UNIVERSITI PUTRA MALAYSIA

DEVELOPMENT OF BLAST-RESISTANT RICE VARIETY DERIVED FROM CROSSING BETWEEN MR219 AND PONGSU SERIBU 1 THROUGH MARKER-ASSISTED SELECTION

GOUS MIAH

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By

GOUS MIAH

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfillment of the Requirement for the Degree of Doctor of Philosophy

January 2015

DEDICATIONS

I dedicate this thesis to my beloved parents, wife, son and daughter, brother and sisters for their kind and loving support.

Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirement for the Degree of Doctor of Philosophy

DEVELOPMENT OF BLAST-RESISTANT RICE VARIETY DERIVED FROM CROSSING BETWEEN MR219 AND PONGSU SERIBU 1 THROUGH MARKER-ASSISTED SELECTION

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Chairman: Professor Mohd Rafii Yusop, PhD.

Institute: Tropical Agriculture

Marker-assisted selection (MAS) is very effective and powerful method for efficient selection of the target gene. MAS can potentially accelerate breeding programs for varietal resistance. Marker-assisted backcrossing (MABC) is the most-effective way of transferring specific gene(s) to an agronomically superior variety. Rice blast disease, caused by the fungus *Magnaporthe oryza*, is one of the most devastating and destructive disease causing significant yield loss worldwide as well as Malaysia. The most-effective approach to preventing this disease is the genetic improvement using resistant varieties. In this study, blast resistance gene (putative *Piz)* was transferred from an *indica* rice donor Pongsu Seribu 1, using MABC method, into a blast susceptible elite *indica* rice variety, MR219. Therefore, a cross between rice variety MR219 and Pongsu Seribu 1 was performed to incorporate blast resistance gene(s) into MR219 variety without losing their quality. Sixteen microsatellite markers tightly linked to the blast resistant genes were selected and used in this study to determine potential association with blast resistance gene. These polymorphic foreground markers were used for confirmation of blast resistant genes in F_1 population. After that only two microsatellite markers, RM6836 and RM8225, that conferred blast resistance gene (putative *Piz)* located on chromosome 6 were used to BC_1F_1, BC_2F_1 and BC_2F_2 populations related to resistance against the most-virulent Malaysian rice blast pathotype P7.2 of *Magnaporthe oryzae*. Out of 375-microsatellite markers, 70 markers were found to have polymorphism between the parental lines and were used for background analysis in each generation. The inheritance of the resistance gene against the pathotype P7.2 was investigated on BC_2F_1 and BC_2F_2 populations. The parent MR219 showed susceptible reaction with lesion score 5 to 7, whereas Pongsu Seribu 1 was found as resistant producing lesion score 0 to 2 after exposing to P7.2 inoculum in the glasshouse. In BC_2F_1 population, 333 plants were challenged with pathotype P7.2. Among them, 159 plants showed

resistant reaction and another 174 plants showed susceptible reaction to blast. The observed frequencies were tested for goodness of fit with chi-square (χ^2) test for single dominant gene model. The goodness of fit (p=0.4463) to the expected test cross ratio (1:1) showed that the resistance is controlled by a single nuclear gene. The plants resistant to blast pathotype P7.2 from BC_2F_1 population showed good fit with two markers, RM6836 (χ^2=0.20; p=0.6547) and RM8225 (χ^2=1.20; p=0.2733) with expected test cross ratio (1:1) for single gene model. These two markers were found suitable for marker-assisted selection conferring blast resistance gene against the pathotype P7.2. The phenotypic reaction on the blast incidence of BC_2F_2 population segregated in 3:1 ratio (resistance to susceptible). The genotypic segregation of BC_2F_2 population using RM6836 and RM8225 markers showed 1:2:1 ratio. Results confirmed that single dominant gene governs blast resistance in Pongsu Seribu 1 variety. The background analysis of the improved lines indicated recurrent parent genome recovery ranging from 75.40 % to 91.30 % in BC_1F_1, 80.40% to 96.70% in BC_2F_1 and 92.7% to 97.7% in BC_2F_2 generation. The average proportion of the recurrent parent in BC_2F_2 selected improved lines was 95.98%, explaining the very close similarity at phenotypic level with the parental variety, MR219. Thirteen homozygous plants consist of blast resistant gene which is phenotypically similar with MR219 backgrounds were selected as an improved blast resistant breeding lines. The agronomic characters showed no significant difference between MR219-parent and blast resistant MR219 improved lines. The improved lines possessing blast resistant gene (putative *Piz)* with desirable agronomic traits that can be used as a valuable source for further blast resistance rice breeding programs. In conclusion, from this research rice blast resistance in Pongsu Seribu 1 is governed by a single dominant gene located on chromosome 6, which is linked to RM6836 and RM8225 markers. This information could be used in MAS for blast resistance in other rice crosses involving Pongsu Seribu 1.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

PEMBANGUNAN VARIETI PADI RINTANG KARAH DARI KACUKAN ANTARA MR219 DAN PONGSU SERIBU 1 MELALUI PEMILIHAN BANTUAN PENANDA

Oleh

GOUS MIAH

Januari 2015

Pengerusi: Profesor Mohd Rafii Yusop, PhD

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Pemilihan bantuan penanda (MAS) adalah kaedah yang sangat berkesan dan berkeupayaan tinggi dalam memilih gen yang dikehendaki. MAS juga berpotensi untuk mempercepatkan program pemilihan varieti yang rintang penyakit. Kacuk balik bantuan penanda (MABC), adalah cara paling berkesan untuk memindahkan gen spesifik ke varieti yang mempunyai ciri agronomi yang unggul. Penyakit karah padi, yang disebabkan oleh kulat *Magnaporthe oryza*, adalah salah satu penyakit yang paling utama dan merosakkan tanaman, yang mengakibatkan penurunan hasil yang ketara dalam pengeluaran padi di seluruh dunia dan juga Malaysia. Pendekatan yang paling berkesan untuk mencegah penyakit ini adalah dengan memperbaiki kandungan genetik menggunakan varieti yang rintang penyakit. Dalam kajian ini, gen rintang karah (putatif *Piz*) telah dipindahkan dari penderma padi *indica* (Pongsu Seribu 1), menggunakan kaedah MABC, ke satu varieti padi *indica* unggul yang rentan karah, MR219. Oleh itu, kacukan antara varieti padi MR219 dan Pongsu Seribu 1 telah dijalankan untuk menggabungkan gen rintang karah ke atas varieti penerima, padi MR219 tanpa kehilangan kualiti asal MR219. Enam belas penanda mikrosatelit yang berkait rapat dengan gen kerintangan karah (*Pi*-gen) telah dipilih dan digunakan dalam kajian ini bagi menentukan potensi pengabungannya dengan gen kerintangan karah. Penanda polimorfik utama ini telah digunakan bagi mengenal pasti gen kerintangan karah pada populasi F_1. Selepas itu hanya dua penanda mikrosatelit, RM6836 dan RM8225, yang menentukan gen kerintangan karah (putatif *Piz*) yang terletak di atas kromosom 6 telah digunakan pada populasi BC_1F_1, BC_2F_1 dan BC_2F_2 yang menunjukkan kerintangan terhadap patotip P7.2 *Magnaporthe oryzae*, iaitu, patogen karah yang paling virulen di Malaysia. Daripada 375 penanda mikrosatelit, 70 penanda didapati polimorfik di antara kedua induk dan telah digunakan untuk analisis pemulihan dalam setiap generasi. Pewarisan gen kerintangan karah padi terhadap patotip P7.2 telah dinilai ke atas populasi BC_2F_1 dan BC_2F_2. Induk MR219 menunjukkan reaksi paling rentan dengan

skor *lesion* 5 hingga 7, manakala induk Pongsu Seribu 1 yang mempunyai kerintangan tinggi dengan skor *lesion* dari 0 hingga 2 apabila dirawat dengan inokulum P7.2 di rumah kaca. Pada populasi BC_2F_1, 333 pokok telah diinokulasi dengan patotip P7.2. Dari jumlah tersebut, didapati 159 pokok menunjukkan kerintangan dan 174 pokok lagi didapati reaksi rentan karah. Frekuensi yang dicerap telah diuji untuk keserasian menggunakan ujian khi-kuasa dua (χ^2) bagi model gen tunggal. Keserasian (p=0.4463) kepada ujian nisbah kacuk yang dijangka (1:1) menunjukkan kerintangan tersebut dikawal oleh gen tunggal. Pokok rintang karah terhadap patotip P7.2 dari populasi BC_2F_1 menunjukkan padanan yang baik dengan dua penanda RM6836 (χ^2=0.20; p=0.6547) dan RM8225 (χ^2=1.20; p=0.2733) bagi nisbah dijangka (1:1) untuk model gen dominan tunggal. Kedua-dua penanda ini didapati sesuai digunakan untuk pemilihan bantuan penanda bagi gen kerintangan karah patotip P7.2. Reaksi fenotip jangkitan karah pada populasi BC_2F_2 bersegregasi pada nisbah 3:1 (nisbah rintang ke rentan). Segregasi genotip dalam populasi BC_2F_2 dengan mengunakan penanda RM6836 dan RM8225 memberikan nisbah 1:2:1. Keputusan mengesahkan bahawa gen dominan tunggal yang mengawal kerintangan terhadap karah pada varieti Pongsu Seribu 1. Analisa pemulihan pada titisan maju menunjukkan pemulihan genom induk penerima dari 75.40% kepada 91.30% pada BC_1F_1, 80.40% kepada 96.70% pada BC_2F_1 dan 89.7% kepada 97.7% pada generasi BC_2F_2. Purata pemulihan genom titisan induk penerima pada BC_2F_2 terpilih adalah 95.98%, yang menunjukkan persamaan yang rapat pada fenotip dengan varieti induk, MR219. Tiga belas pokok homozigot mempunyai gen rintang karah dengan fenotip yang sama dengan MR219 telah dipilih bagi membangunkan varieti yang rintang karah. Ciri agronomi menunjukkan tiada perbezaan yang bererti di antara induk MR219 dan waris MR219 maju rintang karah. Titisan maju yang telah diperbaiki memiliki putatif gen *Piz* mempunyai ciri agronomi yang dikehendaki dan boleh digunakan secara langsung sebagai sumber untuk program seterusnya bagi pembiakbakaan padi kerintangan karah. Kesimpulannya, hasil dari penyelidikan kerintangan terhadap karah padi Pongsu Seribu 1, ianya dikawal oleh gen dominan tunggal yang terletak pada kromosom 6, yang berkait dengan penanda RM6836 dan RM8225. Maklumat ini boleh digunakan dalam MAS untuk kerintangan karah pada kacukan padi lain yang melibatkan varieti Pongsu Seribu 1.

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This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfillment of the requirements for the degree of Doctor of Philosophy. The members of the Supervisory Committee were as follows:

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LIST OF ABBREVIATIONS

bp	Base pair
cM	Centi Morgan
cm	Centimeter
CTAB	Cetyltrimethylammonium bromide
χ^2	Chi-square
^oC	Degree celsius
df	Degree of freedom
DNA	Deoxyribonucleic acid
EDTA	Ethyenediaminetetraacetic acid
EST	Expressed sequence tag
g	Gram
MABC	Marker-assisted backcrossing
MAS	Marker-assisted selection
Mbp	Mega base pair
m	Metre
µ	Micro
ml	Milliliter
mm	Millimeter
min	Minute
M	Molar
n	Nano
PCR	Polymerase chain reaction
QTL	Quantitative trait loci
%	Percentage
RPG	Recurrent parent genome
SSR	Simple sequence repeat
RAPD	Randomly amplified polymorphic DNA
RIL	Recombinant inbred line

RFLP	Restriction fragment length polymorphism
RH	Relative humidity
RNA	Ribonucleic acid
rpm	Rounds per minute
s	Second
SMA	Single-marker analysis
SNP	Single-nucleotide polymorphism
SES	Standard evaluation score
TE	Tris/EDTA
UV	Ultra violet
V	Volt
v/v	Volume/volume
w/v	Weight/volume
β-ME	β-mercaptoethanol
ddH_2O	Double distilled water
BLD	Blast lesion degree
BLT	Blast lesion type
%DLA	Percent diseased leaf area
GDP	Gross domestic product

CHAPTER 1

INTRODUCTION

1.1 General introduction

Rice (*Oryza sativa* L.) is one of the most vital food sources of humans and the second major global calories contributor (FAO, 2008). Rice is also the staple food of Malaysia, which is the significant source of employment and earnings to the rural farmers. Rice is prone to a range of man-made environmental or natural stresses. All these stresses cause modifications in an extensive range of physiological, biochemical and molecular processes in plants which ultimately lead to poor growth and low crop yield (Ashraf and Harris, 2013; Ashraf, 2014). The rice consumer is increasing, and demand for rice is also moving up due to better living standards. Various studies have shown that to meet the increasing demand for rice, production has to be increased more than 40 % by 2030 (Khush, 2005). This challenge has to be overcome by the development of high-yielding rice varieties with resistance or tolerance to biotic and abiotic stresses (Selvaraj *et al.,* 2011). Among the biotic stresses, blast disease is the most harmful threat to high productivity of rice (Fahad *et al.,* 2014). The rice yield loss should be minimized in order to help the marginal and poor farmers of developing countries (Latif *et al.,* 2011a). However, the potential yield of rice in Malaysia is around 10 tons ha^{-1} (Abdullah *et al.,* 2010). Unfortunately, until now the rice production in Malaysia has not met the national demand (Ghee-Thean *et al.,* 2012). Consequently, research is needed to expand and to increase rice yields by preventing diseases in order to supply sufficient food for a rising population. Malaysia is targeting 80% rice-sufficiency by 2020 that is why the government has increased four new granary areas under rice cultivation around 2.5% in year 2013 (FAO, 2013).

At least 85% of the Malaysian rice farmers reported that pests and diseases are the major problems in rice production (Amir *et al.,* 2012). The evolution of new biotypes of pests and diseases, and the pressures of climate change, pose thoughtful challenges to rice breeders, who would like to increase rice production by introducing resistance to numerous biotic and abiotic stresses (Miah *et al.,* 2013). Blast disease can be managed by the use of genetic resistance rice varieties, with cultural practices and the use of fungicides (Fahad *et al.,* 2014). In modern years, many techniques have been developed to control the rice blast disease. The chemical and biological methods, cultivation practices and disease forecasting methods are applied widely to control the spread of this disease (Jeger *et al.,* 2007). Unfortunately, these methods are not very effective. The use of fungicides is expensive as well as neither practical nor environmental-friendly. The use of resistant rice varieties is a powerful tool to reduce the use of environmentally destructive fungicides.

The molecular role of some blast resistance genes has been defined and many quantitative trait loci (QTLs) for blast resistance have been mapped (Dai *et al.,* 2007). New information and knowledge gained from molecular biology research on disease

resistance gene-mediated defense responses which is undoubtedly offer new perceptions into the nature of rice disease resistance. So, understanding and application of molecular biology is a prerequisite for accelerating the development of the blast resistance. Many rice researchers and breeders (Zhao *et al.,* 2010; Wang *et al.,* 2011; Swamy and Sarla, 2011) have developed new improved cultivated rice for resistance against the blast through molecular breeding approach involving DNA markers, marker-assisted selection (MAS) and genetic transformation. The PCR-based allele-specific markers provide an efficient marker system for MAS for blast resistance breeding (Latif *et al.,* 2011b). Conventional rice breeding is a slow process, typically requires 10 to 15 years from initiation to varietal release and the release of improved varieties cannot be assured (Werner *et al.,* 2005; Zhang *et al.,* 2006). Moreover, MAS offer better selection tactics in rice breeding with a short period. Marker-assisted selection is more efficient, effective and reliable than phenotypic selection. Advent of DNA marker technology, development of numerous types of molecular markers and molecular breeding approaches offered possibilities to plant breeders and geneticists to overcome several problems faced during conventional breeding. In specific, microsatellite-based methods offer a fascinating high-throughput and non-labor-intensive technique to tag blast resistance genes in rice breeding programs.

Oryza sativa ssp. *indica* cv. MR219 a Malaysian elite rice variety which have the characteristics of high-grain yield, short maturation period and good eating quality (Alias, 2002). MR219 is the premier variety released by Malaysian Agricultural Research and Development Institute (MARDI) in 2001 and widely planted in Malaysia. The highest potential yield recorded is 10.75 tons ha^{-1} and with long panicles at 23.2 cm (Alias, 2002). MR219 is grown more than 90% of rice fields in Malaysia due to its high-production potentiality (Fasahat *et al.,* 2012). When MR219 is released by MARDI, it was moderately resistant against blast fungal. But after a longtime cultivation and regeneration of seeds and due to climate change new blast pathotypes have been developed and recently MR219 broken down blast resistant ability and affected severely with blast pathogens. These informations highlighted the opportunity to develop additional high-yielding varieties that are adapted to other regions or environments. Here, the objective of this research was to convert widely cultivated variety MR219 to blast resistant variety with MR219 genetic backgrounds through backcross breeding and MAS. MR219 is not a blast resistant variety, and farmers are facing either very low yield or did not get any yield in the affected area. More supportable and everlasting solutions are needed to overcome this problem. One of the most encouraging solutions is to develop high-yielding varieties that are blast disease resistant and that are more likely to be rapidly adopted by the farmers in the target regions.

Pongsu Seribu 1 is Malaysian local rice variety which is resistant against blast fungal *Magnaporthe oryzae*. The choice of Pongsu Seribu 1 as a donor parent for the current breeding program was based on the fact that this variety is blast resistant, has a great percentage of the existing genetic difference for *Oryza* genus even though it's phenotype is agronomically unattractive. Information on genetic control of blast resistance in Pongsu Seribu 1 is very limited.

Recent advances in rice genomics have now made it possible to identify and map a number of genes through linkage to existing DNA markers. There are more noteworthy examples of molecular markers that tightly linked with the genes in rice confer resistance to blast. Therefore, in combination with conventional breeding methods, MAS can be used in breeding populations to monitor the presence or lack of these genes. For instance, MABB has been used to incorporate important genes with meaningfully biological effects into a number of regularly grown rice varieties. The use of finely mapped microsatellite markers and MAS strategies provide opportunities for breeders to develop high-yield, blast resistance rice varieties. Therefore, there is an urgent need to develop novel strategies to breed new rice varieties that confer high and stable resistance to this important rice disease in order to ensure food security in this country. Taking consideration above all these things in mind, blast resistant gene was introgressed into the rice genotype, MR219 which will help much to reduce yield losses of rice, as well as improvement livelihood to the people of Malaysia. In this study, microsatellite markers were successfully used to introgress blast resistance gene into a popular Malaysian rice variety MR219 having high-yield potential through marker-assisted backcrossing (MABC).

1.2 Significance of the study

In agriculture, one of the main objectives of plant breeder is to improve the existing varieties, which are deficient in one or more traits by crossing such varieties with lines that possess the desired traits. Conventional breeding program is laborious and time consuming; involving several crosses, several generations and careful phenotypic selection, and the linkage drag may make it further difficult to achieve the desired objectives. Molecular breeding approach involving MAS for resistance against blast has been used in developing new improved rice varieties by many rice researchers and breeders (Zhao *et al.*, 2010; Wang *et al.*, 2011; Swamy and Sarla, 2011). Marker-assisted selection is a recent tool in breeding to improve resistance to rice blast (Chowdhury *et al.*, 2012). Marker-asisted selection provides the potential solution to some of the problems that conventional breeding cannot resolve. In recent years, blast resistant genes have introgressed into Luhui 17, G46B, Zhenshan 97B, Jin 23B, CO39, IR50, Pusa1602 and Pusa1603 lines through MAS. Introduction of exotic genes for resistance induced the occurrence of new races of blast fungus; therefore, breeding work should be concentrated in local resistance genes (Miah *et al.*, 2013b). In Malaysia, several upland and traditional rice varieties are known to be resistant to blast disease. Among them, Pongsu Seribu 1 is one of the Malaysian local rice variety which is resistant against blast fungal. A better understanding of resistant genes is needed to enhance the development of blast-resistant varieties especially those with long-lasting, durable resistance (Tyng *et al.*, 2010). Information on genetic control of blast resistance in Pongsu Seribu 1 is very limited. Therefore, Pongsu Seribu 1 can be used in order to develop new rice variety with blast resistant in the current Malaysian rice breeding program. In the present study molecular marker technology and MABC were used to

introgress blast resistant gene in MR219 rice variety and to identify tightly linked markers conferring blast resistance against the most virulent rice blast fungus *Magnaporthae oryzae* pathotype P7.2. The improved blast resistant MR219-rice variety will reduce the yield loss and helpful to achieve rice production at self-sufficiency level in Malaysia.

1.3 Problem statement

Rice blast disease, caused by the fungus pathogen *Magnaporthe oryzae*, is one of the most serious diseases of rice. More than 85 countries around the world have reported the blast occurrence (Wang *et al.*, 2014), leading to the yield loss 10 million tons of rice every year (Wen and Gao, 2011). Therefore, rice blast is a significant economic and humanitarian problem. In Malaysia, rice blast has become a considerable disease of rice. Outbreaks often occur in seasons and off-seasons across the rice growing areas. The most popular rice variety MR219 is susceptible to blast disease. In Malaysia, a severe outbreak of blast disease occurred in 2006 at Kemubu Agriculture Development Authority (KADA) and Kelantan and yield losses were more than 60% from 4,000 hectares of rice cultivated area (Ashkani, 2011). In the recent years, in Malaysia, frequency of blast occurrence has increased with invasion into new areas. Moreover, there is no cultivated blast resistant rice variety in Malaysia. These results highlighted the opportunity to develop additional blast resistant high-yielding MR219 rice variety that will be adapted to Malaysia.

1.4 Objectives of the research

1. To analyse SSR markers linked with blast resistant gene in BC_2F_1 population derived from crosses between MR219 and Pongsu Seribu 1.
2. To analyse the recurrent parent genome recovery contribution in marker-assisted backcross breeding programs for the introgression of blast resistant gene.
3. To introgress blast resistant gene in MR219-rice variety through marker-assisted selection.

REFERENCES

Abdullah, A.M., Arshad, F.M., Radam, A., Ismail, M.M. and Mohamed, Z.A. et al. (2010). Studies on the impacts of subsidized fertilizer scheme and subsidized paddy price scheme provided by the federal government. Ministry of Agriculture and Agro-based Industry Malaysia, Putrajaya, Malaysia.

Abdullah, M.Z., Mohamad, O., Hadzim, K. and Othman, O. (1991). Vareiti padi traditional di Malaysia. *Teknologi Padi Jil.,* 7: 11-18.

Ahloowalia, B.S., Maluszynski, M. and Nichterlein, K. (2004). Global impact of mutation-derived varieties. *Euphytica*, 135: 187–204.

Ahn, S.N., Kim, Y.K., Hong, H.C., Han, S.S., Choi, H.C., McCouch, S.R. and Moon, H.P. (1997). Mapping of genes conferring resistance to Korean isolates of rice blast fungus using DNA markers. *Korean Journal of Breeding*, 29: 416–423.

Akagi, H., Yokozeki, Y., Inagaki, A. and Fujimura, T. (1996). Microsatellite DNA markers for rice chromosomes. *Theoretical and Applied Genetics*, 93: 1071–1077.

Alias, I. (2002). MR219, a new high-yielding rice variety with yields of more than 10 mt/ha. MARDI, Malaysia. FFTC: *An international information center for small scale farmers in the Asian and Pacific region*.

Allard, R.W. (1999). *Principles of plant breeding*, 2nd edn. Wiley and Sons, New York.

Allard, R.W. (1960). *Principles of plant breeding.* John Wiley and Sons, Inc., New York.

Amir, H.M., Shamsudin, M.N., Mohamed, Z.A., Hussein, M.A. and Radam, A. (2012). Economic evaluation of rice IPM practices in MADA, Malaysia. *Journal of Economics and Sustainable Development,* 3: 47-55.

Annual report. (1982). *International Rice Research Institute*. Los Banos, Laguna, Philippines.

Arunakanthi, B., Srinivasprasad, M., Madhanmohan, K., Balachandran, S.M., Madhav, M.S., Reddy, C.S. and Viraktamath, B.C. (2008). Introgression of major blast resistance genes *Pi-1*, *Pi-2* and *Pi-kh* in indica rice varieties Samba Mahsuri and Swarna. *Journal of Mycology and Plant Pathology,* 38: 625-630.

Ashkani S., Rafii, M.Y., Sariah, M., Abdullah, S.N.A., Rusli, I., Rahim, H.A. and Latif, M.A. (2011). Analysis of simple sequence repeat markers linked with blast disease resistance genes in a segregating population of rice (*Oryza sativa*). *Genetics and Molecular Research,* 10: 1345–1355.

Ashkani, S. (2011). Molecular dissection and QTL mapping of rice blast disease resistance using simple sequence repeat markers. Ph.D Thesis, Universiti Putra Malaysia.

Ashkani, S., Rafii, M.Y., Harun, A.R. and Latif, M.A. (2013). Genetic dissection of rice blast resistance by QTL mapping approach using an F_3 population. *Molecular Biology Reports***,** 40: 2503–2515.

Ashkani, S., Rafii, M.Y., Rusli, I., Sariah, M., Abdullah, S.N.A., Rahim, H.A.and Latif, M.A. (2012). SSRs for Marker-Assisted Selection for Blast Resistance in Rice (*Oryza sativa* L.). *Plant Molecular Biology Reports,* 30: 79–86.

Ashraf, M. (2009). Biotechnological approach of improving plant salt tolerance using antioxidants as markers. *Biotechnology Advances,* 27: 84–93.

Ashraf, M. (2014). Stress-induced changes in wheat grain composition and quality. *Critical Reviews in Food Science and Nutrition*, *54*, 1576–1583.

Ashraf, M. and Akram, N.A. (2009). Improving salinity tolerance of plants through conventional breeding and genetic engineering: An analytical comparison. *Biotechnology Advances,* 27: 744–752.

Ashraf, M. and Foolad, M. R. (2013). Crop breeding for salt tolerance in the era of molecular markers and marker-assisted selection. *Plant Breeding,* 132: 10–20.

Ashraf, M. and Harris, P.J.C. (2013). Photosynthesis under stressful environments: An overview. *Photosynthetica*, 51: 163-190.

Ashraf, M., Akram, N. A., Rahman, M., and Foolad M. R. (2012). Marker-assisted selection in plant breeding for salinity tolerance. Sergey Shabala and Tracey Ann Cuin (eds.), *Plant Salt Tolerance: Methods and Protocols, Methods in Molecular Biology* (pp. 305-333), vol. 913, © Springer Science+Business Media, LLC 2012.

Azlan, S., Alias, I., Saad, A. and Habibuddin, H. (2004). Performance of potential mutant lines of MR180. In: Sivaprasagam et al. (eds) Modern rice farming. *Proceedings of the international rice conference*, Serdang, Malaysia: MARDI, 2003, 293–296.

Ballini, E., Morel, J.B., Droc, G., Price, A., Courtois, B., Notteghem, J.L. and Tharreau, D. (2008). A genome-wide meta-analysis of rice blast resistance genes and quantitative trait loci provides new insights into partial and complete resistance. *Molecular Plant Microbe Interactions*, 21: 859–868.

Ballini, E., Nguyen, T.T.T. and Morel, J. (2013). Diversity and genetics of nitrogen-induced susceptibility to the blast fungus in rice and wheat. *Rice*, 6: 32.

Barman, S.R., Gowda, M., Venu, R.C. and Chattoo, B.B. (2004). Identification of a major blast resistance gene in the rice variety 'Tetep'. *Plant Breeding,* 123: 300–302.

Basavaraj, S.H., Singh, V.K., Singh, A.T., Singh, A.S., Singh, A.N., Anand, D., Yadav, S., Ellur, R.K., Singh, D., Gopalakrishnan, S., Nagarajan, M., Mohapatra, T., Prabhu, K.V. and Singh, A.K. (2010). Marker assisted improvement of bacterial blight resistance in parental lines of PusaRH10, a superfine grain aromatic rice hybrid. *Molecular Breeding*, 26: 293-305.

Berruyer, R., Adreit, H., Milazzo, J., Gaillard, S., Berger, A., Dioh, W., Lebrun, M. H. and Tharreau, D. (2003). Identification and fine mapping of *Pi33*, the rice resistance gene corresponding to the *Magnaporthe grisea* avirulence gene ACE1. *Theoretical and Applied Genetics*, 107: 1139–1147.

Beyer, B.M., Haley, S.D., Lapitan, N.L.V., Peng, J.H. and Peairs, F.B. (2011). Inheritance of Russian wheat aphid resistance from tetraploid wheat accessions during transfer to hexaploid wheat. *Euphytica*, 179: 247-255.

Bhatia, D., Sharma, R., Vikal, Y., Mangat, G.S., Mahajan, R., Sharma, N., Lore, J.S., Singh, N., Bharaj, T.S. and Singh, K. (2011). Marker-assisted development of bacterial blight resistant, dwarf, and high yielding versions of two traditional Basmati rice varieties. *Crop Science*, 51: 759–770.

Bhatt, J.C., Singh, R.A., Mani, S.C. and Shoran, J. (1994). Inheritance of blast resistance in rice. *Indian Journal of Genetics*, 54: 142-148.

Bhuiyana, M.A.R., Narimaha, M.K., Rahim, H.A., Abdullahc, M.Z. and Wickneswaria, R. (2011). Transgressive variants for red pericarp grain with high yield potential derived from *Oryza rufipogon* × *Oryza sativa*: Field evaluation, screening for blast disease, QTL validation and background marker analysis for agronomic traits. *Field Crops Research*, 121: 232–239.

Bonman, J.M. (1992). Durable resistance to rice blast-environmental influences. *Euphytica*, 63: 115-123.

Bonman, J.M., Khush, G.S. and Nelson, R.J. (1992). Breeding rice for resistance to pests. *Annual Review of Phytopathology*, 30: 507-528.

Bonnett, D.G., Rebetzke, G.J. and Spielmeyer, W. (2005). Strategies for efficient implementation of molecular markers in wheat breeding. *Molecular Breeding*, 15: 75-85.

Bormans, C.A. (2002). Development of genetic markers for blast resistance genes in rice (*Oryza sativa* L.) for use in marker assisted selection. Doctoral dissertation, Texas A & M University.

Brondani, C., Rangel, P.H.N., Borba, T.C.O. and Brondani, R.P.V. (2003). Transferability of microsatellite and sequence tagged site markers in *Oryza* species. *Hereditas,* 138: 187-192.

Bryan, G.T., Wu, K.S., Farrall, L., Hershey, H.P., McAdams, S.A., Faulk, K.N., Donaldson, G.K., Tarchini, R. and Valent, B. (2000b). A single amino acid difference distinguishes resistant and susceptible alleles of the rice blast resistance gene *Pi-ta*. *Plant Cell,* 12: 2033–2046.

Campos-Soriano, L., Vale, G., Lupotto, E. and San Segundo, B. (2013). Investigation of rice blast development in susceptible and resistant rice varieties using a gfp-expressing *Magnaporthe oryzae* isolate. *Plant Pathology,* 62: 1030–1037.

Cao, L.Y., Zhuang, J.Y., Zhan, X.D., Zheng, K.L. and Cheng, S.H. (2003). Hybrid rice resistant to bacterial blight developed by marker assisted selection. *Chinise Journalof Rice Science,* 17: 184–186.

Causse, M A., Fulton, T.M., Cho, Y.G., Ahn, S.N., Chunwongse, J., Wu, K.S., Xiao, J.H., Yu, Z.H., Ronald, P.C., Harrington, S.E., Second, G., McCouch, S. and Tanksley, S.D. (1994). Saturated molecular map of the rice genome based on an interspecific backcross population. *Genetics,* 138: 1251–1274.

Chauhan, S., Farman, M.L., Zhang, H.B. and Leong, A. (2002). Genetic and physical mapping of a rice blast resistance locus, *PiCO39(t),* that corresponds to the avirulence gene AVR1-CO39 of *Magnaporthe grisea*. *Molecular Genetics and Genomics,* 267: 603–612.

Chen, D.H., dela Viña, M., Inukai, T., Mackill, D.J., Ronald, P.C. and Nelson, R.J. (1999). Molecular Mapping of the blast resistance gene, *Pi44(t),* in a line derived from a durably resistant rice variety. *Theoretical and Applied Genetics,* 106: 1457-1466.

Chen, H., Lin, Y. and Zhang, Q. (2010). Rice. F. Kempken and C. Jung (eds.), Genetic modification of plants. *Biotechnology in Agriculture and Forestry,* 64: 423.

Chen, H.Q., Chen, Z.X., Ni, S., Zuo, S.M., Pan, X.B. and Zhu, X.D. (2008). Pyramiding three genes with resistance to blast by marker assisted selection to improve rice blast resistance of Jin 23B, application, Zhongguo Shuidao Kexue. *Chinese Journal of Rice Science,* 22: 23–27.

Chen, J., Henny, R., Devanand, P. and Chao, C. (2006). AFLP analysis of nephthytis (Syngonium podophyllum Schott) selected from somaclonal variants. *Plant Cell Reports,* 24: 743–749.

Chen, X.W., Li, S.G., Xu, J.C., Zhai, W.X., Ling, Z.Z., Ma, B.T., Wang, Y.P., Wang, W.M., Cao, G., Ma, Y.Q., Shang, J.J., Zhao, X.F., Zhou, K.D. and Zhu, L.H. (2004). Identification of two blast resistance genes in a rice variety, Digu. *Journal of Phytopathology,* 152: 77–85.

Chen, Z.W., Guan, H.Z., Wu, W.R., Zhou, Y.C. and Han, Q.D. (2005). The screening of molecular markers closely linked to rice blast resistant gene *Pi-1* and their application. *Journal of Fujian Agriculture and Forestry University,* 34: 74-77.

Chowdhury M.R., Yu-Lin, J. and Cartwright, R.D. (2012b). Structure, function, and co-evolution of rice blast resistance genes. *Acta Agronomica Sinica*, 38: 381−393.

Chowdhury, M.R., Jia, Y., Jackson, A., Jia, M.H., Fjellstrom, R. and Cartwright R.D. (2012). Analysis of rice blast resistance gene *Pi-z* in rice germplasm using pathogenicity assays and DNA markers. *Euphytica,* 184: 35–46.

Clergeot, P.H., Gourgues, M., Cots, J., Laurans, F., Latorse, M.P., Pepin, R., Tharreau, D., Notteghem, J.L. and Lebrun, M.H. (2001). *PLS1*, a gene encoding a tetraspanin-like protein, is required for penetration of rice leaf by the fungal pathogen *Magnaporthe grisea*. *Proceedings of the National Academy of Sciences,* USA, 98: 6963–6968.

Collard, B.C.Y. and Mackill, D.J. (2007). Marker-assisted selection: An approach for precision plant breeding in the twenty-first rst century. *Philosophical Transactions of the Royal Society of London*. Series B: *Biological Sciences,* 17: 1–16.

Collard, B.C.Y. and Mackill, D.J. (2008). Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philosophical Transactions of the Royal Society B,* 363: 557–572.

Collard, B.C.Y., Cruz, C.M., McNally, K.L., Virk, P.S., Mackill, D.J. (2008). Rice molecular breeding laboratories in the genomics era: Current status and future and considerations. *Int. J. Plant Genomics*, doi:10.1155/2008/524847.

Conaway-Bormans, C.A., Marchetti, M.A., Johnson, C.W., McClung, A.M. and Park, W.D. (2003). Molecular markers linked to the blast resistance gene *Pi-z* in rice for use in marker-assisted selection. *Theoretical and Applied Genetics*, 107: 1014-102.

Correa-Victoria, F.J. and Zeigler, R.S. (1993). Pathogenic variability in *Pyricularia grisae* at a rice blast ‘‘hot spot’’ breeding site in Eastern Colombia. *Plant Disease*, 77: 1029–1035.

Couch, B.C. and Kohn, L.M. (2002). A multilocus gene genealogy concordant with host preference indicates segregation of new species, *Magnaporthe oryzae* from *M.* grisea. *Mycologia,* 94: 683–693.

Cuc, L.M., Huyen, L.T.N., Hien, P.T.M., Hang, V.T.T., Dam, N.Q., Mui, P.T., Quang, V.D., Ismail, A.M. and Ham, L.H. (2012). Application of marker assisted backcrossing to introgress the submergence tolerance QTL SUB1 into the Vietnam elite rice variety-AS996. *American Journal of Plant Sciences,* 3: 528-536.

Dai, L., Liu, X., Xiao, Y. and Wang, G. (2007). Recent advances in cloning and characterization of disease resistance genes in rice. *Journal of Integration Plant Biology,* 49(1): 112–119.

Dean, R.A., Talbot, N.J., Ebbole, D.J., Farman, M.L., Mitchell, T.K., Orbach, M.J., Thon, M., Kulkarni, R., Xu, J.R., Pan, H., Read, N.D., Lee, Y.H., Carbone, I., Brown, D., Oh, Y.Y., Donofrio, N., Jeong, J.S., Soanes, D.M., Djonovic, S., Kolomiets, E., Rehmeyer, C., Li, W., Harding, M., Kim, S., Lebrun, M.H., Bohnert, H., Coughlan, S., Butler, J., Calvo, S., Ma, L.J., Nicol, R., Purcell, S., Nusbaum, C., Galagan, J.E. and Birren, B.W. (2005). The genome sequence of the rice blast fungus *Magnaporthe grisea*. *Nature,* 434: 980‑986.

Deng, Y., Zhu, X., Shen, Y. and He, Z. (2006). Genetic characterization and fine mapping of the blast resistance locus *Pigm(t)* tightly linked to *Pi2* and *Pi9* in a broad-spectrum resistant Chinese variety. *Theoretical and Applied Genetics,* 113: 705–713.

Deng, Y., Zhu, X., Xu, J., Chen, H. and He, Z. (2009). Map-based cloning and breeding application of a broad-spectrum resistance gene *Pigm* to rice blast, in: G.L. Wang, B. Valent (Eds.), *Advances in Genetics, Genomics and Control of Rice Blast*, Springer of Congress + Business Media B.V., USA, 161–171.

Divya, B., Robin, S., Rabindran, R., Senthil, S., Raveendran, M. and John Joel A. (2014). Marker assisted backcross breeding approach to improve blast resistance in Indian rice (*Oryza sativa*) variety ADT43. *Euphytica,* doi. 10.1007/s10681-014-1146-9.

Doyle, J.J. and Doyle, J.L. (1990). Isolation of plant DNA from fresh tissue. *Focus*, 12: 13-15.

Duke, J.A. (1983). Handbook of energy crops. http://www.hort.purdue.edu/newcrop/duke_energy/Oryza_sativa.htm#references.

Dutta, R.K., Baset Mia, M.A. and Khanam, S. (2002). Plant architecture and growth characteristics of fine grain and aromatic rice and their relation with grain yield. *IRC Newsletter,* 51: 51-56.

Dwivedi, S.L., Crouch, J.H., Mackill, D.J., Xu, Y., Blair, M.W., Ragot, M., Upadhyaya, H.D. and Ortiz, R. (2007). The molecularization of public sector crop breeding: Progress, problems, and prospects. *Advances in Agronomy,* 95: 163–318.

Fahad, S., Nie, L., Khan, F.A., Chen, Y., Hussain, S., Wu, C., Xiong, D., Jing, W., Saud, S., Khan, F.A., Li, Y., Wu, W., Khan, F., Hassan, S., Manan, A., Jan, A. and Huang, J. (2014) Disease resistance in rice and the role of molecular breeding in protecting rice crops against diseases. *Biotechnology Letter,* 36: 1407-1420.

FAO (Food and Agriculture Organization). (2008). Food Consumption: Pattern of main food items-share in total dietary energy consumption. FAO (Food and Agricultural Organization of the United States) Statistic Division. Bulletin.

FAO (Food and Agriculture Organization) (2013). Rice Market Monitor. Trade and Markets Division, Food and Agriculture Organization of the United Nations, July 2013 Volume XVI - Issue No. 3.

FAOSTAT (2013). Statistical database of the food and agriculture of the United Nations. FAO, Rome. (http://www.fao.org/economic/est/publications/rice-publications/rice-market-monitor-rmm/en/).

Farooq, S. and Azam, F. (2002). Molecular markers in plant breeding I: concepts and characterization. *Pakistan Journal of Biological Sciences,* 5: 1135- 1140.

Fasahat, P., Kharidah, M., Aminah, A. and Ratnam, W. (2012). Proximate nutritional composition and antioxidant properties of *Oryza rufipogon*, a wild rice collected from Malaysia compared to cultivated rice, MR219. *Australasian Journal of Crop Science*, 6: 1502-1507.

Fjellstrom, R., McClung, A.M. and Shank, A.R. (2006). SSR markers closely linked to the *Pi-z* locus are useful for selection of blast resistance in a broad array of rice germplasm. *Molecular Breeding*, 17: 149–157.

Flores-Gaxiola, J.A., Nuque, F.L., Crill, J.P. and Khush, G.S. (1983). Inheritance of blast *Pyricularia oryzae* resistance in rice. *International Rice Research Newsletter*, 8: 5-6.

Frisch, M. (1999). Comparison of selection strategies for marker assisted backcrossing of a gene. *Crop Science*, 39: 1295-1301.

Frisch, M. (2005). Optimum design of marker-assisted backcross programs. In: Loerz H, Wenzel G (eds) *Biotechnology in Agriculture and Forestry* vol 55. Springer, Berlin, 319–334.

Frisch, M. and Melchinger, A.E. (2001a). Marker-assisted backcrossing for simultaneous introgression of two genes. *Crop Science*, 41: 1716-1725.

Frisch, M. and Melchinger, A.E. (2005). Selection theory for marker-assisted backcrossing. *Genetics*, 170: 909-917.

Frisch, M., Bohn, M. and Melchinger, A.E. (1999a). Minimum sample size and optimal positioning of flanking markers in marker-assisted backcrossing for transfer of a target gene. *Crop Science,* 39: 967-975.

Frisch, M., Bohn, M. and Melchinger, A.E. (1999b). Comparison of selection strategies for marker-assisted backcrossing of a gene. *Crop Science,* 39: 1295-1301.

Fu, C., Wu, T., Liu, W., Wang, F., Li, J., Zhu, X., Huang, H., Liu, Z.R., Liao, Y., Zhu, M., Chen, J. and Huang, Y. (2012). Genetic improvement of resistance to blast and bacterial blight of the elite maintainer line Rongfeng B in hybrid rice (*Oryza sativa* L.) by using marker-assisted selection. *African Journal of Biotechnology,* 11: 13104–13124.

Fujii, K., Hayano-Saito, Y., Saito, K., Sugiura, N., Hayashi, N., Tsuji, T., Izawa, T., Iwasaki, M. (2000). Identification of RFLP marker tightly linked to the panicle blast resistance gene *Pb1* in rice. *Breeding Science,* 50: 183–188.

Fujimaki, H. (1979). Recurrent selection by using male sterility for rice improvement. *Jpn Agricultural Research,* 13: 153–156.

Fujita, D., Ebron, L. A., Kobayashi, N. and Fukuta, Y. (2006). Comparison of DNA marker analysis of the blast resistance genes *Pib* and *Pita* in IRRI-bred rice varieties with gene estimation by conventional genetic analysis. *Development and characterization of blast resistance using differential varieties in rice*. Japan International Research Center for Agricultural Sciences (JIRCAS), Japan, working report No. 63.

Fujita, D., Yoshimura, A. and Yasui, H. (2010). Development of nearisogenic lines and pyramided lines carrying resistance genes to green rice leafhopper (Nephotettix cincticeps Uhler) with the Taichung 65 genetic background in rice (*Oryza sativa* L.). *Breeding Science,* 60: 18–27.

Fukuoka, S. and Okuno, K. (2001). QTL analysis and mapping of *Pi21,* a recessive gene for field resistance to rice blast in Japanese upland rice. *Theoretical and Applied Genetics,* 103: 185-190.

Fukuoka, S., Yamamoto, S., Mizobuchi, R., Yamanouchi, U., Ono, K., Kitazawa, N., Yasuda, N., Fujita, Y., Nguyen, T.T.T., Koizumi, S., Sugimoto, K., Matsumoto, T. and Yano, M. (2013). Multiple functional polymorphisms in a single disease resistance gene in rice enhance durable resistance to blast. *Scientific Reports,* 4: 45-50.

Fukuta, Y., Yanoria, M.J.T., Mercado-Escueta, D., Ebron, L.A., Fujita, Y., Araki, E., Khush, G.S. (2004). Quantitative trait loci (QTL) reactions to rice blast isolates from Japan and the Philippines. In: Kawasaki S (ed) *Rice blast: interaction with rice and control* (pp. 113–121). Kluwer, Dordrecht.

Gao, L.Z., Zhang, C.H., Chang, L.P., Ji, J.Z., Qiu, Z.E. and Dong, Y.S. (2005). Microsatellite diversity within *Oryza sativa* with emphasis on *indica-japonica* divergence. *Genetics Research,* 85: 1-14.

Gao, X., Liu, H., Wang, H., Fu, S., Guo, Z. and Liang, G. (2013). Southern most Asia is the source of Japanese encephalitis virus (genotype 1) diversity from which the viruses disperse and evolve throughout Asia. *PLOS Neglected Tropical Diseases,* 7: e2459.

Garris, J., Thomas, H.T., Coburn, J., Kresovich, S. and McCouch, S. (2005). Genetic structure and diversity in *Oryza sativa* L. *Genetics Society of America,* 169: 1631-1638.

Ghee-Thean, L., Ismail, M.M. and Harron, M. (2012). Measuring technical efficiency of malaysian paddy farming: An application of stochastic production frontier approach. *Journal of Applied Science,* 12: 1602-1607.

Ghislain, M., Spooner, D.M., Rodrı´guez, F., Villamo´n, F., Nu´n˜ez, J., Va´squez. C et al. (2004). Selection of highly informative and user-friendly microsatellites (SSRs) for genotyping of cultivated potato. *Theoretical and Applied Genetics,* 108: 881–890.

Gopalakrishnan, S., Sharma, R.K., Rajkumar, K.A., Joseph, M., Singh, V.P., Singh, A.K., Bhat, K.V., Singh, N.K. and Mohapatra, T. (2008). Integrating marker assisted background analysis with foreground selection for identification of superior bacterial blight resistant recombinants in Basmati rice. *Plant Breeding,* 127: 131-139.

Goto, I. (1970). Genetic sutudies on the resistance of rice plant to the blast fungus. I. Inheritance of resistance in crosses Sensho x H-79 and Imochishirazu x H-79. *Annual Phytopathology Society Japan,* 36: 304-312.

Goto, I. (1988). Genetic studies on resistance of rice plant to blast fungus (VII). Blast resistance genes of Kuroka. *Annual Phytopathology Society Japan,* 54: 460–465.

Goto, I., Jaw, Y.L. and Baluch, A.A. (1981). Genetic studies on resistance of rice plant to blast fungus IV. Linkage analysis of four genes, *Pi-a, Pi-k, Pi-z* and *Pi-i. Annual Phytopathology Society Japan,* 47: 252–254.

Gouda, P.K., Saikumar, S., Varma, C.M.K., Nagesh, K., Thippeswamy, S., Shenoy, V., Ramesha, M.S. and Shashidhar, H.E. (2013). Marker-assisted breeding of *Pi-1* and *Piz-5* genes imparting resistance to rice blast in PRR78, restorer line of Pusa RH-10 Basmati rice hybrid. *Plant Breeding,* 132: 61–69.

Gowda, M., Barman-Roy, S. and Chatoo, B.B. (2006). Molecular mapping of a novel blast resistance gene *Pi38* in rice using SSLP and AFLP markers. *Plant Breeding,* 125: 596–599.

Gregorio, G.B., Aliyu, R., Adamu, A.K., Muazu, S. and Alonge, S.O. (2010). Tagging and validation of SSR markers to salinity tolerance QTLs in rice (*Oryza spp*). *International conference on biology, environment and chemistry, 1*(pp.328-332), IACSIT Press, Singapore.

Gu, Y.Q., Coleman-Derr, D., Kong, X. and Anderson, O.D. (2004). Rapid genome evolution revealed by comparative sequence analysis of orthologous regions from four Triticeae genomes. *Plant Physiology,* 135: 459-470.

Guimara˜es, E. P. and Correa-Victoria, F. (2000). Use of recurrent selection for develop resistance Pyricularria grisea Sacc. On rice. In: Guimara˜es EP (ed) *Advances in rice population improvement* (pp. 165–175). Embrapa Rice and Beans, Santo Antonio de Goias.

Guo, S., Wei, Y., Li, X., Liu, K., Huang, F., Chen, C. and Gao, G. (2013). Development and Identification of Introgression Lines from Cross of *Oryza sativa* and *Oryza minuta*. *Rice Science,* 20: 95−102.

Hadzim, K., Ajimilah, N.H., Othman, O., Arasu, N.T., Latifah, A. and Saad, A. (1988). Mutant Mahsuri: Baka untuk beras bermutu. *Teknology Padi,* 4: 7–13.

Hamer, J.E., Howard, R.J., Chumley, F.G. and Valent, B. (1988). A mechanism for surface attachment in spores of a plant pathogenic fungus. *Science,* 239: 288-290.

Hari Y., Rao, K.S., Viraktamath, B.C., Prasad, A.S.H., Laha, G.S., Ahmed, M.I., Kumar, P.N., Sujatha, K., Prasad, M.S., Pandey, M., Ramesha, M.S., Neeraja, C.N., Balachandran, S.M., Rani, N.S., Kemparaju, B., Mohan, K.M., Sama, V.S.A.K., Shaik, H., Balachiranjeevi, C., Pranathi, K., Reddy, G.A., Madhav, M.S. and Sundaram, R.M. (2013). Marker-assisted introgression of bacterial blight and blast resistance into IR58025B, an elite maintainer line of rice. *Plant Breeding,* 132: 586–594.

Hashimoto, N., Higuchi, K., Koiwa, M., Yasuda, K. and Daigen, M. (1998). Selection of individual having Pi-z, the rice blast true resistance gene, using RFLP markers in resistance sensitive cross progeny. *Breeding Science, 48*(Suppl. 2): 109.

Hayashi, K., Hashimoto, N., Daigen, M. and Ashikawa, I. (2004). Development of PCR-based SNP markers for rice blast resistance genes at the *Piz* locus. *Theoretical and Applied Genetics,* 108: 1212–1220.

Hayashi, K., Yoshida, H. and Ashikawa, I. (2006). Development of PCR-based allele-specific and InDel marker sets for nine rice blast resistance genes. *Theoretical Applied Genetics,* 113: 251–260.

He, Z., Deng, Y., Xu, J., Chen, H. and Zhu, X. (2007). Functional and evolutionary of the broad spectrum resistance locus *Pigm(t)* to rice blast Magnaporthe oryzae. *In Proceeding of the 4th Int'l Rice Blast Conference,* pp. 31.

He, Z.H. and Shen, Z.T. (1990). Studies on blast resistance genes in indica rice. *International Rice Research Newsletter*, 15: 4.

Hirabayashi, H., Sato, H., Nonoue, Y., Kuno-Takemoto, Y., Takeuchi, Y., Kato, H., Nemoto, H., Ogawa, T., Yano, M., Imbe, T. and Ando, I. (2010). Development of introgression lines derived from *Oryza rufipogon* and *O. glumaepatula* in the genetic background of japonica cultivated rice (*O. sativa* L.) and evaluation of resistance to rice blast. *Breeding Science,* 60: 604–612.

Hittalmani, S., Parco, A., Mew, T.V., Zeigler, R.S. and Huang, N. (2000). Fine mapping and DNA marker-assisted pyramiding of the three major genes for blast resistance in rice. *Theoretical and Applied Genetics*, 100: 1121–1128.

Hospital, F. (2005). Selection in backcross programme. *Philosophical Transactions of the Royal Society,* 360: 1503 –1511.

Hospital, F. and Charcosset, A. (1997). Marker assisted introgression of quantitative trait loci. *Genetics,* 147: 1469-1485.

Hospital, F. and Decoux, G. (2002). Popmin: a program for the numerical optimization of population sizes in marker-assisted backcross programs. *Journal of Heredity,* 93: 383-384.

Hospital, F., Chevalet, C. and Mulsant, P. (1992). Using markers in gene introgression breeding programs. *Genetics*, 132: 1119-1120.

Hossain, M.B., Islam, M.O. and Hasanuzzaman, M. (2008). Influence of different nitrogen levels on the performance of four aromatic rice varieties. *International Journal of Agriculture Biology,* 10: 693-696.

Hua, L., Wu, J., Chen, C., Wu, W., He, X., Lin, F., Wang, L., Ashikawa, I., Matsumoto, T., Wang, L. and Pan, Q. (2012). The isolation of *Pi1*, an allele at the *Pik* locus which confers broad spectrum resistance to rice blast, *Theoretical and Applied Genetics,* 125: 1047–1055.

Huyen, L.T., Luu, N., Cuc, M., Ismail, A. M. and Ham, Le H. (2012). Introgression the salinity tolerance QTLs Saltol into AS996, the elite rice variety of Vietnam. *American Journal of Plant Sciences,* 3: 981-987.

Ibrahim, M.N., Talab, K.T., Spotar, S., Kharidah, M. and Rosnita, A.T. (2013). Desorption isotherm model for a Malaysian rough rice rariety (MR219). *Pertanika Journal of Tropical Agricultural Science,* 36: 189 – 198.

Iftekharudaula, K.M. (2008). *Comparison of new selection strategies or marker assisted backcrossing for a submergence tolerant gene in rice*. Doctoral dissertation. Bangladesh Agricultural University, Mymensingh, Bangladesh, 1-205.

Iftekharuddaula, K.M., Salam, M.A., Newaz, M.A., Ahmed, H.U., Collard, B.C.Y., Septiningsih, E.M., Sanchez, D.L., Pamplona, A.M. and Mackill, D.J. (2012). Comparison of phenotypic versus marker-assisted background selection for the SUB1 QTL during backcrossing in rice. *Breeding Science*, 62: 216–222.

Imbe, T. and Matsumoto, S. (1985). Inheritance of resistance of rice varieties to the blast fungus strains virulent to the variety ‘‘Reiho’’. *Japanese Journal of Breeding*, 35: 332–339.

Imbe, T., Yanoria, M.J. and Tsunematsu, H. (1997). A new gene for blast resistance in rice variety, IR24. *Rice Genetics Newsletter*, 14: 60-62.

Inukai, T., Nelson, R.J., Zeigler, R.S., Sarkarung, S., Mackill, D.J., Bonman, J.M., Takamure, I. and Kinoshita, T. (1994). Allelism of blast resistance genes in near-isogenic lines of rice. *Phytopathology*, 84: 1278-1283.

Inukai, T., Zeigler, R.S., Sarkarung, S., Bronson, M., Dung, L.V., Kinoshita, T. and Nelson, R.J. (1996b). Development of pre-isogenic lines for rice blast-resistance by marker-aided selection from a recombinant inbred population. *Theoretical and Applied Genetics*, 93: 560-567.

IRRI. (1996). Standard Evaluation System for Rice. 4th edn. *The International Network for Genetic Evaluation of Rice* (pp. 52). Genetic Resources Center. International Rice Research Institute, Manila.

Ise, K. (1991). Linkage analysis of some blast resistance gene in rice, *Oryza sativa* L. *Japanese Journal of Breeding*, 42(Suppl. 2): 388–389.

Jeger, M.J., Pautasso, M., Holdenrieder, O., Shaw, M.W. (2007). Modelling disease spread and control in networks: implications for plant sciences. *New Phytology*, 174: 279–297.

Jena, K. K. and Mackill, D.J. (2008). Molecular markers and their use in marker-assisted selection in rice. *Crop Science*, 48: 1266-1276.

Jeon, J.S., Chen, D., Yi, G.H., Wang, G.L. and Ronald, P.C. (2003). Genetic and physical mapping of *Pi5(t)*, a locus associated with broad spectrum resistance to rice blast. *Molecular Genetics and Genomics*, 269: 280–289.

Jeung, J., Kim, B., Cho, Y., Han, S., Moon, H., Lee, Y. and Jena, K. (2007). A novel gene, *Pi40(t)*, linked to the DNA markers derived from NBS-LRR motifs confers broad spectrum of blast resistance in rice. *Theoretical and Applied Genetics*, 115: 1163–1177.

Jia, Y. (2009). Artificial introgression of a large chromosome fragment around the rice blast resistance gene Pi-ta in backcross progeny and several elite rice varieties. *Heredity*, 103: 333–339.

Jia, Y., Bryan, G.T., Farrall, L. and Valent, B. (2003). Natural variation at the *Pi-ta* rice blast resistance locus. *Phytopathology,* 93: 1452-1459.

Jiang, G.H., Xu, C.G., Tu, J.M., Li, X.H., He, Y.Q. and Zhang, Q.F. (2004). Pyramiding of insect-and disease-resistance genes into an elite *indica*, cytoplasm male sterile restorer line of rice, 'Minghui 63.' *Plant Breeding,* 123: 112-116.

Joseph, M., Gopalakrishnan, S., Sharma, R.K., Singh, A.K., Singh, V.P., Singh, N.K. and Mohapatra, T. (2004). Combining bacterial blight resistance and Basmati quality characteristics by phenotypic and molecular marker assisted selection in rice. *Molecular Breeding,* 13: 377-387.

Kankanala, P., Czymmek, K. and Valent, B. (2007). Roles for rice membrane dynamics and plasmodesmata during biotrophic invasion by the blast fungus. *Plant Cell,* 19: 706–724.

Khanh, T.D., Linh, L.H., Linh, T.H., Ham, L.H. and Xuan, T.D. (2013). Rapid and high-precision marker assisted backcrossing to introgress the SUB1 QTL into the Vietnamese elite rice variety. *Journal of Plant Breeding and Crop Science,* 5: 26-33.

Khush, G.S. (1989). Multiple disease and insect resistance for increased yield stability in rice. In: Progress in irrigated rice research (pp.79–92). International Rice Research Institute, Manila, Philippines.

Khush, G.S. (2005). What it will take to feed 5.0 billion rice consumers in 2030. *Plant Molecular Biology,* 59: 1–6.

Khush, G.S. (2013). Strategies for increasing the yield potential of cereals: case of rice as an example. *Plant Breeding,* 132: 433–436.

Khush, G.S. and Jena, K.K. (2009). Current status and future prospects for research on blast resistance in rice (*Oryza sativa* L.), In: Wang GL, Valent B (eds) *Advances in genetics, genomics and control of rice blast disease* (pp. 1-10). Springer, Dordrecht.

Kingsolver, C.H., Barksdale, T.H. and Marchetti, M.A. (1984). Rice Blast Epidemiology. *Bulletin of the Pennsylvania Agricultural Experiment Station,* 853: 1-33.

Kinoshita, T. and Kiyosawa, S. (1997). Some considerations on linkage relationships between *Pii* and *Piz* in the blast resistance of rice. *Rice Genetics Newsletter,* 14: 57–59.

Kiyosawa, S. (1967). The inheritance of resistance of the Zenith type varieties of rice to the blast fungus. *Japanese Journal of Breeding,* 17: 99-107.

Kiyosawa, S. (1972). The inheritance of blast resistance transferred from some *indica* varieties of rice. *Bulletin of the National Institute of Agricultural Sciences,* 23: 69-95.

Kiyosawa, S. (1982). Gene analysis for blast resistance. *Oryza,* 18: 196–203.

Koide, Y., Kobayashi, N., Xu, D. and Fukuta, Y. (2009). Resistance genes and DNA selection markers for blast disease in rice *Oryza sativa* L. *Japan Agricultral Researc Quarterly,* 43: 255-280.

Koizumi, S. (2007). Durability of resistance to rice blast disease. *JIRCAS Working Report,* 53: 1–10.

Korinsaka, S., Sirithunyab, P., Meakwatanakarnd, P., Sarkarunge, S., Vanavichitc, A., Toojindaa, T. (2011). Changing allele frequencies associated with specific resistance genes to leaf blast in backcross introgression lines of Khao Dawk Mali 105 developed from a conventional selection program. *Field Crops Research,* 122: 32–39.

Kou, Y. and Wang, S. (2012). Toward an understanding of the molecular basis of quantitative disease resistance in rice. *Journal of Biotechnology,* 159: 283-290.

Kumar, M., Mishra, G.P., Singh, R., Kumar, J., Naik, P.K. and Singh, S.B. (2009). Correspondence of ISSR and RAPD markers for comparative analysis of genetic diversity among different apricot genotypes from cold arid deserts of trans-Himalayas. *Physiology and Molecular Biology of Plant,* 15: 225‑235.

Kumbhar, S.D., Kulwal, P.L., Patil, J.V., Gaikwad, A.P. and Jadhav, A.S. (2013). Inheritance of blast resistance and identification of SSR marker associated with it in rice variety RDN 98-2. *Journal of Genetics*, 92: 317-321.

Latif, M.A., Badsha, M.A., Tajul, M.I., Kabir, M.S., Rafii, M.Y. and Mia, M.A.T. (2011a). Identification of genotypes resistant to blast, bacterial leaf blight, sheath blight and tungro and efficacy of seed treating fungicides against blast disease of rice. *Scientific Research Essays,* 6: 2804–2811.

Latif, M.A., Rafii, M.Y., Rahman, M.M. and Talukdar, M.R.B. (2011b). Microsatellite and minisatellite markers based DNA fingerprinting and genetic diversity of blast and ufra resistant genotypes. *Comptes Rendus Biologies,* 334: 282–289.

Lee, Y.H. and Dean, R.A. (1993). cAMP regulates infection structure formation in the plant pathogenic fungus *Magnaporthe grisea*. *Plant Cell*, 5: 693–700.

Lei, C., Wu, J., Ling, Z., Zhuang, J., Wang, J., Zheng, K. and Wan, J. (2006). Research progress on rice blast disease and resistance breeding in China. *A differential system for blast resistance for stable rice production environment*. Japan International Research Center for Agricultural Sciences (JIRCAS), Japan, working report No. 53.

Lei, C.L., Huang, D.Y., Li, W., Wang, J.L., Liu, Z.L., Wang, X.T., Shi, K., Cheng, Z.J., Zhang, X., Ling, Z.Z. and Wan, J.M. (2005). Molecular mapping of a blast resistance gene in an *indica* rice variety Yanxian No. 1. *Rice Genetics Newsletter,* 22: 76–77.

Lewis, R.S. and Kernodle, S.P. (2009). A method for accelerated trait conversion in plant breeding. *Theoretical and Applied Genetics,* 118: 1499-1508.

Li, D., XuXu, M. H., YaoYao, C.X. and Long, S.Q. (2008). SSR identification of rice blast resistance gene *Pi-d(t)* in the core germplasm of Yunnan indigenous rice varieties. *Southwest China Journal of Agricultural Sciences,* 21: 1583-1586.

Li, Y.B., Wu, C.J., Jiang, G.H., Wang, L.Q. and He, Y.Q. (2007). Dynamic analyses of rice blast resistance for the assessment of genetic and environmental effects. *Plant Breeding,* 126: 541–547.

Lin, F., Chen, S., Que, Z.Q., Wang, L., Liu, X.Q. and Pan, Q.H. (2007). The blast resistance gene *Pi37* encodes a nucleotide binding site-leucine rich repeat protein and is a member of a resistance gene cluster on rice chromosome 1. *Genetics,* 177: 1871–1880.

Linh, L.H., Linh, T.H., Xuan, T.D., Ham, L.H., Ismail, A.M., Khanh, T.D. (2012). Molecular breeding to improve salt tolerance of rice (*Oryza sativa* L.) in the Red River Delta of Vietnam. *International Journal of Plant Genomics,* 1-9.

Litt, M., and Lutty, J.A. (1989). A hypervariable microsatellite revealed by in vitro amplication of a dinucleotide repeat within the cardiac muscle actin gene. *Americam Journal of Human Genetics,* 44: 397–401.

Liu, B., Zhang, S., Zhu, X., Yang, Q., Wu, S., Mei, M., Mauleon, R., Leach, J., Mew, T., Leung, H. (2004). Candidate defense genes as predictors of quantitative blast resistance in rice. *Molecular Plant Microbe Interaction,* 17: 1146–1152.

Liu, G., Lu, G., Zeng, L. and Wang, G.L. (2002). Two broad-spectrum blast resistance genes, *Pi9(t)* and *Pi2(t),* are physically linked on rice chromosome 6. *Molecular Gene and Genomics,* 267: 472‑480.

Liu, J., Wang, X., Mitchell, T., Hu, Y., Liu, X., Dai, L. and Wang, G.L. (2010). Recent progress and understanding of the molecular mechanisms of the rice-*Magnaporthe oryzae* interaction. *Molecular Plant Pathology*, 11: 419-427.

Liu, S.P., Li, X., Wang, C.Y., Li, X.H. and He, Y.Q. (2003). Improvement of resistance to rice blast in Zhenshan 97 by molecular marker aided selection. *Acta Botanica Sinica*, 45: 1346-1350.

Liu, W.G., Jin, S. J., Zhu, X.Y., Wang, F., Li, J.H., Liu, Z.R., Liao, Y.L., Zhu, M.S., Huang, H.J. and Liu, Y.B. (2008). Improving blast resistance of a thermo-sensitive genic male sterile rice line GD-8S by molecular marker-assisted selection. *Rice Science*, 15: 179-185.

Liu, X., yang, Q., Lin, F., Hua, L., Wang, C., Wang, L. and Pan, Q. (2007). Identification and fine mapping of *Pi39(t)*, a major gene conferring the broad-spectrum resistance to Magnaporthe oryzae. *Molecular Genetics and Genomics*, 278: 403-410.

Liu, X.Q., Wang, L., Chen, S., Lin, F. and Pan, Q.H. (2005). Genetic and physical mapping of *Pi36(t)*, a novel rice blast resistance gene located on rice chromosome 8. *Molecular Gene Genetics*, 274: 394–401.

Lopez-Gerena, L. (2006). *Mapping QTL Controlling Durable Resistance to Rice Blast in Variety Oryza llanos 5*. Doctoral dissertation, Kansas State University, Manhattan, KS, USA.

Luo, K., Huang, S.Y., Wang, G.P. and Wan, W.J. (1985). Genetic analysis of the resistance of the rice varieties Zenlong 13 and Zhaiyeqing 8 to *Pyricularia oryzae. Acta Phytopathology Sinica*, 15: 115-119.

Mackill, D.J. (2007). Molecular markers and marker-assisted selection in rice. *Genomics assisted crop improvement*, 2: 147–168.

Mackill, D.J. and Bonman, J.M. (1992). Inheritance of blast resistance in near-isogenic lines of rice. *Phytopathology*, 82: 746-749.

Mackill, D.J. and Ni, J.J. (2001). Molecular mapping and marker-assisted selection for major-gene traits in rice. In: Khush GS, Brar DS, Hardy B (eds) Rice genetics IV (pp. 137–151). Science Publishers, New Delhi.

Mackill, D.J., Bonman, J.M., Suh, H.S. and Srilingam, R. (1985). Genes for resistance to Philippine isolates of the rice blast pathogen. *Rice Genetics Newsletter*, 2: 80-81.

Maheshwari, R. and Sharma, I.R. (2013). Soil status in relation to blast disease in bundi district of Rajasthan, India. *International Journal of Pure and Applied Bioscience*, 1: 13-19.

Manibhushan, R.K. (1994). Rice Blast Disease. 1st Ed., Daya Publishing House, Delhi.

MARDI (2002). MR219, A new high yielding rice variety with yields of more than 10 t/ ha. MARDI Publisher.

Matsuo, T., Futsuhara, Y., Kikuchi, F. and Yamaguchi, H. (1997). Science of the rice plant. In: Matsuo T, Futsuhara Y, Kikuchi F, Yamaguchi H (eds) *Food and Agriculture Policy Research Center*, Tokyo.

Mazid, M.Z., Rafii, M.Y., Hanafi, M.M., Rahim, H.A. and Latif, M.A. (2013). Agro-morphological characterization and assessment of variability, heritability, genetic advance and divergence in bacterial blight resistant rice genotype. *South African Journal of Botany*, 86: 15-22.

Marzukhi, H., Ali, A.H. and Hassan, S. (1991). Kehadiran penyakit baru padi di estet padi Seberang Perak. *Teknologi Padi*, 7: 49–52.

McCouch, S.R., Sweeney, M., Li, J., Jiang, H., Thomson, M., Septiningsih, E., Edwards, J., Moncada, P., Xiao, J., Garris, A., Tai, T., Martinez, C., Tohme, J., Sugiono, M., McClung, A., Yuan, L.P., Ahn, S. N. (2007). Through the genetic bottleneck: *O. rufipogon* as a source of trait-enhancing alleles for *O. sativa*. *Euphytica*, 154: 317-339.

McCouch, S.R., Teytelman, L., Xu, Y., Lobos, K.B., Clare, K., Walton, M., Fu, B., Maghirang, R., Li, Z., Xing, Y., Zhang, Q., Kono, I., Yano, M., Fjellstrom, R., DeClerck, G., Schneider, D., Cartinhour, S., Ware, D. and Stein, L. (2002). Development of 2240 new SSR markers for rice. *DNA Research*, 9: 199–220.

Mehta, Y.R. and Baier, A. (1998). Variação patogênica entre isolados de *Magnaporthe grisea* atacando triticale 332 e trigo no estado do Paraná. *Summa Phytopathology*, 24: 119-125.

Miah, G., Rafii, M.Y., Ismail M.R., Puteh, A.B., Rahim, H.A., Asfaliza, R. and Latif, M.A. (2013). Blast resistance in rice: A review of conventional breeding to molecular approaches. *Molecular Biology Reports*, 40: 2369‑2388.

Miah, G., Rafii, M.Y., Ismail, M.R., Puteh, A.B., Rahim, H.A., Islam, K.N. and Latif, M.A. (2013b). A review of microsatellite markers and their applications in rice breeding programs to improve blast disease resistance. *International Journal of Molecular Sciences*, 14: 22499-22528.

Ministry of Agriculture and Agro-based Industry Malaysia, (2011). *Agricultural Statistical Handbook 2010*. Ministry of Agriculture and Agro-based Industry Malaysia, Malaysia.

Mohamad, O., Abdullah, M.Z. and Rahman, M.A. (2005). Molecular markers as a breeding tool in rice breeding: new paradigms and opportunities. In : *Proceedings of the 6th National Congress on Genetics*, Genetics Society of Malaysia, Kuala Lumpur, Malaysia.

Mohamad, O., Nazir, B. M., Alias, I., Azlan, S., Rahim, H. A., Abdullah, M. Z., Othman, O., Hadzim, K., Saad, A., Habibuddin, H. and Golam, F. (2006). Development of improved rice varieties through the use of induced mutations in Malaysia. *Plant Mutation Report,* 1: 27–33.

Mohammadi, S.A. and Prasanna, B.M. (2003). Analysis of genetic diversity in crop plants - salient statistical tools and considerations. *Crop Science,* 43: 1235-1248.

Mohanty, C.R. and Gangopadhyay, S. (1982). Testing of blast resistance in F2 rice seedlings in different doses of nitrogen and seasons. *Annals Phytopathological Society of Japan*, 48: 648-658.

Mondal, U., Khanom, M.S.R., Hassan, L. and Begum, S.N. (2013). Foreground selection through SSRs markers for the development of salt tolerant rice variety. *Journal of Bangladesh Agricultural University*, 11: 67–72.

Morgante, M., Hanafey, M. and Powell, W. (2002). Microsatellites are preferentially associated with nonrepetitive DNA in plant genomes. *Nature Genetics,* 30: 194-200.

Nakamura, S., Asakawa, S., Ohmido, N., Fukui, K., Shimizu, N. and Kawasaki, S. (1997). Construction of an 800-kb contig in the nearcentromeric region of the rice blast resistance gene *Pi-ta2* using a highly representive rice BAC library. *Molecular Gene Genetics,* 254: 611–620.

Naqvi, N.I. and Chattoo, B.B. (1996). Molecular genetic analysis and sequence characterized amplified region-assisted selection of blast resistance in rice. In: Khush GS (ed) Rice genetics III (pp. 570–576). *Proceeding of the third international rice genetics symposium*. International Rice Research Institute, Manila, Philippines.

Narayanan, N.N., Baisakh, N., Vera Cruz, C.M., Gnanamanickam, S.S., Datta, K., Datta, S.K. (2002). Molecular breeding for the development of blast and bacterial blight resistance in rice cv. IR50. *Crop Science,* 42: 2072–2079.

Neeraja, C., Maghirang-Rodriguez, R., Pamplona, A., Heuer, S., Collard, B., Septiningsih, E. et al. (2007). A marker-assisted backcross approach for developing submergence-tolerance rice varieties. *Theoretical and Applied Genetics*, 115: 767 –76.

Nguyen, T.T., Koizumi, S., La, T.N., Zenbayashi, K.S., Ashizawa, T., Yasuda, N., Imazaki, I. and Miyasaka, A. (2006). *Pi35(t),* a new gene conferring partial resistance to leaf blast in the rice variety Hokkai 188. *Theoretical and Applied Genetics*, 113: 697–704.

NEKA MARDI. (2012). Breeding and improvement of MARDI fragrant rice varieties (MRQ74 and MRQ76) against blast and brown plant hopper. http://nkea.mardi.gov.my/index.php/epp-pertanian/epp/44-sub-epp9-breeding-and-improvement-of-mardi-fragrant-rice-varieties-mrq-74-and-mrq-76-againsts-blast-and-brown-plant-hopper-bph.

Nordin, M.S., Ariffin, Z., Jajuli, R., Abdullah, W.D.W. and Denis M.G. (2007). Country report on The State of Plant Genetic Resources For Food and Agriculture in Malaysia (1997-2007), 19.

Oliveira, E.J., Padua, J.G., Zucchi, M.I., Vencovsky, R. and Vieira, M. L. C. (2006). Origin, evolution and genome distribution of microsatellites. *Genetics and Molecular Biology,* 29: 294–307.

Olufowote, J.O., Xu, Y., Chen, X., Park, W.D., Beachell, H.M., Dilday, R.H., Goto, M. and McCouch, S.R. (1997). Comparative evaluation of within-variety variation of rice (*Oryza sativa* L.) using microsatellite and RFLP markers. *Genome,* 38: 1170–1176.

Ou, S.H. and Jennings, P.R. (1969). Progress in the development of disease-resistant rice. *Annual Review of Phytopathology,* 7: 383–410.

Padmanabhan, S.Y., Mathur, S.C. and Mishra, R.K. (1974). Breeding for blast resistance in India. *Indian Journal of Genetics*, 34A: 424-429.

Padmavathi, G., Ram, T., Satyanarayana, K. and Mishra, B. (2005). Identification of blast (*Magnaporthe grisea*) resistance genes in rice. *Current Science,* 88: 628-630.

Pan, Q., Wang, L., Ikehashi, H., Taniska, T. (1996). Identification of a new blast resistance gene in the indica rice variety Kasalath using Japanese differential varieties and isozyme markers. *Phytopathology,* 86: 1071–1075.

Pan, Q.H., Hu, Z.D., Tanisaka, T. and Wang, L. (2003). Fine mapping of the blast resistance gene *Pi15,* linked to *Pii* on rice chromosome 9. *Acta Botanica Sinica,* 45: 871–877.

Pan, Q.H., Tanisaka, T. and Ikehashi, H. (1997). Studies on the genetics and breeding of blast resistance in rice VII. Gene analysis for the blast resistance of Indian native variety, Aus 373. *Breed Science, 47*(Suppl. 1): 35.

Powell, W., Machray, G.C. and Provan, J. (1996). Polymorphism revealed by simple sequence repeats. *Trends in Plant Sciences,* 1: 215–222.

Prabhu, A.S., de Castro, E.M., de Araujo, L.G. and Berni, R.F. (2003). Resistance spectra of six elite breeding lines of upland rice to *Pyricularia grisea. Pesquisa Agropecuária Brasileira,* 38: 203-210.

Prabhu, A.S., Filippi, M.C. and Zimmermann, F.J.P. (1996) Genetic control of blast in relation to nitrogen fertilization in upland rice. *Pesquisa Agropecuária Brasileira,* 31: 339-347.

Prigge, V., Maurer, H.P., Mackill, D.J., Melchinger, A.E. and Frisch, M. (2008). Comparison of the observed with the simulated distributions of the parental genome contribution in two marker-assisted backcross programs in rice. *Theoretical and Applied Genetics*, 116: 739–744.

Qu, S., Liu, G., Zhou, B., Bellizzi, M. and Zeng, L. et al. (2006). The broad-spectrum blast resistance gene pi9 encodes a nucleotide-binding site-leucine-rich repeat protein and is a member of a multigene family in rice. *Genetics,* 172: 1901–1914.

Rafii, M.Y., Zakiiah, M.Z., Asfaliza, R., Iffah Hanifaa, M.D., Latif, M.A. and Malek, M.A. (2014). Grain quality performance and heritability estimation in selected F1 rice genotypes. *Sains Malaysiana,* 43(1): 1-7.

Ragimekula, N., Varadarajula, N.N., Mallapuram, S.P., Gangimeni, G., Reddy, R.K. and Kondreddy, H.R. (2013). Marker assisted selection in disease resistance breeding. *Journal of Plant Breeding and Genetics,* 1: 90-109.

Rahim, H. A., Zarifth, S. K., Bhuiyan, M.A.R, Narimah, M.K., Wickneswari, R., Abdullah, M.Z, Anna, L.P.K, Sobri, H., Rusli and Khairuddin, A.R. (2012). Evaluation and characterization of advanced rice mutant line of rice (*Oryza sativa*), MR219-4 and MR219-9 under drought condition. *Research and Development seminar 26-28 September 2012,* 44: 1-15.

Rahim, H.A., Bhuiyan, M.A.R., Saad, A., Azhar, M. and Wickneswari, R. (2013). Identification of virulent pathotypes causing rice blast disease (*Magnaporthe oryzae*) and study on single nuclear gene inheritance of blast resistance in F_2 population derived from Pongsu Seribu 2 × Mahshuri. *Australian Journal of Crop Science*, 7: 1597-1605.

Rai, A.K., Kumar, S.P., Gupta, S.K., Gautam, N., Singh, N.K. and Sharma, T.R. (2011). Functional complementation of rice blast resistance gene *Pi-kh(Pi54)* conferring resistance to diverse strains of *Magnaporthe oryzae*. *Journal of Plant Biochemistry and Biotechnology,* 20: 55–65.

Rajpurohit, D., Kumar, R., Kumar, M., Paul, P., Awasthi, A.A., Basha, P.O., Puri, A., Jhang, T., Singh, K. and Dhaliwal, H.S. (2011). Pyramiding of two bacterial blight resistance and a semi dwarfing gene in Type 3 Basmati using marker-assisted selection. *Euphytica,* 178: 111–126.

Ramkumar, G., Sivaranjani, A.K.P., Pandey, M.K., Sakthivel, K., Shobha Rani, N., Sudarshan, I., Prasad, G.S.V., Neeraja, C.N., Sundaram, R.M., Viraktamath, B.C. and Madhav, M.S. (2010). Development of a PCR-based SNP marker system for effective selection of kernel length and kernel elongation in rice. *Molecular Breeding,* 26: 735–740.

Rathour, R., Chopra, M. and Sharma, T.R. (2008). Development and validation of microsatellite markers linked to the rice blast resistance gene *Pi-z* of Fukunishiki and Zenith. *Euphytica*, 163: 275–282.

Razak, A.A., Zainudin, N.A.I.M., Sidiqe, S.N.M., Ismail, N.A., Mohamad, N.M.I.N. and Salleh, B. (2009). Sheath brown rot disease of rice caused by *Pseudomonas fuscovaginae* in the Peninsular Malaysia. *Journal of Plant Protection Research,* 49 (3): 244-249.

Ribaut, J.M., Jiang, C. and Hoisington, D, (2002b). Simulation experiments on efficiencies of gene introgression by backcrossing. *Crop Science,* 42: 557-565.

Ribot, C., Hirsch, J., Balzergue, S., Tharreau, D., Notteghem, J.H., Lebrun, M.H. and Morel, J.B. (2008). Susceptibility of rice to the blast fungus, *Magnaporthe grisea*. *Journal of Plant Physiology,* 165: 114-24.

Rohlf, F. (2002). *NTSYS-pc: Numerical Taxonomy and Multivariate Analysis System, 2*. 1st ed. Department of Ecology and Evolution, State University of NY, Stony Brook.

Sabu, K.K., Abdullah, M.Z., Lim, L.S., Wickneswari, R. (2006). Development and evaluation of advanced backcross families of rice for agronomically important traits. *Communications in Biometry and Crop Science,* 1: 111–123.

Saad, A. and Habibuddin, H. (2010). Pathotypes and virulence of *Xanthomonas oryzae* causing bacterial blight disease of rice in Peninsular Malaysia. *Journal of Tropical Agriculture and Food. Science,* 38(2): 257– 266.

Salem, A.H., Abdel-Sayyed, S.M. and Shatta, M.A. (1983). Gene effects and selection efficiency of leaf blast resistance in the rice cross Yabani (15) X PI (1). *Annual Agricultural Science,* 28: 1575-1592.

Salina, E., Dobrovolskaya, O., Efremova, T., Leonova, I., Roder, M.S. (2003). Microsatellite monitoring of recombination around the *Vrn-B1* locus of wheat during early backcross breeding. *Plant Breeding,* 122: 116–119.

Sallaud, C., Lorieux. M., Roumen, E., Tharreau, D., Berruyer, R., Svestasrani, P., Garsmeur, O., Ghesquiere, A., Notteghem, J.L. (2003). Identification of five new blast resistance genes in the highly blast-resistant rice variety IR64 using a QTL mapping strategy. *Theoretical and Applied Genetics,* 106: 794–803.

Sambrook, J. and Russell, D.W. (2001). *Molecular cloning – a laboratory manual* (3rd ed.) Cold Spring Harbour Laboratory Press, New York.

Sang, N.A., Kim, Y., Hong, H., Han, S., Kwon, S., Choi, H., Moon, H. and McCouch, S.R. (1996). Molecular mapping of a new gene for resistance to rice blast (*Pyricularia grisea* Sacc). *Euphytica*, 116: 17-22.

Scheuermann, K.K., Raimondi, J.V., Marschalek, R., de Andrade, A. and Wickert, E. (2012). *Magnaporthe oryzae* genetic diversity and its outcomes on the search for durable resistance. *Molecular Basis Plant Genetics Diversity*, 331–356.

Sellamuthu, R., Liu, G.F., Ranganathan, C.B. and Serraj, R. (2011). Genetic analysis and validation of quantitative trait loci associated with reproductive-growth traits and grain yield under drought stress in a doubled haploid line population of rice (*Oryza sativa* L.). *Field Crops Research*, 124: 46-58.

Selvaraj, C.I., Nagarajan, P., Thiyagarajan, K., Bharathi, M. and Rabindran, R. (2011). Studies on heterosis and combining ability of well known blast resistant rice genotypes with high yielding varieties of rice (*Oryza sativa* L.). *International Journal of Plant Breeding and Genetics*, 5: 111–129.

Semagn, K., Bjørnstad, Å. and Ndjiondjop, M.N. (2006). Progress and prospects of marker assisted backcrossing as a tool in crop breeding programs. *African Journal of Biotechnology*, 5: 2588-2603.

Septiningsih, E.M., Pamplona, A.M., Sanchez, D.L., Neeraja, C.N., Vergara, G.V., Heuer, S., Ismail, A.M. and Mackill, D.J. (2009). Development of submergence tolerant rice varieties: the Sub1 locus and beyond. *Annual Botany*, 103: 151–160.

Servin, B. and Hospital, F. (2002). Optimal positioning of markers to control genetic background in marker-assisted backcrossing. *Journal of Heredity*, 93: 214–217.

Sesma, A. and Osbourn, A.E. (2004). The rice blast pathogen undergoes developmental processes typical of root-infecting fungi. *Nature*, 431: 582–586.

Shang, J., Tao, Y., Chen, X., Zou, Y., Lei, C., Wan, J. and Zhu, L. (2009). Identification of a new rice blast resistance gene, *Pid3*, by genomewide comparison of paired nucleotide-binding site leucine-rich repeat genes and their pseudogene alleles between the two sequenced rice genomes. *Genetics*, 182: 1303−1311.

Shanti, M.L., Shenoy, V.V., Devi, G.L., Kumar, V.M., Premalatha, P., Kumar, G.N., Shashidhar, H.E., Zehr, U.B. and Freeman, W.H. (2010). Marker-assisted breeding for resistance to bacterial leaf blight in popular varieties and parental lines of hybrid rice. *Journal of Plant Pathology*, 92: 495–501.

Sharma, R.C., Shrestha, S.M. and Pandey, M P. (2007). Inheritance of blast resistance and associated microsatellite markers in rice variety "Laxmi. *Journal of Phytopathology*, 155: 749-753.

Sharma, T.R., Madhav, M.S., Singh, B.K., Shanker, P., Jana, T.K., Dalal, V., Pandit, A., Singh, A., Gaikwad, K., Upreti, H.C. and Singh, N.K. (2005). High resolution mapping, cloning and molecular characterization of the *Pi-kh* gene of rice, which confers resistance to *M. grisea*. *Molecular Genetics and Genomics*, 274: 569–578.

Sharma, T.R., Rai, A.K., Gupta, S.K., Vijayan, J., Devanna, B.N. and Ray, S. (2012). Rice blast management through host resistance: retrospect and prospects. *Agricultural Science*, 1: 37-52.

Shi, C., Zhu, J., Wu, J. and Fan, L. (2000). Genetic and genotype × environment interaction effect from embryo, endosperm, cytoplasm and maternal plant for rice grain shape traits of *indica* rice. *Field Crops Research*, 68: 191-198.

Shinoda, H., Toriyama, K., Yunoki, T., Ezuka, A. and Sakurai, Y. (1971). Studies on the varietal resistance of rice to blast. 6. Linkage relationship of blast resistance genes. *Bulletin Chugoku Agricultural Experiment Station Series A*, 20: 1-25.

Shu, Q. Y. (2009). Induced plant mutations in the genomics era. Food and Agriculture Organization of the United Nations, Rome, 425–427.

Shu, Q., Wu, D. and Xia, Y. (1997). The most widely cultivated rice variety 'Zhefu 802' in China and its geneology. *Mutation Breeding Newsletter*, 43: 3–5.

Siangliwa, J.L., Jongdeeb, B., Pantuwanc, G. and Toojinda, T. (2007). Developing KDML105 backcross introgression lines using marker-assisted selection for QTLs associated with drought tolerance in rice. *Science Asia*, 33: 207-214.

Singh, A., Singh, V.K., Singh, S.P., Pandian, R.T.P., Ellur, R.K., Singh, D., Bhowmick, P.K., Krishnan, S.G., Nagarajan, M., Vinod, K.K., Singh, U.D., Prabhu, K.V., Sharma, T.R., Mohapatra, T. and Singh, A.K. (2012). Molecular breeding for the development of multiple disease resistance in Basmati rice. *AoB PLANTS*, pls029.

Singh, A.K., Gopala Krishnan, S., Singh, V.P., Prabhu, K.V., Mohapatra, T., Singh, N.K., Sharma, T., Nagarajan, M., Vinod, K.K., et al. (2011). Marker Assisted Selection: a paradigm shift in Basmati breeding. *Indian Journal of Genetics*, 71: 1–9.

Singh, V. K., Singh, A., Singh, S. P., Ellur, R. K., Singh, D., Krishnan, S. G., Bhowmick, P. K., Nagarajan, M., Vinod, K.K., Singh, U.D., Mohapatra, T., Prabhu, K.V. and Singh, A.K. (2013). Marker-assisted simultaneous but stepwise backcross breeding for pyramiding blast resistance genes *Piz5* and *Pi54* into an elite Basmati rice restorer line 'PRR78'. *Plant Breeding*, 132: 486–495.

Singh, V.K., Singh, A., Singh, S.P., Ellur, R.K., Choudhary, V., Sarkel, S., Singh, D., Krishnan, S.G., Nagarajan, M., Vinod, K.K., Singh, U.D., Rathore, R., Prashanthi, S.K., Agrawal, P.K., Bhatt, J.C., Mohapatra, T., Prabhu, K.V. and Singh, A.K. (2012a). Incorporation of blast resistance into ''PRR78'', an elite Basmati rice restorer line, through marker assisted backcross breeding. *Field Crops Research,* 128: 8–16.

Skamnioti, P. and Gurr, S.J. (2009). Against the grain: safeguarding rice from rice blast disease. *Trends Biotechnology,* 27: 141–150.

Sreewongchai, T., Toojinda, T., Thanintorn, N., Kosawang, C., Vanavichit, A., Tharreau, D. and Sirithunya, P. (2010). Development of elite *indica* rice lines with wide spectrum of resistance to Thai blast isolates by pyramiding multiple resistance QTLs. *Plant Breeding,* 129: 176–180.

Srinivasachary, Hittalmani, S., Shivayogi, S., Vaishali, M.G., Shashidar, H.E. and Kumar, K.G. (2002). Genetic analysis of rice blast fungus of souther Karnataka using DNA marker and reaction of popular rice genotypes. *Current Science,* 82: 732-735.

Steele, K.A., Price, A.H, Shashidhar, H.E. and Witcombe J.R. (2006). Marker-assisted selection to introgress rice QTLs controlling root traits into an Indian upland rice variety. *Theoretical and Applied Genetics,* 112: 208–221.

Suh, J.P., Jeung, J.U., Noh, T.H., Cho, Y.C., Park, S.H., Park, H.S., Shin, M.S., Kim, C.K. and Jena, K.K. (2013). Development of breeding lines with three pyramided resistance genes that confer broad-spectrum bacterial blight resistance and their molecular analysis in rice. *Rice* , 6: 5.

Suh, J.P., Roh, J.H., Cho, Y.C., Han, S.S., Kim, Y.G. and Jena, K.K. (2009). The *Pi40* gene for durable resistance to rice blast and molecular analysis of *Pi40*-advanced backcross breeding lines. *Phytopathology,* 99: 243-250.

Suh, J.P., Yang, S.J., Jeung, J.U., Pamplona, A., Kim, J.J., Lee, J.H., Hong, H.C., Yang, C.I., Kim, Y.G. and Jena, K.K. (2011). Development of elite breeding lines conferring *Bph18* gene-derived resistance to brown planthopper (BPH) by marker-assisted selection and genome-wide background analysis in *japonica* rice (*Oryza sativa* L.). *Field Crops Research,* 120: 215–222.

Sundaram, R.M., Vishnupriya, M.R., Biradar, S.K., Laha, G.S., Reddy, G.A., ShobhaRani, N., Sarma, N.P. and Sonti, R.V. (2008). Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite *indica* rice variety. *Euphytica,* 160: 411-422.

Sundaram, R.M., Vishnupriya, M.R., Laha, G.S., ShobhaRani, N., SrinivasRao, P., Balachandaran, S.M., Reddy, G.A., Sarma, N.P., Shonti, R.V. (2009). Introduction of bacterial blight resistance into Triguna, a high yielding, mid-early duration rice variety. *Biotechnology Journal,* 4: 400-407.

Swamy, B.P.M. and Sarla, N. (2011). Meta-analysis of yield QTLs derived from inter-specific crosses of rice reveals consensus regions and candidate genes. *Plant Molecular Biology Reports*, 29(3): 663–680.

Tabien, R.E., Li, Z., Paterson, A.H., Marchetti, M.A., Stansel, J.W. and Pinson, S.R.M. (2000). Mapping of four major rice blast resistance genes from 'Lemont' and 'Teqing' and evaluation of their combinatorial effect for field resistance. *Theoretical and Applied Genetics*, 101: 1215–1225.

Takahashi, Y. (1965). Genetics of resistance to the rice blast disease. In: The Rice Blast Disease (pp. 303-329). Johns Hopkins Press, Baltimore. Maryland.

Takeuchi, Y., Ebitani, T., Yamamoto, T., Sato, H. et al. (2006). Development of isogenic lines of rice variety Koshihikari with early and late heading by marker-assisted selection. *Breeding Science*, 56: 405-413.

Tanksley SD, Young ND, Patterson AH, Bonierbale MW (1989). RFLP mapping in plant breeding: New tools for an old science. *Bio-Technology*, 7: 257-263.

TeBeest, D.O., Guerher, C. and Ditmore, M. (2007). Rice blast. *The plant health instructor. DOI:10.1094/PHI-I-2007-0313-07. Reviewed 2012*.

Temnykh, S., Park, W.D., Ayers, N. Cartinhour, S., Hauck, N., Lipovich, L., Cho, Y.G., Ishii, T. and McCouch, S.R. (2000). Mapping and genome organization of microsatellite sequences in rice (*Oryza sativa* L.). *Theoretical and Applied Genetics*, 100: 697–712.

Terashima, T., Fukuoka, S., Saka, N. and Kudo, S. (2008). Mapping of a blast field resistance gene *Pi39(t)* of elite rice strain Chubu 111. *Plant Breeding*, 127: 485–489.

Tian, F., Li, D.J., Fu, Q., Zhu, Z.F., Fu, Y.C., Wang, X.K. and Sun, C.Q. (2006). Construction of introgression lines carrying wild rice (*Oryza rufipogon* Griff.) segments in cultivated rice (*Oryza sativa* L.) background and characterization of introgressed segments associated with yield-related traits. *Theoretical and Applied Genetics*, 112: 570-580.

Tohme, J., Montenegro, M.V., Correa, F., Martinez, C., Zeigler, R.S. and Roca, W. (1993). Implications of molecular markers in breeding for Colombian lineages of rice blast. In: Proc 6th, Chiang Mai, Thailand. *Annual Meeting International Program on Rice Biotechnology*, 45: 22-24.

Toojinda, T., Tragoonrung, S., Vanavichit, A., Siangliw, J.L., Pan, N., Jantaboon, J., Siangliw, M. and Fukai, S. (2005). Molecular breeding for rainfed lowland rice in the Mekong region. *Plant Production Science*, 8: 330–333.

Torres, A. M. (2010). Application of Molecular Markers for Breeding Disease Resistant Varieties in Crop Plants, In: S. M. Jain and D. S. Brar, Eds., *Molecular Techniques in Crop Improvement*, Springer Science and Business Media B.V, Dordrecht.

Tyng, C.F., Maniam, K.V. and Latip, M.A. (2010). Determining polymorphism in upland rice varieties, using microsatellite markers associated with blast resistant genes. *Genetic Bulletin of the Genetics Society of Malaysia,* 17: 15-19.

USDA. (2013). Malaysia Grain and Feed Annual 2013. *GAIN Report Number: MY3002*. USDA foreign Agricultural Service.

Van Berloo, R. (2008). GGT 2.0: versatile software for visualization and analysis of genetic data. *Journal of Heredity,* 99: 232–236.

Variar, M., Vera Cruz, C.M., Carrillo, M.G., Bhatt, J.C., Sangar, R.B.S. (2009). Rice blast in India and strategies to develop durably resistant varieties. In: Liang, Wang, G., Valent, B. (Eds.), *Advances in Genetics, Genomics and Control of Rice Blast Disease* (pp. 359–374). Springer Publication.

Visscher, P.M. (1996). Proportion of the variation in genomic composition in backcrossing programs explained by genetic markers. *Journal of Heredity,* 87: 136–138.

Visscher, P.M. (1996a). Marker assisted introgression in backcross breeding programs. *Genetics,* 144: 1923-1932.

Visscher, P.M., Haley, C.S. and Thompson, R. (1996). Marker assisted introgression in back cross breeding programs. *Genetics*, 144: 1923-1932.

Wang, B., Zhu, C., Liu, X., Wang, W., Ding, H., Jiang, M., Li, G., Liu, W. and Ya, F. (2011). Fine mapping of qHD4-1, a QTL controlling the heading date, to a 20.7-bDNAfragment in rice (*Oryza sativa* L.). *Plant Molecular Biology Reports,* 29: 702–713.

Wang, G.L., Mackill, D.J., Bonman, J.M., McCouch, S.R., Champoux, M.C. and Nelson, R.T. (1994). RFLP mapping of genes conferring complete and partial resistance to blast in durably resistance rice varieties. *Genetics,* 136: 1421-1434.

Wang, L., Zhang, Z., Wei, L., Zhang, D., Teng, F., Tao, Y. and Zheng, Y. (2009). The residual background genome from a donor within an improved line selected by marker-assisted selection: impact on phenotype and combining ability. *Plant Breeding,* 128: 429- 435.

Wang, X., Lee, S., Wang, J., Ma, J., Bianco, T. and Jia, Y. (2014). Current advances on genetic resistance to rice blast disease. InTech: Rice-Germplasm, Genetics and Improvement, 195-217. http://dx.doi.org/10.5772/56824.

Wang, Z., Jia, Y., Rutger, J. N. and Xia, Y. (2007). Rapid survey for presence of a blast resistance gene *Pi-ta* in rice varieties using the dominant DNA markers derived from portions of the *Pi-ta* gene. *Plant Breeding*, 126: 36-42.

Wang, Z.X., Yano, M., Yamanouchi, U., Iwamoto, M., Monna, L., Hayasaka, H., Katayose, Y. and Sasaki, T. (1999). The *Pib* gene for rice blast resistance belongs to the nucleotide binding and leucine rice repeat class of plant disease resistance genes. *Plant Journal*, 19: 55–64.

Wen, S. and Gao, B. (2011). Introgressing blast resistant gene *Pi-9(t)* into elite rice restorer Luhui17 by marker-assisted selection. *Rice Genomics and Genetics*, 2: 31-36.

Werner, K., Friedt, W. and Ordon, F. (2005). Strategies for pyramiding resistance genes against the barley yellow mosaic virus complex (BaMMV, BaYMV, BaYMV-2). *Molecular Breeding*, 16: 45–55.

William, H.M., Morris, M., Warburton, M. et al. (2007a) Technical, economic, and policy considerations on marker assisted selection in crops: lesons from the experience at an international agriculture research center. In: Guimaraes E, Ruane J, Scerf B, Sonnino A, Dargie J (eds), *Marker assisted selection. Current status and future perspectives in crops, livestock, forestry and fish*. Food and Agriculture Organization of the United Nations, Rome.

Wu, J.L., Fan, Y.Y., Li, D.B., Zheng, K.L., Leung, H. and Zhuang, J.Y. (2005). Genetic control of rice blast resistance in the durably resistant variety Gumei 2 against multiple isolates. *Theoretical and Applied Genetics*, 111: 50–56.

Wu, K.S., Martinez, C., Lentini, Z., Tohme, J., Chumley, F.G., Scolnik, P.A. and Valent, B. (1996). Cloning a blast resistance gene by chromosome walking. In: Khush GS (ed) Rice genetics III (pp. 669–674). *Proceeding of the third international rice genetics symposium*. International Rice Research Institute, Manila, Philippines.

Xi, Z.Y., He, F.H., Zeng, R.Z., Zhang, Z.M., Ding, X.H., Li, W.T. and Zhang, G.Q. (2008). Development of a wide population of chromosome single-segment substitution lines in the genetic background of an elite variety of rice (*Oryza sativa* L.). *Genome*, 49: 476–484.

Xiao, J., Grandillo, S., Ahn, S.A., McCouch, S.R., Tanksley, S.D., Li, J. and Yuan, L. (1996b). Genes from wild rice improve yield. *Nature*, 384: 223-224.

Xiao, J., Li, J., Yuan, L., McCouch, S.R. and Tankley, S.D. (1996a). Genetic diversity and its relationship to hybrid performance and heterosis in rice as revealed by PCR-based markers. *Theoretical and Applied Genetics*, 92: 637–643.

Xu, X., Chen, H., Fujimura, T. and Kawasaki, S. (2008). Fine mapping of a strong QTL of field resistance against rice blast, *Pikahei-1(t*), from upland rice Kahei, utilizing a novel resistance evaluation system in the greenhouse. *Theoretical and Applied Genetics*, 117: 997–1008.

Xu, Y. and Crouch, J.H. (2008). Marker-assisted selection in plant breeding: from publications to practice. *Crop Science*, 48: 391-407.

Xue, Q.Z. and Chen, H.S. (1987). Genetic study of disease resistance in Dan 209, a rice variety bred by anther culture. *Acta Genetics Sinica*, 14: 349-354.

Yamasak, Y.I., Kiyosawa, S. (1966). Studies on inheritance of resistance of rice varieties to blast. I. Inheritance of resistance of Japanese varieties to several strains of the fungus. *Bulletin of the National Institute of Agricultural Sciences, Japan*, 14: 39-69.

Yang, Q.Z., Lin, F., Feng, S.J., Wang, L. and Pan, Q.H. (2009). Recent progress on molecular mapping and cloning of blast resistance genes in rice (*Oryza sativa* L.). *Science Agriculture Sinica*, 42: 1601–1615.

Ye, G. (2010). Marker-assisted gene pyramiding for variety development. *Plant Breeding Reviews*, 33: 219–256.

Ye, G. and Smith, K.F. (2008). Marker-assisted gene pyramiding for inbred line development: Basic principles and practical guidelines. *International Journal of Plant Breeding*, 2: 1-10.

Yi, G., Lee, S.K., Hong, Y.K., Cho, Y.C., Nam, M.H., Kim, S.C., Han, S.S., Wang, G.L., Hahn, T.R., Ronald, P.C. and Jeon, J.S. (2004). Use of *Pi5(t)* markers in marker-assisted selection to screen for varieties with resistance to *Magnaporthe grisea*. *Theoretical and Applied Genetics*, 109: 978-985.

Yokoo, M.K.S. (1970). Inheritance of blast resistance of the rice variety, Toride 1, selected from the cross Norin 8 x TKM 1. *Japanese Journal of Breeding*, 20: 129-132.

Young, N.D. and Tanksley, S.D. (1989a). RFLP analysis of the size of chromosomal segments retained around the *Tm-2* locus of tomato during backcross breeding. *Theoretical and Applied Genetics*, 77: 353-359.

Young, N.D. and Tanksley, S.D. (1989b). Restriction fragment length polymorphism maps and the concept of graphical genotypes. *Theoretical and Applied Genetics*, 77: 95-101.

Yu, H. Z., Mackill, D.J. and Bonman, J.M. (1987). Inheritance of resistance to blast in some traditional and improved rice varieties. *Phytopathology*, 77: 323-326.

Yu, S.B., Xu, W.J., Vijayakumar, C.H.M., Ali, J., Fu, B.Y., Xu, J.L., Jian, Y.Z., Marghirang, R., Domingo, J., Aquino, C., Virmani, S.S. and Li, Z.K. (2003). Molecular diversity and multi locus organization of the parental lines used in the International Rice Molecular Breeding Program. *Theoretical and Applied Genetics*, 108: 131-140.

Yu, Z.H., Mackill, D.J., Bonman, J.M. and Tanksley, S.D. (1991). Tagging genes for blast resistance in rice via linkage to RFLP markers. *Theoretical and Applied Genetics*, 81: 471- 476.

Zenbayashi, K., Ashizawa, T., Tani, T. and Koizumi, S. (2002). Mapping of the QTL conferring partial resistance to leaf blast in rice variety Chubu 32. *Theoretical and Applied Genetics*, 104: 547–552.

Zhan, X., Zhou, H., Chai, R., Zhuang, J., Cheng, S. and Cao, L. (2012). Breeding of R8012, a rice restorer line resistant to blast and bacterial blight through marker-assisted selection. *Rice Science*, 19: 29-35.

Zhang, J.F., Gong, L.G., Qu, Y. and Qu, H.L. (2005). The rice ears were seriously damaged by the fifth and sixth generation of small brown planthopper in Changshu City in 2004. *China Plant Protection*, 25: 39.

Zhang, Y.S., Luo, L.J., Xu, C.G., Zhang, Q.F. and Xing, Y.Z. (2006). Quantitative trait loci for panicle size, heading date and plant height co-segregating in trait-performance derived near-isogenic lines of rice (*Oryza sativa*). *Theoretical Applied Genetics*, 113: 361–368.

Zhao, F., Cai, Z., Hu, T., Yao, H., Wang, L., Dong, N., Wang, B., Ru, Z. and Zhai, W. (2010). Genetic analysis and molecular mapping of a novel gene conferring resistance to rice stripe virus. *Plant Molecular Biology Reports*, 28: 512–518.

Zheng, K.L., Zhuang, J.Y., Lu, J., Qian, H.R. and Lin, H.X. (1996). Identification of DNA markers tightly linked to blast resistance genes in rice. In Khush, G.S. ed. *Rice genetics III* (pp. 565-569). IRRI, Manila, Philippines.

Zhou, B., Qu, S., Liu, G., Dolan, M., Sakai, H., Lu, G., Bellizzi, M. and Wang, G.L. (2006). The eight amino acid divergences within three leucine-rich repeats between *Pi2* and *Piz-t* resistance proteins determine the resistance specificity to *Magnaporthe grisea*. *Molecular Plant Microbe Interactions*, 19: 1216–1228.

Zhou, J.H., Wang, J.L., Xu, J.C., Lei, C.L. and Ling, Z.Z. (2004). Identification and mapping of a rice blast resistance gene *Pi-g(t)* in the variety Guangchangzhan. *Plant Pathology*, 53: 191–196.

Zhou, Y.L., Uzokwe, V.N.E., Zhang, C.H., Cheng, L.R., Wang, L., Chen, K., Gao, X., Sun, Q., Chen, Y., Zhu, J.J., Zhang, L.H., Ali, Q., Xu, J.L. and Li, Z.K. (2011). Improvement of bacterial blight resistance of hybrid rice in China using the Xa23 gene derived from wild rice (*Oryza rufipogon*). *Field Crop Research,* 30: 637–644.

Zhu, M., Wang, L. and Pan. Q. (2004). Identification and characterization of a new blast resistance gene located on rice chromosome 1 through linkage and differential analyses. *Phytopathology*, 94: 515-519.

Zhuang, J. Y., Chai, R. Y., Ma, W. B., Lu, J., Jin, M. Z. and Zheng, K. L. (1997). Genetic analysis of the blast resistance gene at vegetative and reproductive stages in rice. *Rice Genetics Newslellter,* 14: 62–64.

Zhuang, J. Y., Wu, J. L., Fan, Y. Y., Rao, Z. M. and Zheng, K. L. (2001). Genetic drag between a blast resistance gene and QTL conditioning yield trait detected in a recombinant inbred line population in rice. *Rice Genetics Newsletter*, 18: 69–70.

Zou, J. H., Pan, X. B., Chen, Z. X., Xu, J. Y., Lu, J. F., Zhai, W. X. and Zhu, L. H. (2000). Mapping quantitative trait loci controlling sheath blight resistance into rice varieties (*Oryza sativa* L.). *Theoretical and Applied Genetics,* 101: 569-573.

Zuraida, A. R., Zulkifli, A. S., Habibuddin, H. and Naziah, B. (2012). Regeneration of Malaysian rice variety MR219 via somatic embryogenesis. *Journal of Tropical Agriculture and Food Science,* 39: 167– 177.