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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 devastating 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, Lvyingzhan, 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 conducted 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

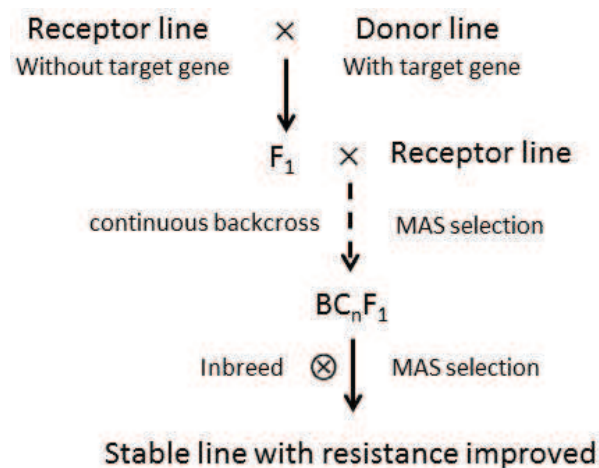


Figure 1.
 The breeding course with marker-assisted selection and backcross.

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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References

- [1] Wu B, Hu W, Xing YZ. The history and prospect of rice genetic breeding in China. *Hereditas*. 2018;**40**:841-857
- [2] Yuan LP. The strategy for hybrid rice development. *Hybrid Rice*. 2018;**33**:1-2
- [3] Zeng B, Sun SX, Wang J. Registration of main rice varieties and its application in recent 30 years in China. *Crops*. 2018;**2**:1-5
- [4] Hu ZX, Tian Y, Xu QS. Review of extension and analysis on current status of hybrid rice in China. *Hybrid Rice*. 2016;**31**:1-8
- [5] Yi NA, Li W, Dai LY. Advances in the cloning of rice blast resistance gene and its molecular breeding. *Molecular Plant Breeding*. 2015;**13**:1653-1659
- [6] Huang F, Ye HZ, Xie R, Liu CY. Screening for good quality rice germplasm resources resistant to rice blast. *Acta Agronomica Sinica*. 2006;**32**:1549-1553
- [7] Ma BT, Yang L, Wang LX, Yang TZ, Zhao XY, Gao XG, et al. Resistance evaluation and breeding of rice varieties (lines) to rice blast in nursery. *Chinese Agricultural Science Bulletin*. 2005;**21**:263-267
- [8] Xin W, Wang JG, Sun J, Liu HL, Guo LY, Jiang SD, et al. Physiological races of rice blast in Heilongjiang province and species identification of resistance to resource. *Acta Agriculturae Boreali-Sinica*. 2016;**31**:130-137
- [9] Feng AQ, Yang JY, Chen S, Zeng LX, Yang QY, Su J, et al. Evaluation on qualitative and quantitative resistance of rice germplasm to *Magnaporthe oryzae*. *Guangdong Agricultural Sciences*. 2015;**42**:27-32
- [10] Feng GP, Liu EM, Huang HM, Lv JL, Yan WT, Bai ZA, et al. Identification of resistance of 121 rice varieties against *Magnaporthe grisea*. *Hybrid Rice*. 2010;**25**:79-81
- [11] Min J, Mao SC, Long HP, Yi GL, Sun MY. Results and analysis of blast resistance of rice varieties in the united comparison test of rice in Hunan province. *Hybrid Rice*. 2018. DOI: 10.16267/j.cnki.1005-3956.20180322.091
- [12] Zeng FS, Xiang LB, Yang LJ, Yang XL, Yang JS, Yu DZ. Diversity analysis for resistance of 251 rice (*Oryza sativa* L.) varieties (lines) to rice blast disease. *Acta Phytopathologica Sinica*. 2011;**41**:399-410
- [13] Li XS, Xiang XJ, Shen CC, Yang LW, Chen K, Wang XW, et al. Identification and evaluation of blast resistance for resequenced rice core collections. *Acta Agronomica Sinica*. 2017;**43**:795-810
- [14] Ruan HC, Yang XJ, Chen SL, Dong RX, Chen FR, Wang WX, et al. Identification and evaluation of rice new varieties resistant to *Magnaporthe grisea* in Fujian Province. *Fujian Journal of Agricultural Sciences*. 2006;**21**:304-307
- [15] Du YX, Ruan HC, Wang MM, Guan RF, Yang XJ, Gan L, et al. Resistance evaluation of leading rice varieties to rice blast disease in Fujian province. *Chinese Agricultural Science Bulletin*. 2010;**26**:217-221
- [16] Li G, Yuan CY, Cao KR, Sun XL, Li J, Wang J, et al. Evaluation and distribution of the blast resistance genes of 544 rice materials. *Journal of China Agricultural University*. 2018;**23**: 22-28
- [17] Jiang JS, Wang SP. Identification of a 118kb DNA fragment containing the locus of blast resistance gene Pi2(t) in rice. *Molecular Genetics and Genomics*. 2008;**268**:249-252

- [18] Qu SH, Liu GF, Zhou B, Bellizzi M, Zeng LR, Dai LY, et al. The broad-spectrum blast resistance gene Pi9 encodes a nucleotide-binding site leucine-rich-repeat protein and a member of a multi gene family in rice. *Genetics*. 2006;**172**:1901-1904
- [19] Hua LX, Wu JZ, Chen CX, Wu WH, He XY, Lin F, et al. The isolation of Pi1, an allele at the Pik locus which confers broad spectrum resistance to rice blast. *Theoretical and Applied Genetics*. 2012;**125**:1047-1055
- [20] Liu Y, Xu PZ, Zhang HY, Xu JD, Wu FQ, Wu XJ. Marker-assisted selection and application of blast resistant gene Pib in Rice. *Scientia Agricultura Sinica*. 2008;**41**:9-14
- [21] Jia YL, Wang ZH, Singh P. Development of dominant rice blast Pi-ta resistance gene markers. *Crop Science*. 2002;**42**:2145-2149
- [22] Gao LJ, Deng GF, Gao HL, Gao GQ, Zhou M, Zhou WY, et al. Establishment and application of gene tagging linked to rice blast resistance Gene Pi-d2. *Southwest China Journal of Agricultural Sciences*. 2010;**23**:77-82
- [23] Ramkumar G, Srinivasarao K, Madhan Mohan K, Sudarshan I, AKP S, Gopalakrishna K, et al. Development and validation of functional marker targeting an InDel in the major rice blast disease resistance gene Pi54 (Pikh). *Molecular Breeding*. 2011;**27**:129-135
- [24] Zeng SY, Li C, Du CC, Sun LT, Jing DD, Lin TZ, et al. Development of specific markers for Pigm in marker-assisted breeding of panicle blast resistant Japonica rice. *Chinese Journal of Rice Science*. 2018;**32**:453-461
- [25] Akira T, Nagao H, Akio M, Hirohiko H. Unique features of the rice blast resistance Pish locus revealed by large scale retrotransposon tagging. *BMC Plant Biology*. 2010;**10**:175
- [26] Wang WJ, Zhou JY, Wang CY, Su J, Feng JQ, Chen B, et al. Distribution of eight rice blast resistance genes in Indica hybrid rice in China. *Chinese Journal of Rice Science*. 2017;**31**:299-306
- [27] Feng H, Yang CM, Wu XB, Liu YS, Peng YL. Detection and analysis of rice blast resistance gene in some hybrid rice parents and 32 resistant materials of Sichuan province. *Southwest China Journal of Agricultural Sciences*. 2013;**26**:987-993
- [28] Wang J, Yang J, Chen ZD, Fan FJ, Zhu JY, Yang JH, et al. Pyramiding resistance gene Pi-ta, Pi-b, and Stv-bi by marker-assisted selection in rice (*Oryza sativa* L.). *The Crop Journal*. 2011;**37**:975-981
- [29] Chen HL, Chen BT, Zhang DP, Xie YF, Zhang Q. Pathotypes of *Pyricularia grisea* in rice fields of central and southern China. *Plant Disease*. 2001;**85**:843-850
- [30] Liu G, Lu G, Zeng L, Wang GL. Two broad-spectrum blast resistance genes, Pi9 (t) and Pi2 (t), are physically linked on rice chromosome 6. *Molecular Genetics and Genomics*. 2002;**267**:472-480
- [31] Deng YW, Zhai K, Xie Z, Yang DY, Zhu XD, Liu JZ, et al. Epigenetic regulation of antagonistic receptors confers rice blast resistance with yield balance. *Science*. 2017;**355**:962
- [32] Yin DS, Xia MY, Li JB, Wan BL, Zha ZP, Du XS, et al. Development of STS marker linked to rice blast resistance gene Pi9 in marker-assisted selection breeding. *Chinese Journal of Rice Science*. 2011;**25**:25-30
- [33] Liu WQ, Li XX, Li YC, Pan XW, Sheng XN, Duan YH. Improvement of rice blast resistance of Xiangwanxian No.13 with high quality by molecular marker-assisted selection. *Molecular Plant Breeding*. 2017;**15**:3063-3069

- [34] Chen HQ, Chen ZX, Ni S, Zuo SM, Pan XB, Zhu XD. Pyramiding three genes with resistance to blast by marker-assisted selection to improve rice blast resistance of Jin 23B. *Chinese Journal of Rice Science*. 2008;**22**:23-27
- [35] Liu WG, Wang F, Liu ZR, Zhu XY, Li JH, Huang HJ, et al. Improvement of rice blast resistance in CMS line Rongfeng A by pyramiding Pi-1 and Pi-2 with molecular marker techniques. *Molecular Plant Breeding*. 2012;**10**:575-582
- [36] Chen XW, Li SG, Ma YQ, Li HY, Zhou KD, Zhu LH. Marker-assisted selection and pyramiding for three blast resistance genes, Pi-d(t)1, Pi-b, Pi-ta2 in Rice. *Chinese Journal of Biotechnology*. 2004;**20**:708-714
- [37] Chen HL, Li YC, Liu XL, Liu JL, Yang FY, Xing X, et al. Improving blast resistance of Indica rice restorer R599 and its hybrid by MAS technology. *Hybrid Rice*. 2017;**32**:61-65
- [38] Xing X, Liu XL, Chen HL, Yang FY, Li YC, Liao H, et al. Improving blast resistance of rice restorer R288 by molecular marker-assisted selection of Pi9 Gene. *Crop Research*. 2016;**30**:487-491
- [39] Zhang H, Zhou P, Tu SH, Zheng JT, Zhang JF, Xie HA. Developing new restorer lines with blast-resistance gene Pi9 for hybrid rice by marker assistance selection (MAS). *Molecular Plant Breeding*. 2015;**13**:1918-1922
- [40] Yang P, Zou GX, Chen CL, Huang YP, Lan B, Xiong YH, et al. Improvement of rice blast resistance of Chunhui350 by using molecular-marker assisted selection. *Molecular Plant Breeding*. 2015;**13**:741-747
- [41] Zhang JP, Hao M, Zeng G, Cao Z, Jiang HY, Huang XG, et al. Polymerization of Pi9 and Pi49 loci by marker assisted selection to improve blast resistance of dual-purpose genic sterile rice Chuang 5S. *Molecular Plant Breeding*. 2018;**16**:7372-7379
- [42] Dong RX, Wang HF, Dong LF, Zhou P, Tu SH, You QR, et al. Improving the rice blast resistance for a CMS line of rice Zhenda A and its hybrids using molecular marker-assistant selection. *Journal of Plant Genetic Resources*. 2017;**18**:573-586
- [43] Cao Z, Zeng G, Hao M, Sheng HW, Ye NZ, Xiao YH. Improving blast resistance of dual-purpose genic sterile line C815S by using molecular marker-assisted selection. *Molecular Plant Breeding*. 2015;**13**:1193-1200
- [44] Wang H, Chen JJ, Yan Z, Zhou GX, Shen GL, Jiang JP, et al. Improving the rice blast resistance of sterile line 03S by molecular marker-assisted selection. *Journal of Yangzhou University*. 2015;**36**:74-78
- [45] Jin SJ, Liu WG, Zhu XY, Wang F, Li JH, Liu ZR, et al. Improving blast resistance of a thermo-sensitive genic male sterile line GD-8S by molecular marker-assisted selection. *Chinese Journal of Rice Science*. 2007;**21**:599-604
- [46] Dong W, Li X, Yan B, Wu CJ, Gao GJ, Bao L, et al. Improving the blast resistance of Peiai64S through marker-assisted selection. *Molecular Plant Breeding*. 2010;**8**:853-860
- [47] Zhao HJ, Wang XY, Jia YL, Minkenberg B, Wheatley M, Fan JB, et al. The rice blast resistance gene Ptr encodes an atypical protein and confers broad spectrum disease resistance. *Nature Communications*. 2018;**9**:2039. DOI: 10.1038/s4147-018-04369-4
- [48] Xing JJ, Jia YL, Peng ZR, Shi YF, He Q, Shu F, et al. Characterization of molecular identity and pathogenicity of rice blast fungus in Hunan province of China. *Plant Disease*. 2017;**101**:557-561