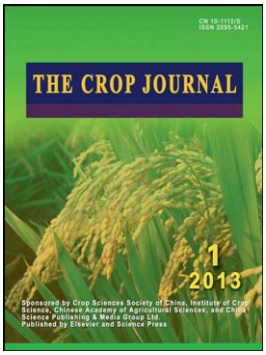

Mapping stripe rust resistance genes by BSR-Seq: *YrMM58* and *YrHY1* on chromosome 2AS in Chinese wheat lines Mengmai 58 and Huaiyang 1 are *Yr17*

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PII: S2214-5141(17)30032-6
DOI: doi:10.1016/j.cj.2017.03.002
Reference: CJ 223

To appear in: *The Crop Journal*

Received date: 10 February 2017
Revised date: 20 March 2017
Accepted date: 20 March 2017

Please cite this article as: Yong Wang, Huaizhi Zhang, Jingzhong Xie, Bingmin Guo, Yongxing Chen, Huaiyu Zhang, Ping Lu, Qiuhong Wu, Miaomiao Li, Deyun Zhang, Guanghao Guo, Jian Yang, Panpan Zhang, Yan Zhang, Xicheng Wang, Hong Zhao, Tingjie Cao, Zhiyong Liu, Mapping stripe rust resistance genes by BSR-Seq: *YrMM58* and *YrHY1* on chromosome 2AS in Chinese wheat lines Mengmai 58 and Huaiyang 1 are *Yr17*, *The Crop Journal* (2017), doi:10.1016/j.cj.2017.03.002

Mapping stripe rust resistance genes by BSR-Seq: *YrMM58* and *YrHY1* on chromosome 2AS in Chinese wheat lines Mengmai 58 and Huaiyang 1 are *Yr17*

Yong Wang[a], Huaizhi Zhang[a], Jingzhong Xie[b], Bingmin Guo[a], Yongxing Chen[b], Huaiyu Zhang[c], Ping Lu[b], Qiuhong Wu[b], Miaomiao Li[a], Deyun Zhang[a], Guanghao Guo[a], Jian Yang[b], Panpan Zhang[b], Yan Zhang[d], Xicheng Wang[e], Hong Zhao[e], Tingjie Cao[e,*], Zhiyong Liu[b,*]

[a] College of Agronomy and Biotechnology, China Agricultural University, Beijing 100193, China

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

[c] College of Life Science, Sichuan Agricultural University, Ya'an 625014, Sichuan, China

[d] College of Horticulture, China Agricultural University, Beijing 100193, China

[e] Wheat Research Institute, Henan Academy of Agriculture Sciences, Zhengzhou 450002, Henan, China

Abstract: Stripe rust (yellow rust), caused by *Puccinia striiformis* f. sp. *tritici* (PST), is one of the most devastating fungal diseases in common wheat (*Triticum aestivum* L.) in China and worldwide. Resistance breeding is the most effective strategy to control diseases in crop plants. Chinese wheat lines Mengmai 58 and Huaiyang 1 are highly resistant to PST race CYR34 (V26) at the adult plant stage. To genetically map the underlying resistance genes we developed segregating populations by crossing Mengmai 58 and Huaiyang 1 with the susceptible cultivar Nongda 399. The stripe rust resistances in Mengmai 58 and Huaiyang 1 were both controlled by single dominant genes, provisionally designated *YrMM58* and *YrHY1*, respectively. Bulked segregant RNA-Seq (BSR-Seq) analysis showed that *YrMM58* and *YrHY1* were located in the same distal ~16 Mb region on chromosome 2AS. Comparative genomics analysis with the physical map of *Aegilops tauschii* proved useful for developing additional markers to saturate the genetic linkage map. *YrMM58* and *YrHY1* were mapped to the distal end of chromosome arm 2AS, with the closest marker *WGGB148* being 7.7 cM and 3.8 cM from the resistance gene, which was considered to be *Yr17*. These markers can be used in marker-assisted selection.

Keywords: Genetic mapping; Stripe rust; *Triticum aestivum*

1. Introduction

Common wheat is a major food crop and wheat production is continually challenged by several diseases, including stripe rust, stem rust, leaf rust, powdery mildew, and Fusarium head blight. Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (PST), is one of the most severe of those diseases worldwide [1]. Breeding stripe rust resistant cultivars by deployment of effective stripe rust resistance genes is the main strategy for control [2, 3]. More than 70 stripe rust resistance genes have been formally named and some of them have been widely used in breeding [4–6]. However, new virulent pathogen races are a constant threat once resistance genes are deployed [7]. For example, *Yr9* on the 1RS.1BL translocation became ineffective following emergence of the virulent race CYR29 in the late 1990s [8], and the *Yr24*/*Yr26*/*YrCH42* was recently overcome by race CYR34 (V26) [9].

*Corresponding authors: Zhiyong Liu, E-mail address: zyliu@genetics.ac.cn, Tingjie Cao, E-mail address: caotingjie893@163.com.

Received: 2017-2-10; Revised: 2017-3-20; Accepted: 2017-04-16.