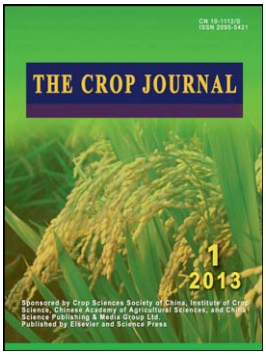

A journey to understand wheat fusarium head blight resistance in the Chinese wheat landrace Wangshuibai

Haiyan Jia, Jiyang Zhou, Shulin Xue, Guoqiang Li, Haisheng Yan, Congfu Ran, Yiduo Zhang, Jinxing Shi, Li Jia, Xin Wang, Jing Luo, Zhengqiang Ma

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Review

A journey to understand wheat fusarium head blight resistance in the Chinese wheat landrace Wangshuibai

Haiyan Jia[1], Jiyang Zhou[1], Shulin Xue, Guoqiang Li, Haisheng Yan, Congfu Ran, Yiduo Zhang, Jinxing Shi, Li Jia, Xin Wang, Jing Luo, Zhengqiang Ma[*]

The Applied Plant Genomics Laboratory, Nanjing Agricultural University, Nanjing 210095, Jiangsu, China

Abstract: Fusarium head blight (FHB) or scab caused by *Fusarium graminearum* is a major threat to wheat production in China as well as in the world. To combat this disease, multiple efforts have been carried out internationally. In this article, we review our long-time effort in identifying the resistance genes and dissecting the resistance mechanisms by both forward and reverse genetics approaches in the last two decades. We present recent progress in resistance QTL identification, candidate functional gene discovery, marker-assisted improvement of FHB resistant varieties, and findings in investigating association of signal molecules, such as Ca^{++}, SA, JA, and ET, with FHB response, with the assistance from rapidly growing genomics platforms. The information will be helpful for designing novel and efficient approaches to curb FHB.

Keywords: Fusarium head blight; QTL; Gene discovery; Marker-assisted selection; *Triticum aestivum*

1 Introduction

Fusarium head blight (FHB), caused by *Fusarium graminearum*, is arguably the most destructive disease in wheat. It greatly reduces yield and kernel quality in epidemic years and is almost not curable due to lack of immune germplasm [1–2]. More than that, the fungal mycotoxin contaminated kernels render the grain unsuitable for food or feed [3]. It has been a great challenge for wheat producers to avoid consequent economic damage. Among the measures adopted to curb this disease, deployment of scab-resistant varieties is the most preferred strategy for its economy and environmental friendliness.

Resistance to FHB in wheat is controlled by polygenes that usually have small effects and are vulnerable to environmental influences [4, 5]. Resistance is further complicated by its different manifestations, such as type I resistance against initial penetration, type II against fungal spread within spikes [6], type III for toxin decomposition [7], and less kernel infection and yield tolerance [8]. Because of these complexities, understanding of the resistance mechanisms was very limited and progress in scab resistance breeding was slow and far from meeting our needs.

Since the end of last century, the application of molecular genetics to crops has greatly speeded up FHB resistance research in wheat. Buerstmayr et al. [9] summarized findings from 52 studies on FHB resistance QTL mapping using various germplasm accessions. Currently, more than 250 QTL distributed on all 21 chromosomes have been documented [10–28]. As expected, most QTL have small effects and are yet to be verified. The effort is ongoing to cloning the FHB resistance QTL. Besides fine mapping of four major-effect QTL identified in

[*]Corresponding author: Zhengqiang Ma, E-mail address: zqm2@njau.edu.cn.
[1] Haiyan Jia and Jiyang Zhou contributed equally to this work.
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