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The Utilization of Rice Blast Resistance Genes in Hybrid Rice Breeding in China

Junjie Xing, Huafeng Deng and Longping Yuan

Abstract

Hybrid rice has demonstrated promises of yield gain for over several decades since its conception and massive deployment in China. One of the common bottlenecks of hybrid rice is the availability of suitable breeding lines as parents to produce marketable rice grains. Due to limitation of genetic diversity of breeding parent, hybrid rice is extremely vulnerable to rice blast disease caused by the fungal pathogen *Magnaporthe oryzae*. *M. oryzae* is a highly adaptive fungus that often gains new virulence to reduce crop resistance resulting in massive yield loss and crop failure. To secure yield gain of hybrid rice, identification and integration of diverse sources of resistance genes into hybrid rice are super critical. In this chapter, we will present strategies to identify, characterize, and stack effective blast resistance genes in hybrid rice breeding in China.

Keywords: rice blast, resistance gene, hybrid rice

1. Introduction

In China, the research on hybrid rice has gone on for more than 50 years. Professor Yuan first found the male sterility in 1964 and started hybrid rice research in China and, subsequently, creatively proposed the three-line, two-line, and one-line breeding conception [1]. Three-line hybrid rice was defined as restorer line, cytoplasmic male sterile line, and maintainer line; two-line hybrid rice was defined as restorer line and photo-thermosensitive genic male sterile; one-line hybrid rice was defined to maintain the heterosis by diploid line through apomixes [2]. Until now, hybrid rice breed with three-line or two-line method has successfully been applied in rice production.

From 1975, hybrid rice has gone through fast-speed development. More than 5000 varieties have been authorized by the government and planted for more than 500 million hm² in China and play important function for national food safety [3, 4]. Rice blast disease caused by *Magnaporthe oryzae* is popular and devastative on rice. The vulnerability of hybrid rice to rice blast brought huge yield damage. The utilization of resistant varieties was the most economical and environmental method to control the rice blast. Up to now, more than 90 resistance (*R*) genes have been identified, in which more than 20 genes are cloned [5]. Hence, rice lines containing major resistant genes have been widely used directly or indirectly as parents of hybrid rice. In this chapter, we will introduce the utilization of resistance genes in hybrid rice breeding.

2. The utilization of rice blast resistance genes

2.1 Identification of the resistant rice parents

The resistance level of parents is directly related with the resistance performance of hybrid rice. The resistance evaluation for breeding lines is a very important prerequisite work for resistance breeding of hybrid rice. For traditional breeders, field nursery or artificial inoculation with blast isolates in greenhouse was normally used for resistance identification. Amounts of rice lines with middle or high resistance have been identified in different provinces with diverse ecology. The detailed information was listed in **Table 1**. These identified rice materials provided rich selection as parents or resistant resource for hybrid rice breeding. As we know, genetic mechanism of rice blast resistance followed the gene for gene interaction. It was unclear about background and resistant genes in these materials, and the presence of one *R* gene masked another *R* gene; and also, the stationary field nursery only can stand for limited ecological districts. Hence, blast evaluation cannot identify any particular resistance gene, and it will lead to huge uncertainty in resistance of later generations in breeding. Phenotype identification cooperated with precise analysis of resistant genes will more effectively serve for hybrid rice resistance breeding.

2.2 Characterization and stack effective *R* genes in hybrid rice

Following the clone of resistant genes and the development of related functional molecular makers, marker screening has been widely applied on resistance identification and innovation of parents of hybrid rice. Up to now, molecular makers of blast resistance genes, *Pi2*, *Pi9*, *Pi1*, *Pib*, *Pita*, *Pid2*, *Pikh*, *Pigm*, and *Pish*, have been developed and used on detecting the related *R* genes [17–25]. In Jiangsu, a total of 544 rice materials were assessed for blast resistance and resistance genes distribution by inoculation and marker screening; results showed that 968, Xiushui 134, Jia 58, Jindao 263, Huaidao 20, Yandao 10, and Gumei 4 contained the majority of resistance genes; and *Pi5*, *Pita*, *Pi9*, and *Pib* exhibited high resistance to six major blast races [14]. In South China, with functional marker of *Pi1*, *Pik-p*, *Pikh*, *Pi2*, *Pi9*,

Province	Resistance resource	Reference
Sichuan	IR99–35, Miyang 46, IR 1544, Tetep, Gumei 2, 6326, Suhui162, and Suhui 527	[6, 7]
Heilongjiang	Suijing 12, Mudanjiang 26, Longdun 105, Longjing 20, Longjing 31, Dongnong 415, Songjing 9, Longdao 12, Hejiang 23, and Wuyoudao 3	[8]
Guangdong	Sanhuangzhan 2 Hao, Qingliuai 1 Hao, Jingxian 89, IR36, and 28 Zhan	[9]
Hunan	Xiangzao 143, Fengyuanyou 299, Jinyou 207, Liangyou 222, Quanfengyou 610, Hanyou 983, Lvyinzhan, Bingyou C278, Yuenongsimiao, and Zhuoliangyou 249	[10, 11]
Hubei	Zhenke, Jinlong 1, Fanyu 1, Ningwan 1, Sanqizao, Nanjing 15, Aiyinnuo, Jinzao 47, Yunjin 23, and Quanzhen 10	[12, 13]
Fujian	Yixiangyou 673, Dyou 15, Gangyou 148, Guyou 527, Jiafuzan, and Teyou 627	[14, 15]
Jiangsu	Longjing 968, Xiushui 134, Jia 58, Jindao 263, Huaidao 20, Yandao 10, and Gumei 4	[16]

Table 1.
Selected rice varieties with different resistant resources to blast in China.

Piz-t, *Pita*, and *Pii*, 328 hybrid rice combinations were screened, in which *Pita* and *Pii* were found in high frequency, but *Pi2* and *Pi1* displayed highly effective resistance contribution to local rice [26]. In Sichuan Province, with molecular markers closely linked to *Pi-9*, *Pi-2*, *Pi-kh*, and *Pi-km*, general rice parents of hybrid rice were analyzed and selected for the resistance resources [27]. The *R* gene screening make breeders directly utilize related resistance resources on purpose.

The hybridization, backcross, and marker-assisted selection (MAS) were the general method for the introduction of *R* genes into the restorer line, maintainer line, and sterile line of hybrid rice. MAS conduced to selectively breeding based on the genotype and accelerate the breeding course [28]. The procedure for MAS was shown in **Figure 1**. As we know, *R* genes, such as *Pi9*, *Pi2*, *Pi1*, and *Pigm*, have been reported to show relatively high resistance in different districts in China [29–31]. Hence, these *R* genes were often used for improvement of rice blast

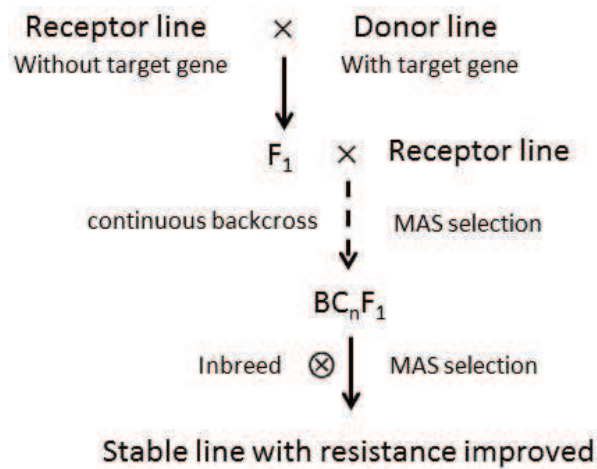


Figure 1.
The breeding course with marker-assisted selection and backcross.

R genes used	Variety improved	Variety type	Reference
<i>Pi9</i>	Yandao 6 Hao	General cultivar	[32]
<i>Pi25</i>	Xiangwanxian 13	General cultivar	[33]
<i>Pi1</i> , <i>Pi2</i> and <i>Pi33</i>	Jin 23B	Maintainer line	[34]
<i>Pi1</i> and <i>Pi2</i>	Rongfeng B	Maintainer line	[35]
<i>Pid(t)</i> , <i>Pib</i> and <i>Pita</i>	G46B	Maintainer line	[36]
<i>Pi9</i>	R599	Maintainer line	[37]
<i>Pi9</i>	R288	Maintainer line	[38]
<i>Pi9</i>	Shuhui527, Minghui 86, and Minhui 3301	Restorer line	[39]
<i>Pigm(t)</i>	Chunhui 350	Restorer line	[40]
<i>Pi9</i> and <i>Pi49</i>	Chuang 5S	Sterile line	[41]
<i>Pi25</i>	Zhenda A	Sterile line	[42]
<i>Pi47</i> and <i>Pi48</i>	C815S	Sterile line	[43]
<i>Pi9</i>	03S	Sterile line	[44]
<i>Pi1</i>	GD-8S	Sterile line	[45]
<i>Pi1</i> and <i>Pi2</i>	Peiai64S	Sterile line	[46]

Table 2.
The improved rice varieties of different types with MAS technique.

resistance (**Table 2**). Recently, a new class resistance gene *Ptr* just cloned encoded an atypical protein and conferred broad-spectrum disease resistance and will provide diverse selection for resistance improvement [47]. To breeding rice cultivars with durable blast resistance, stacking several resistance genes still was the most effective method. To stack resistance gene purposefully, spectrum of each resistance gene must be determined, and also, the identification of differential blast races/isolates that distinguished each resistance gene in different districts was critical for ensuring the effectiveness of resistance gene stacking [48].

3. Conclusions

With identification in the rice blast field nursery or functional marker detecting of major *R* genes, the amount of blast resistance resources was identified and provides diverse selections for hybrid rice resistance breeding. However, the recent finding showed that *Pita* required *Ptr* to function revealed that part of single *R* gene may be not functional as we thought originally [47], and further function analysis of more *R* genes may be necessary.

For conventional rice breeding, all blast *R* genes must be stacked into breeding lines to be effective, whereas hybrid rice can stack blast *R* genes into two parents. For hybrid rice breeding, blast resistance was only a part of index, and other agronomic traits also need to be considered. Lines of Chuang 5 S stacked *Pi9* and *Pi49* have been found obvious differences on plant height, spike length, spike number and stigma exertion rate with the receptor, even though the blast resistance has improved [41]. Hence, blast resistance breeding for hybrid rice was a synthetic work that contained resistance innovation and excellent agronomic trait selection.

In this chapter, it introduced the progress on identification of resistance resources and the utilization of blast resistance genes. Traditional cross technique, combined with MAS, has been used to transfer different major *R* genes into parent's lines to improve the resistance of hybrid rice and achieved remarkable results. Following the improvement of blast resistance of the authorized varieties, it gratefully contributed to decrease the damage of rice blast disease and played important function on protection of rice production safety in China.

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Conflict of interest

The authors declared that there was no conflict of interest.

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