) assay. BM4 has been used as a founder parent, and BM1 has been widely planted, whereas BM2, 3, 5, and 6 have not been used extensively for breeding or planting in China. Phenotypic comparisons revealed that BM4 and BM1 displayed a better overall performance than the other sibling lines. BM1 showed higher thousand-grain weight than BM4, whereas BM4 exhibited lower coefficient of variation for most of the yield-related traits across different years and locations, indicating that BM4 was widely adaptable and more stable in different environments. SNP analysis revealed that BM4 and BM1 inherited similar proportions of the M genome but are dissimilar to BM2, 3, 5, and 6. Both BM1 and BM4 have specific alleles that differ from the other BM lines, and most of these alleles are concentrated in specific chromosomal regions that are found to associate with favorable QTLs, these SNPs and their surrounding regions may carry the genetic determinants important for the superior performance of the two lines. But BM4 has more genetic diversity than BM1 with more specific alleles and pleiotropic regions, indicating that the genome of BM4 may be more complex than the other sibling lines and has more favorable gene resources. Our results provide valuable information that can be used to select elite parents for wheat and self-pollinating crop breeding.

Keywords: wheat, founder parents, widely planted cultivars, SNP

1. Introduction

Wheat (*Triticum aestivum* L.) is one of the most important crops affecting the global economy and food security, and most of the world's wheat is produced by China, which produces >120 million tons per year (National Bureau of Statistics of the Republic of China, <http://www.stats.gov.cn/>; and Food and Agriculture Organization of the United Nations, FAO, <http://www.fao.org/statistics/en/>). Since

Received 7 March, 2017 Accepted 31 May, 2017
CHANG Li-fang, E-mail: longclf116@qq.com; LI Hui-hui, E-mail: lihuihui@caas.cn; Correspondence LI Li-hui, Tel: +86-10-62186670, E-mail: lilihui@caas.cn; LIU Wei-hua, Tel: +86-10-62176077, E-mail: liuweihua@caas.cn

^{*}These authors contributed equally to this study.

© 2018 CAAS. Publishing services by Elsevier B.V. All rights reserved.
doi: 10.1016/S2095-3119(17)61710-6

the 1950s, thousands of wheat cultivars have been bred in pedigree selection programs, which have significantly increased the yield and total production of wheat in China. Pedigree analysis indicates that most released cultivars are derived from 16 founder parents (Zhuang 2003). Among these founder parents, Bima 4, Beijing 8 (Li et al. 2012), Nanda 2419 (Jia et al. 2013), Abbondanza, Funo, Xiaoyan 6, and Youzimai are also widely planted (>667 000 ha) in China (Zhuang 2003). Founder parents have played a crucial role in modern crop breeding for have bred many wheat cultivars, especially widely planted cultivars, and have introduced favorable gene resources, such as the “reduced height genes” (*Rht* genes) from Akakomughi and Norin 10 (Gale and Yousefian 1985; Borojevic and Borojevic 2005a). Pedigree analysis has also been used to identify the founder parents of other crops, including rice (*Oryza sativa* L.; Tian et al. 2006; Zhou et al. 2012; Zhang et al. 2013), maize (*Zea mays* L.; Lu et al. 2009), soybean (*Glycine max* L. Merr.; Lorenzen et al. 1996; Lee et al. 2004), and barley (*Hordeum vulgare* L.; Russell et al. 2000; Sjakste et al. 2003). Many studies have reported the genetic contribution of founder parents to derivative lines, and important founder parents quantitative trait loci (QTLs) have been identified by molecular markers and pedigree analysis (Pestsova and Röder 2002; Borojevic and Borojevic 2005b; Ma et al. 2007; Han et al. 2009; Li et al. 2009, 2012; Zhou et al. 2012; Jia et al. 2013; Xiao et al. 2014; Wu et al. 2015). However, the basic genetic characteristics of founder parents are still poorly understood.

Mazhamai (M), a local landrace of the Guanzhong District in Shaanxi Province of China, was a major founder parent for wheat breeding in the 1950s. M has ecological adaptability, high tolerance to abiotic stress, and a high number of grain numbers per spike (GNS), but it is susceptible to stripe rust. Biyumai (B), which is highly resistant to stripe rust, was introduced from the United States (Zhuang 2003). In China, six wheat cultivars named BM1–6 are derived from the cross M×B. BM1 has been planted over 6 000 000 ha, but few cultivars have been bred from it. BM4 has been planted over 867 000 ha, and 80 released cultivars have been bred from it, including six widely planted cultivars (> 667 000 ha) and the founder parents Beijing 8 (Zhuang 2003; Li et al. 2012) and Jing 411 (Xiao et al. 2014). However, the other four sibling lines (BM2, 3, 5, and 6) have not been used extensively for breeding or planting. Because the six BM sibling lines are derived from the same cross but exhibit different performances, they provide an ideal system to analyze the genetic characteristics of founder parents and widely planted cultivars.

The development of the wheat 9K and 90K single nucleotide polymorphism (SNP) wheat assays has allowed the determination of detailed haplotype structure and the

genetic basis of trait variation (Cavanagh et al. 2013; Wang et al. 2014). These assays have been widely used to identify genomic regions targeted by breeding and improvement selection, to characterize genetic variation in allohexaploid and allotetraploid populations, and to dissect complex traits by QTL (Wu et al. 2015) and association mapping (Sela et al. 2014; Zanke et al. 2014a, b; Maccaferri et al. 2015). In the present study, the wheat 90K SNP assay was used to genotypes BM1–6 and their parents to identify the genomic characteristics of founder parents and widely planted cultivars.

The objectives of the present study were to (1) analyze the phenotypic characteristics of the founder parent BM4 and the widely planted cultivar BM1; (2) analyze the genetic characteristics of BM4 and BM1 by evaluating the genomic similarities and differences of BM1–6. The present study provides theoretical guidance for the selection of parents for wheat and self-pollinating crop breeding.

2. Materials and methods

2.1. Plant materials and field trials

B, M, and BM1–6 were evaluated over three consecutive years from 2007 to 2009 in five major wheat ecological regions in China, including Shijiazhuang in Hebei Province (114.36°E, 37.38°N), Tai'an in Shandong Province (116.02°E, 35.38°N), Yangling in Shaanxi Province (108.82°E, 34.36°N), Chengdu in Sichuan Province (104.06°E, 34.66°N), and Yangzhou in Jiangsu Province (119.4°E, 32.15°N). A randomized complete block design was used at all locations with three replications per site. Each plot consisted of five rows (2 m long and 30 cm wide), and 40 seeds were planted in each row. Ten plants from the center of each plot were harvested for each line to measure eight yield-related traits including plant height (PH), grain number per spike (GNS), thousand-grain weight (TGW), effective tiller number (ETN), spike length (SL), spikelet number per spike (SNS), sterile spikelet number per spike (SS), and heading date (HD). Details about the measurements and timing of measurements are described in Li et al. (2006).

2.2. Statistical analysis

Basic statistics for each trait were calculated for B, M, and BM1–6. Analysis of variance (ANOVA) was used to test the statistical significance of various sources of variation using SAS software (Release 9.1.3; SAS Institute, Cary, NC, USA). Duncan's new multiple range test (MRT) was used to conduct multiple comparison analysis tests for B, M, and BM1–6 (Duncan 1955).

Download English Version:

<https://daneshyari.com/en/article/8875630>

Download Persian Version:

<https://daneshyari.com/article/8875630>

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