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RESEARCH ARTICLE

Novel and favorable genomic regions for spike related traits in a wheat germplasm Pubing 3504 with high grain number per spike under varying environments



CHEN Dan^{1,2*}, WU Xiao-yang^{1*}, WU Kuo², ZHANG Jin-peng¹, LIU Wei-hua¹, YANG Xin-ming¹, LI Xiu-quan¹, LU Yu-qing¹, LI Li-hui¹

¹ National Key Facility for Crop Gene Resources and Genetic Improvement/Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing 100081, P.R.China

² Biotechnology and Germplasm Resources Institute, Yunnan Academy of Agricultural Sciences/Key Laboratory of Southwestern Crop Gene Resources and Germplasm Innovation, Ministry of Agriculture/Scientific Observation for Rice Germplasm Resources of Yunnan, Ministry of Agriculture/Yunnan Provincial Key Laboratory of Agricultural Biotechnology, Kunming 650223, P.R.China

Abstract

Grain number per spike (GNPS) is a major factor in wheat yield breeding. A new wheat germplasm Pubing 3504 shows superior features in spike traits. To elucidate the genetic basis of spike and yield related traits in Pubing 3504, 282 F_{2:3} families were generated from the cross Pubing 3504×Jing 4839, and seven spike and yield related traits, including GNPS, spike length (SL), kernel number per spikelet (KPS), spikelet number per spike (SNS), thousand-grain weight (TGW), spike number per plant (SNP), and plant height (HT) were investigated. Correlation analysis indicated significant positive correlations between GNPS and spike-related traits, including KPS, SNS, and SL, especially KPS. A genetic map was constructed using 190 polymorphic simple sequence repeat (SSR), expressed sequence tag (EST)-SSR, and sequence-tagged-site (STS) markers. For the seven traits measured, a total of 37 quantitative trait loci (QTLs) in a single-environment analysis and 25 QTLs in a joint-environment analysis were detected. Additive effects of 70.3% (in a single environment) and 57.6% (in a joint environment) of the QTLs were positively contributed by Pubing 3504 alleles. Five important genomic regions on chromosomes 1A, 4A, 4B, 2D, and 4D could be stably detected in different environments. Among these regions, the marker interval *Xmag834–Xbarc83* on the short arm of chromosome 1A was a novel important genomic region that included QTLs controlling GNPS, KPS, SNS, TGW, and SNP with stable environmental repeatability. This genomic region can improve the spike trait and may play a key role in improving wheat yield in the future. We deduced that this genomic region was vital to the high GNPS of Pubing 3504.

Keywords: wheat, high GNPS germplasm, QTL mapping, genomic region

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CHEN Dan, E-mail: xiaoyezi09@163.com; WU Xiao-yang,
E-mail: xtwy1@163.com; Correspondance LI Li-hui, Tel: +86-
10-62186670, Fax: +86-10-62189650, E-mail: lilihui@caas.cn

* These authors contributed equally to this study.

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1. Introduction

Wheat (*Triticum aestivum* L.) is one of the most important food crop worldwide. However, wheat production has become increasingly difficult with climate change, environmental

contamination and resource scarcity (FAO 2009). In recent decades, breeders consider that the increase of grain number per spike (GNPS) can effectively improve the yield of wheat (Zhuang 2003). Therefore, identifying the key gene/genomic region from the germplasm with a high GNPS will facilitate crop breeding for high yields in the future.

Wheat yield and yield related traits are controlled by multiple genes and greatly influenced by the environment. Quantitative trait locus (QTL) analysis is an efficient way to determine the molecular mechanism of quantitative traits. Am3 is a synthetic hexaploid wheat line. Using a $BC_5F_{2.3}$ population from a cross between Laizhou 953 and Am3, major QTLs of yield and yield related traits were detected, alleles originating from Am3 could increase TGW by 2.3–4.8 g (Liao et al. 2008; Wang et al. 2008). In addition, W7984 is synthetic hexaploid wheat generated via a cross of *Triticum tauschii* accession CIGM86.940 (DD) with the tetraploid wheat Altar 84 (AABB). Using the recombinant inbred lines (RILs) of W7984×Opata85 population, Börner et al. (2002) mapped 64 major QTLs of 20 traits, including morphological, agronomical, and disease resistance traits. Yu et al. (2014) constructed a high-density genetic map and identified 30 QTLs for five important agronomic traits using a RIL population that was derived from the hybrid of synthetic hexaploid genotype SHW-L1 and the common wheat cultivar Chuanmai 32.

The tetraploid *Agropyron cristatum* L. Gaertn (*A. cristatum*) ($2n=4x=28$, PPPP) is an important gene resource that possesses many desirable traits for wheat genetic improvement. Our laboratory crossed the Japanese wheat cultivar Fukohokomugi (Fukoho) and *A. cristatum* accession Z559 and generated a number of progeny lines 4844 with large spikes with multiple florets and grains (Li et al. 1998). The wheat (*Triticum aestivum* L.) germplasm Pubing 3504 ($2n=6X=42$, 42W, AABBDD) was a genetically stable derivative line obtained from the F_5 progeny of 4844, with high number of spikelets and florets (Chen et al. 2012). Our many studies have investigated these wheat — *A. cristatum* derivative germplasms from the aspects of cytogenetic analysis, molecular markers, QTL mapping, and breeding evaluation (Wu et al. 2006; Zhang et al. 2011). We have mapping a major QTL controlling GNPS on chromosomes 4B in another high GNPS germplasm Pubing 3228, which was a sister line with Pubing 3504 (Wang et al. 2011). Using gene and protein expression profiling analysis, several genes and proteins involved in the formation of the high GNPS phenotype have been identified in these high GNPS wheat germplasms (Chen et al. 2016). Comparing with Pubing 3228, Pubing 3504 possesses higher narrow-sense heritability and more stable environmental adaptability of GNPS (Chen et al. 2012). So we deduce that there might be some different major QTLs controlling GNPS in

Pubing 3504 between Pubing 3228.

The purpose of this paper is to analyze the genetic dissection of spike and yield related traits in the high GNPS germplasm Pubing 3504. We attempted to identify important QTLs and genomic regions associated with spike and yield related traits by QTL analysis in different environments and to provide the molecular basis for marker-assisted selection (MAS) for breeding programs.

2. Materials and methods

2.1. Plant materials

In the 1990s, the Japanese wheat cultivar Fukoho was crossed with *A. cristatum* accession Z559, and progeny line 4844 ($2n=6X=42$ or 44), with a higher number of florets and kernels in a spike, was obtained (Li et al. 1998). Our subsequent analysis demonstrated that the increased number of florets and kernels in a spike of the 4844-12 ($2n=6X=44$, 42W+2P) line was derived from the alien chromosomes of *A. cristatum* (Wu et al. 2006). In this study, the wheat (*Triticum aestivum* L.) germplasm Pubing 3504 ($2n=6X=42$, 42W, AABBDD) was obtained from the F_5 progeny of 4844-12, with a higher number of spikelets and florets, GNPS of 90–130 and kernel number per spikelet (KPS) of 7–9. Jing 4839 is a common wheat cultivar with a GNPS of 30–35, large kernels, and thousand-grain weight (TGW) of 40.8 g (Fig. 1). The genetic population including 282 $F_{2.3}$ lines used in this study was developed from the cross Pubing 3504×Jing 4839.

2.2. Field experiment and trait investigation

The F_2 seeds were grown under field conditions at the experimental station of Chinese Academy of Agricultural Sciences, Beijing, in the 2008–2009 sowing season.



Fig. 1 Morphology of parent. A, plant morphology during maturity. Left, Pubing 3504; right, Jing 4839. B, spike morphology during maturity. Left, Pubing 3504; right, Jing 4839. C, seed of Pubing 3504. D, seed of Jing 4839.

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