



UNIVERSITI PUTRA MALAYSIA

***GENETIC ANALYSIS AND QTL MAPPING OF BROWN PLANTHOPPER
(*Nilaparvata lugens* Stål.) BIOTYPES 2 AND 3 RESISTANCE IN RICE***

MAHMOODREZA SHABANIMOFRAD

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By

MAHMOODREZA SHABANIMOFRAD

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

June 2015

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DEDICATION

To my beloved wife

Thanks for her support, understanding, love and encouragement.



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

**GENETIC ANALYSIS AND QTL MAPPING OF BROWN PLANTHOPPER
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June 2015

Chairman : Professor Mohd Rafii Yusop, PhD
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The use of molecular markers in many aspects of rice (*Oryza sativa* L.) studies such as genetic analysis of insect and diseases resistance genes is on the increase. Molecular markers have played an important role in rice breeding worldwide. Brown planthopper (BPH), *Nilaparvata lugens* is one of the most destructive insect pests in rice growing areas of the world. Several strategies such as QTL mapping are being deployed in breeding for resistance genes into rice varieties have been proposed for combating the BPH insect pest. This study used molecular marker approach in order to analyse molecular genetics of resistance in segregating populations and to identify QTL conferring resistance against two different biotypes of brown planthopper, namely, Biotype 2 and 3, in F₃ generation families derived from the cross between Rathu Heenati (BPH resistant) and MR276 (BPH susceptible) cultivars. One hundred and ten SSR primer pairs related to BPH resistance gene (*Bph* genes) distributed over 12 chromosomes of the rice genome were chosen and used to amplify SSR markers, and to analyse their potential association with *Bph* resistance. Fifty seven of polymorphic markers were used to identify BPH resistant segregation ratios in 176 individuals of F₂ population. Thirty five markers showed a good fit to the expected segregation ratio (1:2:1) for single gene model (df = 1.0, $p \leq 0.05$). The rest of the markers did not fit the expected segregating Mendelian ratios. The F₃ generation families were grown in a greenhouse and infested with two BPH biotypes, Biotype 2 and 3. Chi-square analysis showed a good fit to the phenotypic ratio of 3:1 for the segregation of resistance and susceptibility for the Biotypes 2 and 3 of BPH. Six SSR markers, RM401, RM5953, RM217, RM210, RM242 and RM1103 were found significantly associated with resistance to Biotype 2 and 3 of BPH in rice. These markers showed high selection accuracy for resistant plants with confirmation of resistance effect of about 17 and 20% respectively for phenotypic variation, and can be used in MAS for the resistant gene. The resistance gene markers reported here provide rice breeders and geneticists a valuable tool for marker-assisted selection of the BPH insect resistance gene. A total of 150 F₃ generation families derived from the cross between Rathu Heenati and MR276 were used in this experiment to identify QTLs for resistance to BPH Biotypes 2 and 3. A trait distribution analysis showed continuous variation with normal distribution. Twenty independent QTLs were detected to be associated with BPH resistance on nine chromosomes. Five putative QTL (qBph-1-1, qBph-3-1, qBph-6-1, qBph-7-1 and qBph-3-1) with Logarithmic of Odds (LOD) > 3.0 and five suggestive QTLs (qBph-5-1, qBph-11-1, qBph-6-1, qBph-9-1 and qBph-12-1, LOD < 3.0) were detected for Biotype 2. Meanwhile, two putative QTLs (qBph-3-1 and qBph-6-1) with LOD > 3.0 and eight suggestive QTLs (qBph-1-1, qBph-7-1, qBph-6-1, qBph-9-1, qBph-3-1, qBph-6-1, qBph-10-1 and qBph-12-1, LOD < 3.0) were detected for Biotype 3. The individual locus found in the F₃ population for traits studied, explained 7 to 24% of the

total phenotypic variance in resistance against BPH biotypes. In conclusion, from this research, the QTL identified could help breeders in their programme for marker-assisted selection for rice varietal development with BPH resistance.



Abstrak tesis yang dikemukakan kepada senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk Ijazah Doktor Falsafah

**ANALISIS GENETIK DAN PEMETAAN QTL KERINTANGAN BENA PERANG
(*Nilaparvata lugens* Stål) BIOTIPS 2 DAN 3 TERHADAP PADI**

Oleh

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Penggunaan penanda molekul dalam banyak aspek kajian padi (*Oryza sativa* L.) seperti analisis genetik terhadap gen kerintangan serangga dan penyakit semakin meningkat. Penanda molekul telah memainkan peranan penting dalam pembiakbakaan padi di seluruh dunia. Bena perang (BPH), *Nilaparvata lugens* adalah salah satu serangga perosak yang mengakibatkan kerosakkan yang teruk di kawasan penanaman padi di dunia. Beberapa strategi seperti pemetaan QTL sedang diperluaskan dalam pembiakbakaan untuk gen rintang ke dalam varieti padi telah dicadangkan untuk mengatasi serangga perosak BPH. Kajian ini menggunakan pendekatan penanda molekul untuk menganalisis kerintangan genetik molekul dalam populasi bersegregasi dan mengenal pasti QTL yang memberikan kerintangan terhadap dua biotip berbeza bena perang, iaitu, Biotip 2 dan 3, dalam famili generasi F₃ yang diperolehi daripada kacukan kultivar Rathu Heenati (rintang BPH) dan MR276 (rentan BPH). Seratus sepuluh pasang penanda SSR berkaitan dengan gen kerintangan bena perang (gen-*Bph*) meliputi 12 kromosom genom padi telah dipilih dan digunakan untuk penanda SSR bagi menganalisis potensi hubungannya dengan kerintangan *Bph*. Lima puluh tujuh penanda polimorfik telah digunakan untuk mengenal pasti nisbah segregasi rintangan *Bph* dalam 176 individu populasi F₂. Tiga puluh lima penanda memberikan padanan yang baik dengan nisbah segregasi yang dijangka (1: 2: 1) untuk model gen tunggal ($df = 1.0, p \leq 0.05$). Penanda selebihnya tidak menunjukkan padanan nisbah segregasi dijangka Mendel. Generasi famili F₃ telah ditanam di rumah hijau dan didedahkan dengan serangan dua biotip bena perang, Biotip 2 dan 3. Analisis Chi-kuasa dua menunjukkan padanan yang baik pada nisbah fenotip 3:1 untuk segregasi kerintangan dan kerentanan BPH Biotip 2 dan 3. Enam penanda SSR, RM401, RM5953, RM217, RM210, RM242 dan RM1103 didapati mempunyai perkaitan bererti dengan kerintangan untuk biotip 2 dan 3 BPH ke atas padi. Penanda ini menunjukkan ketepatan pemilihan yang tinggi untuk pokok rintang dengan pengesanan kesan kerintangan sebanyak 17 dan 20% masing-masing untuk variasi fenotip, dan boleh digunakan dalam MAS untuk gen kerintangan. Penanda gen rintang yang diperolehi ini adalah berguna dan dapat membantu ahli biakbaka dan genetik padi untuk pemilihan penanda-berbantu gen rintangan serangga BPH. Sebanyak 150 generasi famili F₃ dari kacukan antara Rathu Heenati dan MR276 telah digunakan dalam eksperimen ini untuk mengenal pasti QTL untuk kerintangan pada biotip BPH 2 dan 3. Analisis serakan ciri menunjukkan variasi secara selanjur dengan bertaburan normal. Dua puluh QTL bebas berkaitan dengan kerintangan BPH telah dikesan pada sembilan kromosom. Lima QTL putatif (qBph-1-1, qBph-3-1, qBph-6-1, qBph-7-1 dan qBph-3-1) dengan Logarithmic of Odds (LOD) > 3.0 dan lima QTL yang dicadang (qBph-5-1, qBph-11-1, qBph-6-1, qBph-9-1 dan qBph-12-1, LOD < 3.0) telah dikesan untuk Biotip 2. Sementara itu, dua QTL putatif (qBph-3-1 dan qBph-6-1) dengan LOD > 3.0 dan lapan QTL yang dicadang (qBph-1-1,

qBph-7-1, qBph-6-1, qBph-9-1, qBph-3-1, qBph-6-1, qBph-10-1 dan qBph-12-1, LOD <3.0) telah dikesan untuk Biotip 3. Locus individu yang terdapat dalam populasi F₃ untuk sifat dinilai, menjelaskan 7 hingga 24% daripada jumlah varians fenotip dalam rintangan terhadap biotip BPH. Kesimpulannya, kajian QTL ini diharapkan dapat membantu ahli biakbaka dalam program pemilihan penanda-berbantu bagi menghasilkan varieti padi dengan ciri kerintangan BPH.



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I certify that a Thesis Examination Committee has met on 15 June 2015 to conduct the final examination of Mahmoodreza Shabanimofrad on his thesis entitled "Genetic Analysis and QTL Mapping of Brown Planthopper (*Nilaparvata lugens* Stål.) Biotypes 2 and 3 Resistance in Rice" in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Doctor of Philosophy.

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TABLE OF CONTENTS

	Page
ABSTRACT	i
ABSTRAK	iii
ACKNOWLEDGEMENTS	v
APPROVAL	vi
DECLARATION	viii
LIST OF TABLES	xii
LIST OF FIGURES	xiii
LIST OF ABBREVIATIONS	xv
CHAPTER	
1 INTRODUCTION	1
2 LITERATURE REVIEW	3
2.1 Rice	3
2.1.1 Rice Taxonomy and Geographic Origin	3
2.1.2 Rice Production	4
2.1.3 The Rice Genome	5
2.1.4 Rice Molecular Genetics Strategy	5
2.2 Brown Planthopper	6
2.2.1 Taxonomy of Brown Planthopper (BPH)	6
2.2.2 Biology and Life Cycle	6
2.2.3 Distribution and outbreak of BPH	8
2.2.4 Brown Planthopper Symptoms	9
2.2.5 Variation of <i>Nilaparvata lugens</i>	10
2.3 Mechanism of Brown Planthopper Resistance	10
2.4 Screening and Genetic of Resistance to BPH	11
2.5 Brown Planthopper Resistance Genes in Rice	13
2.6 Molecular Marker Techniques for Genome Analysis	13
2.7 Marker Application	13
2.7.1 Marker-Assisted Selection	14
2.7.2 Markers and Mapping Experiments	15
2.8 Quantitative Resistance	16
2.9 QTL Mapping	17
2.10 QTL mapping for BPH resistance in rice	17
3 ANALYSIS OF SSR MARKERS LINKED WITH BPH RESISTANCE GENES USING HIGH-RESOLUTION MELT IN RICE	20
3.1 Introduction	20
3.2 Materials and Methods	21
3.2.1 Plant Materials	21
3.2.2 Sample Collection and DNA Extraction	21
3.2.3 SSR Amplification	22
3.2.4 Polymerase Chain Reaction and HRM Analysis	22
3.2.5 Genotyping for Marker Segregation	22
3.2.6 Statistical Analysis	22
3.3 Results	23
3.3.1 Marker Polymorphism between Parents	23
3.3.2 Markers segregation data analysis	25
3.4 Discussion	31

3.5	Conclusion	32
4	MARKER- ASSISTED SELECTION FOR RICE BROWN PLANTHOPPER (<i>Nilaparvata Lugens</i>) RESISTANCE USING LINKED SSR MARKERS	33
4.1	Introduction	33
4.2	Materials and Methods	34
4.2.1	Plant Materials and insects	34
4.2.2	Evaluation of BPH resistance	34
4.2.3	DNA Extraction	35
4.2.4	PCR Amplification for Microsatellite Analysis	35
4.2.5	Marker Genotyping	37
4.2.6	Statistical Analysis	37
4.3	Results	37
4.3.1	Phenotypic Data Analysis	37
4.3.2	Trait Frequency Distribution	39
4.3.3	Molecular Marker Assays	39
4.4	Discussion	42
4.5	Conclusion	43
5	QTL ANALYSIS FOR THE RESISTANCE TO BROWN PLANTHOPPER (<i>Nilaparvata Lugens</i> Stål) BIOTYPES 2 AND 3 IN RICE USING THE F₃ POPULATION	44
5.1	Introduction	44
5.2	Materials and Methods	45
5.2.1	Plant Materials	45
5.2.2	Insect Population	45
5.2.3	Standard Seedbox Screening Test	45
5.2.4	Antibiosis test	46
5.2.5	Antixenosis test	46
5.2.6	QTL Analysis	47
5.3	Results	47
5.3.1	Construction of a Linkage Map with Simple Sequence Repeat (SSR) Markers for Biotype 2	47
5.3.2	Evaluation of BPH Biotype 2 Reaction and QTL Analysis	48
5.3.3	Evaluation for BPH Biotype 3 resistance by standard seedbox screening test and QTL analysis	50
5.3.4	Antibiosis Resistance Test for BPH Biotype 2 and QTL Analysis	53
5.3.5	Antibiosis test and QTL detection for BPH Biotype 3	54
5.3.6	Antixenosis resistance against BPH and QTL Detection for BPH Biotype 2	55
5.3.7	Antixenosis response against BPH and QTL mapping for BPH Biotype 3	56
5.4	Discussion	56
5.5	Conclusion	61
6	GENERAL CONCLUSION AND RECOMMENDATIONS FOR FUTURE RESEARCH	62
	REFERENCES	64
	APPENDICES	83
	BIODATA OF STUDENT	88
	LIST OF PUBLICATIONS	89

LIST OF TABLES

Table	Page
2.1. Chromosome number, genomic composition, reaction to BPH Biotypes and distribution of wild <i>Oryza</i> species with traits of economic importance.	12
2.2. Comparison of commonly used molecular markers.	16
3.1. Fifty seven polymorphic microsatellite markers used for segregation analysis in F ₂ population of rice.	26
3.2. Marker analyses in F ₂ population derived from the cross between MR276 (susceptible) and Rathu Heenati (resistant) rice varieties.	29
4.1. The scoring criteria for BPH resistance.	35
4.2. List of the SSR markers and their sequences used for the analysis of rice genotypes.	36
4.3. Observed and expected segregation ratios of resistant and susceptible plants in the F ₃ population for single genes models (3:1) obtained from cross between the rice cultivars MR276 × Rathu Heenati infested with BPH Biotypes 2 and 3.	38
4.4. Chi-square test for two independent genes (9 : 3 : 3 : 1) for brown planthopper resistance in F ₃ population from cross between the rice cultivars MR276 × Rathu Heenati infested with Biotype 2 and Biotype 3 of BPH.	38
4.5. Marker analysed in the F ₃ progenies derived from cross between the rice cultivars MR276 × Rathu Heenati.	40
4.6. Molecular markers statistics associated with brown planthopper resistance to Biotypes 2 and 3 in the F ₃ progenies.	41
5.1. Standard evaluation criteria of the reaction to BPH in rice seedlings.	46
5.2. QTLs for BPH Biotype 2 resistances detected in the Rathu Heenati/MR276 F ₃ population.	50
5.3. Evaluation of parental and control varieties to BPH by the standard seed box screening test.	50
5.4. QTLs for BPH Biotype 3 resistance detected in the MR276 × Rathu Heenati F ₃ population using three phenotypic screening methods.	53
5.5. QTLs for BPH resistance reported up to 2014.	58

LIST OF FIGURES

Figure	Page
2.1. Scientific classification of rice.	3
2.2. The relationship and demographic history of Asian and African cultivated rices.	4
2.3. Scientific classification of brown planthopper.	6
2.4. Eggs (a), nymphs (b) and (c) adults of brown planthopper.	7
2.5. Brown planthopper life cycle.	8
2.6. Distribution of BPH in Asia, Australasia and the Pacific Islands.	9
2.7. Symptoms of brown planthopper.	10
2.8. Meta analysis of QTLs for BPH resistance in rice identified and localized by different researchers.	19
3.1. Screening to identify the polymorphic microsatellite loci between parental varieties, MR276 (susceptible-red line) and Rathu Heenati (resistant- blue line) for SSR markers RM6 and RM205 using High-Resolution Melting (HRM).	24
3.2. High-Resolution Melting (HRM) curve analysis showing the segregation patterns of F ₂ population derived from a cross between MR276 and Rathu Heenati, at microsatellite locus RM261, RM11 and RM6 located on chromosomes 4, 7 and 2, respectively. Rotor-Gene Screen-Clust HRM software automatically classifies the genotypes of 176 F ₂ individual plants based on curve pattern of parental and F ₁ varieties. 72 and 78 are samples of F ₂ individual plants.	28
4.1. Frequency distribution of score ratings infested with <i>N. lugens</i> on 108F ₂ seedlings of MR276/Rathu Heenati.	39
4.2. PCR products for genotyping with marker RM1103 linked to <i>Bph</i> resistance genes in F ₃ population of rice derived from MR276 (P1) × Rathu Heenati (P2). Running on 3% MetaPhor™ Agarose gel stained with Midori Green, only 26 samples plus the two parents for this marker is shown (M=100bp ladder).	41
5.1. Molecular linkage map constructed by SSR markers assayed on the MR276×Rathu Heenati F ₃ population and quantitative trait loci (QTLs) conferring resistance to BPH Biotype 2. The numbers on the left are the marker position and marker and QTLs names are on the right. The green, red and black colours indicate the standard seedbox screening test (SSST); Honeydew test (HT) and antixenosis test (AXT), respectively.	48

- 5.2. Distribution of BPH Biotype 2 reactions in the MR276×Rathu Heenati F₃ population. (a) Standard seedbox screening test (SSST) for BPH; (b) Honeydew test (HT) for BPH; (c) Antixenosis test (AXT) for BPH. 49
- 5.3. Experimental set up for screening rice genotypes by standard seedbox screening test method. 51
- 5.4. Frequency distribution of BPH Biotype 3 reactions in the MR276×Rathu Heenati F₃ population. (a) Standard seedbox screening test (SSST) for BPH; (b) Honeydew test (HT) for BPH; (c) Antixenosis test (AXT) for BPH. 52
- 5.5. Amount of honeydew exerted by BPH on MR276, Rathu Heenati and F₃ population. 54
- 5.6. Chromosome location of QTLs for the resistance to BPH Biotype 3 in an F₃ population. The numbers on the left are the marker position and marker, and the QTL names are on the right. The green, red and black colours indicate the standard seedbox screening test (SSST), honeydew test (HT) and antixenosis test (AXT), respectively. 55

LIST OF ABBREVIATIONS

AFLP	Amplified Fragment Length Polymorphism
AXT	Antixenosis Test
BPH	Brown Planthopper
CIM	Composite Interval Mapping
cM	Centimorgan
EST	Expressed Sequence Tag
ET	Effector-Triggered
HRM	High Resolution Melt
HT	Honeydew Test
INDELS	Insertions/Deletions
LOD	Log Of Odd
MAS	Marker Assisted Selection
Mb	Million base pair
Mha	Million hectare
Mt	Million tonnes
QTL	Quantitative Trait Loci
RAPD	Random Amplified Polymorphic Dna
RFLP	Restriction Fragment Length Polymorphism
RH	Relative Humidity
SNP	Single Nucleotide Polymorphism
SSR	Simple Sequence Repeat
SSST	Standard Seedbox Screening Test
TN1	Taichung Native 1
χ^2	Chi-square

CHAPTER 1

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important staple food crop for more than two billion people in the world. Brown planthopper (BPH), *Nilaparvata lugens* Stål, is one of the most serious and destructive monophagous insect pests for rice throughout Asia. The brown planthopper damages plants not only causes by sap-sucking, but also acts as a vector of rice stripe virus (RSV), rice grassy stunt (RGSV) and rice ragged stunt virus (RRSV), which often cause significant yield loss in epidemic years.

Application of host-plant resistance cultivars become the major control methods for brown planthopper but their long-term stability is threatened because of the evolution of prolific biotypes (Saxena and Barrion, 1987). Numerous rice cultivars, such as 'IR26', 'IR64', Mudgo and IR46, were found to be resistant against BPH; it reveals that, in some cases, provided important short-term protection against BPH. In some areas BPH populations adapted to new developed resistant rice cultivars, sometimes they are unstable and tend to become susceptible in as little as 3 years of release. Breeding for rice cultivars with BPH resistance, varieties carrying polygenes provide a more durable resistance must be incorporated into individual varieties.

Knowledge about the biotypes of BPH and function of the insect-resistance gene and use them to develop resistant rice varieties is important for controlling this insect pest. Therefore, detailed characterization of the resistant genes against the BPH need to be developed to increase long-term stability resistance, giving security for a long period of time and over a broad geographic region.

Indiscriminate use of pesticides leading to the loss of animal genetic resources, elimination of natural enemies of pests, genetic resistance of BPH to pesticides, chemical contamination and environmental pollution (Chelliah and Gunathilagaraj, 2011). Therefore large efforts have been made to identifying resistance gene resources varieties that help guard against the negative impacts of BPH. Development of broad spectrum resistance capabilities is necessary for crop improvement, therefore use of DNA markers derived from the fine mapped position of the genes and marker assisted selection (MAS) genes for important biological or agronomic traits will provide opportunities for breeders to develop higher yield potential, improved grain quality, and durable resistance rice cultivars.

To develop a sustainable pest management system, it is important to find the right balance between breeding and management strategies to reduce the ecological fitness of BPH and to keep the pest under economic threshold levels. Host-plant resistance is the most practical and economical approach to control insect pests. A very few

information is available about resistance to BPH in Malaysian rice cultivars. The information regarding brown planthopper resistance genes (*Bph* genes) and QTLs existed in local cultivars might be helped in marker assisted selection. So the result of this project will be come up with first SSR-based QTL map of BPH resistance of rice in Malaysia.



REFERENCES

- Adachi, S., Tsuru, Y., Nito, N., Murata, K., Yamamoto, T., Ebitani, T., Ookawa, T. and Hirasawa, T., 2011. Identification and characterization of genomic regions on chromosomes 4 and 8 that control the rate of photosynthesis in rice leaves. *Journal of Experimental Botany* 62, 1927-1938.
- Akkaya, M., Bhagwat, A. and Cregan, P., 1992. Length polymorphisms of simple sequence repeat DNA in soybean. *Genetics* 132, 1131-1139.
- Alam, S.N. and Cohen, M.B., 1998. Detection and analysis of QTLs for resistance to the brown planthopper, *Nilaparvata lugens*, in a doubled-haploid rice population. *Theoretical and Applied Genetics* 97, 1370-1379.
- Ali, M. and Chowdhury, T., 2013. Tagging and mapping of genes and QTLs of *Nilaparvata lugens* resistance in rice. *Euphytica* 195, 1-30.
- Ali, M. and Chowdhury, T., 2014. Tagging and mapping of genes and QTLs of *Nilaparvata lugens* resistance in rice. *Euphytica* 195, 1-30.
- Angeles, E., Khush, G. and Heinrichs, E., 1986. Inheritance of resistance to planthoppers and leafhoppers in rice, *Rice genetics*. Proceedings of the International Rice Genetics Symposium, 27-31 May, 1985, Manila, Philippines. IRRI, pp. 537-549.
- Ashikari, M. and Matsuoka, M., 2006. Identification, isolation and pyramiding of quantitative trait loci for rice breeding. *Trends in Plant Science* 11, 344-350.
- Ashkani, S., Rafii, M., Rahim, H. and Latif, M., 2013. Genetic dissection of rice blast resistance by QTL mapping approach using an F₃ population. *Molecular Biology Reports* 40, 2503-2515.
- Ashkani, S., Rafii, M., Sariah, M., Akmar, A.S.N., Rusli, I., Rahim, H.A. and Latif, M., 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., Rafii, M.Y., Rusli, I., Sariah, M., Abdullah, S.N.A., Rahim, H.A. and Latif, M., 2012. SSRs for marker-assisted selection for blast resistance in rice (*Oryza sativa* L.). *Plant Molecular Biology Reporter* 30, 79-86.
- Athwal, D. and Pathak, M., 1972. Genetics of resistance to rice insects. *Rice Breeding*, 375-386.
- Athwal, D., Pathak, M., Bacalangco, E. and Pura, C., 1971. Genetics of resistance to brown planthoppers and green leafhoppers in *Oryza sativa* L. *Crop Science* 11, 747-750.

- Bao-ju, W., Hong-xing, X., Xu-song, Z., Qiang, F. and Zhong-xian, L., 2010. High temperature modifies resistance performances of rice varieties to brown planthopper, *Nilaparvata lugens* (Stal). *Rice Science* 17, 334-338.
- Blair, M.W., Fregene, M.A., Beebe, S.E. and Ceballos, H., 2007. Marker-assisted selection in common beans and cassava. Marker-assisted selection: Current status and future perspectives in crops, livestock, forestry and fish, *Nature* 81-115.
- Bottrell, D.G. and Schoenly, K.G., 2012. Resurrecting the ghost of green revolutions past: the brown planthopper as a recurring threat to high-yielding rice production in tropical Asia. *Journal of Asia-Pacific Entomology* 15, 122-140.
- Brar, D., Virk, P., Jena, K. and Khush, G., 2009. Breeding for resistance to planthoppers in rice. *Planthoppers: new threats to the sustainability of intensive rice production systems in Asia*. Los Baños (Philippines), International Rice Research Institute 401-409.
- Broekgaarden, C., Snoeren, T.A., Dicke, M. and Vosman, B., 2011. Exploiting natural variation to identify insect-resistance genes. *Plant Biotechnology Journal* 9, 819-825.
- Carlson, C.M., 2012. Genetic control of protein and amino acid content in soybean determined in two genetically connected populations, PhD Thesis. Raleigh, North Carolina, North Carolina State University.
- Cha, Y.-S., Ji, H., Yun, D.-W., Ahn, B.-O., Lee, M.C., Suh, S.-C., Lee, C.S., Ahn, E.K., Jeon, Y.-H. and Jin, I.-D., 2008. Fine mapping of the rice *Bph1* gene, which confers resistance to the brown planthopper (*Nilaparvata lugens* stal), and development of STS markers for marker-assisted selection. *Molecular and Cells* 26, 146-151.
- Chan, E.K., Rowe, H.C., Corwin, J.A., Joseph, B. and Kliebenstein, D.J., 2011. Combining genome-wide association mapping and transcriptional networks to identify novel genes controlling glucosinolates in *Arabidopsis thaliana*. *PLoS Biology* 9, e1001125.
- Chang, W., 1975. Inheritance of resistance to brown planthopper in rice. *Sabrao Journal* 7, 53-60.
- Chelliah, S. and Gunathilagaraj, K., 2011. Pest management in rice-current status and future prospects. Tamil Nadu Agricultural University.
- Chen, H.-q., Chen, Z.-x., Ni, S., Zuo, S.-m., Pan, X.-b. and Zhu, X., 2008. Pyramiding three genes with resistance to blast by marker-assisted selection to improve rice blast resistance of Jin 23B. *Chinese Journal of Rice Science* 1, 005.

- Chen, J., Wang, L., Pang, X. and Pan, Q., 2006. Genetic analysis and fine mapping of a rice brown planthopper (*Nilaparvata lugens* Stal) resistance gene *bph19* (t). *Molecular Genetics and Genomics* 275, 321-329.
- Cheng, C. and Chang, W., 1979. Studies on varietal resistance to the brown planthopper in Taiwan, Brown planthopper: Threat to rice production in Asia. Los Baños (Philippines), International Rice Research Institute, pp. 251-271.
- Cheng, X., Zhu, L. and He, G., 2013. Towards understanding of molecular interactions between rice and the brown planthopper. *Molecular Plant* 6, 621-634.
- Choi, S., Heu, M. and Lee, J., 1979. Varietal resistance to the brown planthopper in Korea, in: Institute, I.R.R. (Ed.), Brown planthopper: threat to rice production in Asia. International Rice Research Institute, Los Baños, pp. 219-232.
- Choudhary, K., Choudhary, O. and Shekhawat, N., 2008. Marker assisted selection: a novel approach for crop improvement. *American-Eurasian Journal of Agronomy* 1, 26-30.
- Cock, J., Gitterle, T., Salazar, M. and Rye, M., 2009. Breeding for disease resistance of Penaeid shrimps. *Aquaculture* 286, 1-11.
- Collard, B.C. 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: Biological Sciences* 363, 557-572.
- Conaway-Bormans, C., Marchetti, M., Johnson, C., McClung, A. and Park, W., 2003. Molecular markers linked to the blast resistance gene *Pi-z* in rice for use in marker-assisted selection. *Theoretical and Applied Genetics* 107, 1014-1020.
- Croxford, A.E., Rogers, T., Caligari, P.D. and Wilkinson, M.J., 2008. High-resolution melt analysis to identify and map sequence-tagged site anchor points onto linkage maps: a white lupin (*Lupinus albus*) map as an exemplar. *New Phytologist* 180, 594-607.
- Darrigues, A., 2007. Dissecting variation in tomato fruit color quality through digital phenotyping and genetic mapping. , PhD Thesis. The Ohio State University.
- Datta, S. K. D. (1981). Principles and practices of rice production a Wiley-Interscience publication, John Wiley & Sons, Inc. Printed in Singapore, (pp 640).
- Deen, R., Ramesh, K., Gautam, S., Rao, Y., Lakshmi, V., Viraktamath, B., Brar, D. and Ram, T., 2010. Identification of new gene for BPH resistance introgressed from *O. rufipogon*. *Rice Genetics Newsletter* 25, 70-72.

- Dekkers, J. and Hospital, F., 2002. The use of molecular genetics in the improvement of agricultural populations. *Nature Reviews Genetics* 3, 22-32.
- Dettori, M., Quarta, R. and Verde, I., 2001. A peach linkage map integrating RFLPs, SSRs, RAPDs, and morphological markers. *Genome* 44, 783-790.
- Dong, S., Ma, Y., Hou, Y., Yu, X. and Ye, G., 2011. Development of an ELISA for evaluating the reproductive status of female brown planthopper, *Nilaparvata lugens*, by measuring vitellogenin and vitellin levels. *Entomologia Experimentalis et Applicata* 139, 103-110.
- Du, B., Zhang, W., Liu, B., Hu, J., Wei, Z., Shi, Z., He, R., Zhu, L., Chen, R. and Han, B., 2009. Identification and characterization of Bph14, a gene conferring resistance to brown planthopper in rice. *Proceedings of the National Academy of Sciences* 106, 22163-22168.
- Duan, C., Su, N., Cheng, Z., Lei, C., Wang, J., Zhai, H. and Wan, J., 2010. QTL analysis for the resistance to small brown planthopper (*Laodelphax striatellus* Fallén) in rice using backcross inbred lines. *Plant Breeding* 129, 63-67.
- Dupo, A. and Barrion, A., 2009. Taxonomy and general biology of delphacid planthoppers in rice agroecosystems, in: Heong, K. and Hardy, B. (Eds.), *Planthoppers: New Threats to the Sustainability of Intensive Rice Production Systems in Asia* International Rice Research Institute, Philippines, pp. 3-156.
- Ellis, J. and Burke, J., 2007. EST-SSRs as a resource for population genetic analyses. *Heredity* 99, 125-132.
- Feng, X., Zhang, Q., Cong, P. and Zhu, Z., 2013. Preliminary study on classification of rice and detection of paraffin in the adulterated samples by Raman spectroscopy combined with multivariate analysis. *Talanta* 115, 548-555.
- Foo, K. and Hameed, B., 2009. Utilization of rice husk ash as novel adsorbent: a judicious recycling of the colloidal agricultural waste. *Advances in Colloid and Interface Science* 152, 39-47.
- Fraley, R.T., 2009. Molecular genetic approaches to maize improvement: an introduction, molecular genetic approaches to maize improvement. Springer, pp. 3-6.
- Fritsche-Neto, R. and Borém, A., 2012. *Plant breeding for biotic stress resistance*, Springer-Verlag, Berlin.
- Fujita, D., Kohli, A. and Horgan, F., 2013. Rice resistance to planthoppers and leafhoppers. *Critical Reviews in Plant Sciences* 32, 162-191.
- Furbank, R.T. and Tester, M., 2011. Phenomics-technologies to relieve the phenotyping bottleneck. *Trends in Plant Science* 16, 635-644.
- Ganopoulos, I., Argiriou, A. and Tsiftaris, A., 2011a. Adulterations in Basmati rice detected quantitatively by combined use of microsatellite and fragrance

typing with High Resolution Melting (HRM) analysis. Food Chemistry 129, 652-659.

Ganopoulos, I., Argiriou, A. and Tsaftaris, A., 2011b. Microsatellite high resolution melting (SSR-HRM) analysis for authenticity testing of protected designation of origin (PDO) sweet cherry products. Food Control 22, 532-541.

Gimenez-Ibanez, S. and Solano, R., 2013. Nuclear jasmonate and salicylate signaling and crosstalk in defense against pathogens. Frontiers in Plant Science 4.

Giri, C. and Vijaya Laxmi, G., 2000. Production of transgenic rice with agronomically useful genes: an assessment. Biotechnology Advances 18, 653-683.

Golding, B., Jeong, H.-J., Jo, Y.D., Park, S.-W. and Kang, B.-C., 2010. Identification of Capsicum species using SNP markers based on high resolution melting analysis. Genome 53, 1029-1040.

Guimarães, E.P., 2007. Marker-assisted selection: current status and future perspectives in crops, livestock, forestry and fish, Food & Agriculture Organization of the United Nations, Rome 471.

Han, Y., Khu, D.-M. and Monteros, M.J., 2012. High-resolution melting analysis for SNP genotyping and mapping in tetraploid alfalfa (*Medicago sativa* L.). Molecular Breeding 29, 489-501.

Hanley, S., Barker, J., Van Ooijen, J., Aldam, C., Harris, S., Ahman, I., Larsson, S. and Karp, A., 2002. A genetic linkage map of willow (*Salix viminalis*) based on AFLP and microsatellite markers. Theoretical and Applied Genetics 105, 1087-1096.

Harini, A.S., Lakshmi, S., Kumar, S., Sivaramakrishnan, S. and Kadirvel, P., 2010. Validation and fine-mapping of genetic locus associated with resistance to brown plant hopper [*Nilaparvata lugens* (Stal.)] in rice (*Oryza sativa* L.). Asian Journal of Bio Science 5, 32-37.

Hashim, H., 1989. Variation of brown planthopper population from major rice regions of Peninsular Malaysia. MARDI Research Journal 17.

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.

He, J., Liu, Y., Liu, Y., Jiang, L., Wu, H., Kang, H., Liu, S., Chen, L., Liu, X. and Cheng, X., 2013. High-resolution mapping of brown planthopper (BPH) resistance gene *Bph27* (*t*) in rice (*Oryza sativa* L.). Molecular Breeding, 1-9.

Heinrichs, E., Medrano, F. and Rapusas, H., 1985. Genetic evaluation for insect resistance in rice, International Rice Research Institute.

- Helliwell, E.E. and Yang, Y., 2013. Molecular strategies to improve rice disease resistance, *Rice Protocols*. Springer, pp. 285-309.
- Heong, K.L. and Hardy, B., 2009. Planthoppers: new threats to the sustainability of intensive rice production systems in Asia, International Rice Research Institute.
- Hirabayashi, H., Angeles, E., Kaji, R., Ogawa, T., Brar, D. and Khush, G., 1998. Identification of brown planthopper resistance gene derived from *O. officinalis* using molecular markers in rice. *Breeding Science* 48, 82.
- Hirabayashi, H., Ideta, O., Sato, H., Takeuchi, Y., Ando, I., Nemoto, H., Imbe, T., Brar, D. and Ogawa, T., 2004. Identification of a resistance gene to brown planthopper derived from *Oryza minuta* in rice. *Breeding Research* 6, 285.
- Huang, B., Xu, J., Hou, M., Ali, J. and Mou, T., 2012a. Introgression of bacterial blight resistance genes *Xa7*, *Xa21*, *Xa22* and *Xa23* into hybrid rice restorer lines by molecular marker-assisted selection. *Euphytica* 187, 449-459.
- Huang, D.-R., Chen, J., Lai, F.-X., Liu, G.-J. and Zhuang, J.-Y., 2012b. Analysis of quantitative trait loci for resistance to brown planthopper in dongxiang wild rice (*Oryza rufipogon* Griff.). *Acta Agronomica Sinica* 38, 210-214.
- Huang, D., Qiu, Y., Zhang, Y., Huang, F., Meng, J., Wei, S., Li, R. and Chen, B., 2013. Fine mapping and characterization of *BPH27*, a brown planthopper resistance gene from wild rice (*Oryza rufipogon* Griff.). *Theoretical and Applied Genetics* 126, 219-229.
- Huang, S., Spielmeier, W., Lagudah, E.S. and Munns, R., 2008. Comparative mapping of HKT genes in wheat, barley, and rice, key determinants of Na⁺ transport, and salt tolerance. *Journal of Experimental Botany* 59, 927-937.
- Huang, Y. J., Qi, A., King, G. J., and Fitt, B. D., 2014. Assessing quantitative resistance against *Leptosphaeria maculans* (phoma stem canker) in *Brassica napus* (oilseed rape) in young plants. *PloS One*, 9(1), e84924.
- Huang, Z., He, G., Shu, L., Li, X. and Zhang, Q., 2001. Identification and mapping of two brown planthopper resistance genes in rice. *Theoretical and Applied Genetics* 102, 929-934.
- Huard-Chauveau, C., Percepied, L., Debieu, M., Rivas, S., Kroj, T., Kars, I., Bergelson, J., Roux, F. and Roby, D., 2013. An atypical kinase under balancing selection confers broad-spectrum disease resistance in Arabidopsis. *PLoS Genetics* 9, e1003766.
- Ilango, S. and Sarla, N., 2010. Microsatellite marker polymorphism in rice varieties rich in iron and zinc endosperm. *Asian Journal of Experimental Biological Science* 1, 751-757.
- Inada, M., Morooka, S., Itoyama, K. and Tojo, S., 2011. Genetic variations in the pre-feeding and pre-oviposition periods among four pure lines in the brown

planthopper, *Nilaparvata lugens* (Hemiptera: Auchenorrhyncha: Delphacidae). Applied Entomology and Zoology 46, 545-551.

IRRI, 1988. Standard evaluation system for rice. International Rice Research Institute Philippine, pp. 54.

IRRI, 1998. Standard Evaluation System for Rice (SES). Philippines, pp. 10 – 35.

Ishii, T., Brar, D., Multani, D. and Khush, G., 1994. Molecular tagging of genes for brown planthopper resistance and earliness introgressed from *Oryza australiensis* into cultivated rice, *O. sativa*. Genome 37, 217-221.

Jairin, J., 2005. Identification of molecular markers linked to brown planthopper resistance in rice (*Oryza Sativa* L.), Unpublished, Ph.D Thesis, Kasetsart University.

Jairin, J., Phengrat, K., Teangdeerith, S., Vanavichit, A. and Toojinda, T., 2007a. Mapping of a broad-spectrum brown planthopper resistance gene, *Bph3*, on rice chromosome 6. Molecular Breeding 19, 35-44.

Jairin, J., Sansen, K., Wongboon, W. and Kothcharek, J., 2010. Detection of a brown planthopper resistance gene *bph4* at the same chromosomal position of *Bph3* using two different genetic backgrounds of rice. Breeding Science 60, 71-75.

Jairin, J., Teangdeerith, S., Leelagud, P., Kothcharek, J., Sansen, K., Yi, M., Vanavichit, A. and Toojinda, T., 2009. Development of rice introgression lines with brown planthopper resistance and KDML105 grain quality characteristics through marker-assisted selection. Field Crops Research 110, 263-271.

Jairin, J., Teangdeerith, S., Leelagud, P., Phengrat, K., Vanavichit, A. and Toojinda, T., 2007b. Detection of brown planthopper resistance genes from different rice mapping populations in the same genomic location. Science Asia 33, 347-352.

Jairin, J., Teangdeerith, S., Leelagud, P., Phengrat, K., Vanavichit, A. and Toojinda, T., 2007c. Physical mapping of *Bph3*, a brown planthopper resistance locus in rice. Maejo International Journal of Science and Technology 1, 166-177.

Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, E., Zhou, B., Li, H., Kim, H. and Yu, Y., 2005. Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction. Plant Physiology 138, 105-115.

Javed, M.A., Huyop, F.Z., Ishii, T., ABD, A., Samad, T., Haider, M.S. and Saleem, M., 2013. Construction of microsatellite linkage map and detection of segregation distortion in indica rice (*oryza sativa*L.). Pakistan Journal of Botany 45, 2085-2092.

- Jena, K., Jeung, J., Lee, J., Choi, H. and Brar, D., 2006. High-resolution mapping of a new brown planthopper (BPH) resistance gene, *Bph18* (t), and marker-assisted selection for BPH resistance in rice (*Oryza sativa* L.). *Theoretical and Applied Genetics* 112, 288-297.
- Jena, K. and Mackill, D., 2008. Molecular markers and their use in marker-assisted selection in rice. *Crop Science* 48, 1266-1276.
- Jena, K., Pasalu, I., Rao, Y., Varalaxmi, Y., Krishnaiah, K., Khush, G. and Kochert, G., 2003. Molecular tagging of a gene for resistance to brown planthopper in rice (*Oryza sativa* L.). *Euphytica* 129, 81-88.
- Jena, K.K., 2010. The species of the genus *Oryza* and transfer of useful genes from wild species into cultivated rice, *O. sativa*. *Breeding Science* 60, 518-523.
- Jena, K.K. and Kim, S.-M., 2010. Current status of brown planthopper (BPH) resistance and genetics. *Rice* 3, 161-171.
- Jeon, Y., Ahn, S., Choi, H., Hahn, T. and Moon, H., 1999. Identification of a RAPD marker linked to a brown planthopper resistance gene in rice. *Euphytica* 107, 23-28.
- Jing, S., Zhang, L., Ma, Y., Liu, B., Zhao, Y., Yu, H., Zhou, X., Qin, R., Zhu, L. and He, G., 2014. Genome-wide mapping of virulence in brown planthopper identifies loci that break down host plant resistance. *PloS One* 9, e98911.
- Kabis, A. and Khush, G., 1988. Genetic analysis of resistance to brown planthopper in rice (*Oryza sativa* L.). *Plant Breeding* 100, 54-58.
- Kartohardjono, A. and Heinrichs, E., 1984. Populations of the brown planthopper, *Nilaparvata lugens* (Stal) (Homoptera: Delphacidae), and its predators on rice varieties with different levels of resistance. *Environmental Entomology* 13, 359-365.
- Katimbang, M., Nokhoda, B., Egdane, J. and Ismail, A., 2012. QTL mapping of IR64 mutants F₂ population for salinity tolerance at seedling stage in rice. *Philippine Journal of Crop Science (Philippines)*.
- Kawaguchi, M., Murata, K., Ishii, T., Takumi, S., Mori, N. and Nakamura, C., 2001. Assignment of a brown planthopper (*Nilaparvata lugens* stal) resistance gene *bph4* to the rice chromosome 6. *Breeding Science* 51, 13-18.
- Khush, G., 1979. Genetics of and breeding for resistance to the brown planthopper. *Brown planthopper: Threat to rice production in Asia*, 321-332.
- Khush, G., Rezaul Karim, A. and Angeles, E., 1985. Genetics of resistance of rice cultivar ARC10550 to Bangladesh brown planthopper teletype. *Journal of Genetics* 64, 121-125.
- Khush, G.S., 2005. What it will take to feed 5.0 billion rice consumers in 2030. *Plant Molecular Biology* 59, 1-6.

- Kim, S.-M. and Sohn, J.-K., 2005. Identification of a rice gene (*Bph 1*) conferring resistance to brown planthopper (*Nilaparvata lugens* Stal) using STS markers. *Molecular and Cells* 20, 30-34.
- Komatsuda, T., Annaka, T. and Oka, S., 1993. Genetic mapping of a quantitative trait locus (QTL) that enhances the shoot differentiation rate in *Hordeum vulgare* L. *Theoretical and Applied Genetics* 86, 713-720.
- Krishnaiah, N., 2014. A global perspective of rice brown planthopper management i-crop-climatic requirement. *International Journal of Molecular Zoology* 4.
- Kubisiak, T., Nelson, C., Nance, W. and Stine, M., 1995. RAPD linkage mapping in a longleaf pine × slash pine F₁ family. *Theoretical and Applied Genetics* 90, 1119-1127.
- Kumar, P., Gupta, V., Misra, A., Modi, D. and Pandey, B., 2009. Potential of molecular markers in plant biotechnology. *Plant Omics* 2, 141.
- Kumari, S., Sheba, J.M., Marappan, M., Ponnuswamy, S., Seetharaman, S., Pothi, N., Subbarayalu, M., Muthurajan, R. and Natesan, S., 2010. Screening of IR50× Rathu Heenati F7 RILs and identification of SSR markers linked to brown planthopper (*Nilaparvata lugens* Stal) resistance in rice (*Oryza sativa* L.). *Molecular Biotechnology* 46, 63-71.
- Kunkel, B.N. and Brooks, D.M., 2002. Cross talk between signaling pathways in pathogen defense. *Current Opinion in Plant Biology* 5, 325-331.
- Lakshminarayana, A. and Khush, G.S., 1977. New genes for resistance to the brown planthopper in rice. *Crop Science* 17, 96-100.
- Lang, N. and Buu, B., 2003. Genetic and physical maps of gene *Bph-10* controlling brown plant hopper resistance in rice (*Oryza sativa* L.). *Omonrice* 11, 35-41.
- Latif, M.A., Guan, T.S., Yusoh, O.M. and Siraj, S.S., 2008. Evidence of sibling species in the brown planthopper complex (*Nilaparvata lugens*) detected from short and long primer random amplified polymorphic DNA fingerprints. *Biochemical Genetics* 46, 520-537.
- Latif, M.A., Rahman, M.M., Ali, M.E., Ashkani, S. and Rafii, M.Y., 2013. Inheritance studies of SSR and ISSR molecular markers and phylogenetic relationship of rice genotypes resistant to tungro virus. *Comptes Rendus Biologies* 336, 125-133.
- Li, C., Wang, X., Dong, N., Zhao, H., Xia, Z., Wang, R., Converse, R.L. and Wang, Q., 2013. QTL analysis for early-maturing traits in cotton using two upland cotton (*Gossypium hirsutum* L.) crosses. *Breeding Science* 63, 154.
- Li, J., 2005. Development of multiple interval mapping for mapping QTL in ordinal traits. PhD Thesis. Raleigh: North Carolina State University.

- Li, R., Li, L., Wei, S., Wei, Y., Chen, Y., Bai, D., Yang, L., Huang, F., Lu, W., Zhang, X., Li, X., Yang, X. and Wei, Y., 2010. The evaluation and utilization of new genes for brown planthopper resistance in common wild rice (*Oryza rufipogon* Griff.). *Molecular Plant Breeding* 4, 365-371.
- Li, W., Xu, X., Li, G., Guo, L., Wu, S., Jiang, Y., Dong, H., Weng, M., Jin, D. and Wu, J., 2012. Characterization and molecular mapping of *RsrR*, a resistant gene to maize head smut. *Euphytica* 187, 303-311.
- Liebhart, R., Gianfranceschi, L., Koller, B., Ryder, C., Tarchini, R., Van de Weg, E. and Gessler, C., 2002. Development and characterisation of 140 new microsatellites in apple (*Malus x domestica* Borkh.). *Molecular Breeding* 10, 217-241.
- Liu, G., Yan, H., Fu, Q., Qian, Q., Zhang, Z., Zhai, W. and Zhu, L., 2001. Mapping of a new gene for brown planthopper resistance in cultivated rice introgressed from *Oryza eichingeri*. *Chinese Science Bulletin* 46, 1459-1462.
- Liu, Y., Su, C., Jiang, L., He, J., Wu, H., Peng, C. and Wan, J., 2009. The distribution and identification of brown planthopper resistance genes in rice. *Hereditas* 146, 67-73.
- Lübberstedt, T., Melchinger, A.E., Klein, D., Degenhardt, H. and Paul, C., 1997. QTL mapping in testcrosses of European flint lines of maize: II. Comparison of different testers for forage quality traits. *Crop Science* 37, 1913-1922.
- Mackay, T.F., 2001. Quantitative trait loci in *Drosophila*. *Nature Reviews Genetics* 2, 11-20.
- Madurangi, S., Ratnasekera, D., Senanayake, S., Samarasinghe, W. and Hemachandra, P., 2013. Antixenosis and antibiosis effects of *Oryza nivara* accessions harbouring *bph2* gene on brown planthopper [*Nilaparvata lugens* (Stal)]. *Journal of the National Science Foundation of Sri Lanka* 41, 147-154.
- Madurangi, S., Samarasinghe, W., Senanayake, S., Hemachandra, P. and Ratnasekera, D., 2011. Resistance of *Oryza nivara* and *Oryza eichingeri* derived lines to brown planthopper, *Nilaparvata lugens* (Stal). *Journal of the National Science Foundation of Sri Lanka* 39, 175-181.
- Manosalva, P.M., 2006. Dissection of quantitative resistance to rice diseases, Department of Plant Pathology Kansas State University
- Martinez, C. and Khush, G.S., 1974. Sources and inheritance of resistance to brown planthopper in some breeding lines of rice. *Crop Science* 14, 264-267.
- McCouch, S., Temnykh, S., Lukashova, A., Coburn, J., DeClerck, G., Cartinhour, S., Harrington, S., Thomson, M., Septiningsih, E. and Semon, M., 2001. Microsatellite markers in rice: abundance, diversity, and applications. *Rice Genetics IV*. IRRI, Manila, Philippines, 117-135.

- Meenakshisundaram, P., Patel, S., Sudha, M., Geethanjali, S., Vinod, K., Selvaraju, K., Govindaraj, P., Arumugachamy, S., Shanmugasundaram, P. and Maheswaran, M., 2011. Microsatellite marker based linkage map construction and mapping of granule bound starch synthase (GBSS) in rich using recombinant inbred lines of the cross Basmati370/ASD16. *Crop Improvement* 38, 155-162.
- Miah, G., Rafii, M.Y., Ismail, M.R., Puteh, A.B., Rahim, H.A., Islam, K.N. and Latif, M.A., 2013. 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.
- Ming High, S., Cohen, M.B., Yao Shu, Q. and Altosaar, I., 2004. Achieving successful deployment of "Bt" rice. *Trends in Plant Science* 9, 286-292.
- Mizoi, J. and Yamaguchi-Shinozaki, K., 2013. Molecular approaches to improve rice abiotic stress tolerance, *Rice Protocols*. Springer, 269-283.
- Montanari, S., Saeed, M., Knäbel, M., Kim, Y., Troglio, M., Malnoy, M., Velasco, R., Fontana, P., Won, K. and Durel, C.-E., 2013. Identification of *Pyrus* single nucleotide polymorphisms (SNPs) and evaluation for genetic mapping in European pear and interspecific *Pyrus* hybrids. *PLoS One* 8, e77022.
- Moorthy, K.K., Babu, P., Sreedhar, M., Sama, V., Kumar, P.N., Balachandran, S. and Sundaram, R., 2011. Identification of informative EST-SSR markers capable of distinguishing popular Indian rice varieties and their utilization in seed genetic purity assessments. *Seed Science and Technology* 39, 282-292.
- Moose, S.P. and Mumm, R.H., 2008. Molecular plant breeding as the foundation for 21st century crop improvement. *Plant Physiology* 147, 969-977.
- Murai, H., Hashimoto, Z., Sharma, P., Shimizu, T., Murata, K., Takumi, S., Mori, N., Kawasaki, S. and Nakamura, C., 2001. Construction of a high-resolution linkage map of a rice brown planthopper (*Nilaparvata lugens* Stal) resistance gene *bph2*. *Theoretical and Applied Genetics* 103, 526-532.
- Murata, K., Fujiwara, M., Kaneda, C., Takumi, S., Mori, N. and Nakamura, C., 1998. RFLP mapping of a brown planthopper (*Nilaparvata lugens* Stal) resistance gene *bph2* of indica rice introgressed into a japonica breeding line 'Norin-PL4'. *Genes & Genetic Systems* 73, 359-364.
- Murata, K., Fujiwara, M., Murai, H., Takumi, S., Mori, N. and Nakamura, C., 2001. Mapping of a brown planthopper (*Nilaparvata lugens* Stal) resistance gene *Bph9* on the long arm of rice chromosome 12. *Cereal Research Communications* 29, 245-250.
- Myint, K.K.M., Fujita, D., Matsumura, M., Sonoda, T., Yoshimura, A. and Yasui, H., 2012. Mapping and pyramiding of two major genes for resistance to the brown planthopper (*Nilaparvata lugens* [Stål]) in the rice cultivar ADR52. *Theoretical and Applied Genetics* 124, 495-504.

- Nagaraju, J., Kathirvel, M., Kumar, R.R., Siddiq, E. and Hasnain, S.E., 2002. Genetic analysis of traditional and evolved Basmati and non-Basmati rice varieties by using fluorescence-based ISSR-PCR and SSR markers. *Proceedings of the National Academy of Sciences* 99, 5836-5841.
- Nagy, E.D., Guo, Y., Tang, S., Bowers, J.E., Okashah, R.A., Taylor, C.A., Zhang, D., Khanal, S., Heesacker, A.F. and Khalilian, N., 2012. A high-density genetic map of *Arachis duranensis*, a diploid ancestor of cultivated peanut. *BMC Genomics* 13, 469.
- Nemoto, H., Ikeda, R. and Kaneda, C., 1989. New Genes for Resistance to Brown Planthopper, *Nilaparvata lugens* Stal, in Rice. *Gene* 1, 3.
- Nemoto, H. and Yokoo, M., 1994. Experimental selection of a brown planthopper population on mixtures of resistant rice lines. *Breeding Science* 44, 133-133.
- Noda, H., Kawai, S., Koizumi, Y., Matsui, K., Zhang, Q., Furukawa, S., Shimomura, M. and Mita, K., 2008. Annotated ESTs from various tissues of the brown planthopper *Nilaparvata lugens*: a genomic resource for studying agricultural pests. *BMC Genomics* 9, 117.
- Ohmido, N., Fukui, K. and Kinoshita, T., 2010. Recent advances in rice genome and chromosome structure research by fluorescence in situ hybridization (FISH). *Proceedings of the Japan Academy. Series B, Physical and Biological Sciences* 86, 103.
- Paran, I. and Zamir, D., 2003. Quantitative traits in plants: beyond the QTL. *Trends in Genetics* 19, 303-306.
- Pashley, C.H., Ellis, J.R., McCauley, D.E. and Burke, J.M., 2006. EST databases as a source for molecular markers: lessons from *Helianthus*. *Journal of Heredity* 97, 381-388.
- Paterson, A.H., Bowers, J.E., Peterson, D.G., Estill, J.C. and Chapman, B.A., 2003. Structure and evolution of cereal genomes. *Current Opinion in Genetics & Development* 13, 644-650.
- Paterson, A.H., Lander, E.S., Hewitt, J.D., Peterson, S., Lincoln, S.E. and Tanksley, S.D., 1988. Resolution of quantitative traits into Mendelian factors by using a complete linkage map of restriction fragment length polymorphisms. *Nature* 335, 721-726.
- Peñalver Cruz, A., Arida, A., Heong, K.L. and Horgan, F.G., 2011. Aspects of brown planthopper adaptation to resistant rice varieties with the *Bph3* gene. *Entomologia Experimentalis et Applicata* 141, 245-257.
- Perumalsamy, S., Bharani, M., Sudha, M., Nagarajan, P., Arul, L., Saraswathi, R., Balasubramanian, P. and Ramalingam, J., 2010. Functional marker-assisted selection for bacterial leaf blight resistance genes in rice (*Oryza sativa* L.). *Plant Breeding* 129, 400-406.

- Pieterse, C.M., Leon-Reyes, A., Van der Ent, S. and Van Wees, S.C., 2009. Networking by small-molecule hormones in plant immunity. *Nature Chemical Biology* 5, 308-316.
- Prasanna, B., 2012. Diversity in global maize germplasm: characterization and utilization. *Journal of Biosciences* 37, 843-855.
- Qiu, Y., Guo, J., Jing, S., Zhu, L. and He, G., 2010. High-resolution mapping of the brown planthopper resistance gene *Bph6* in rice and characterizing its resistance in the 9311 and Nipponbare near isogenic backgrounds. *Theoretical and Applied Genetics* 121, 1601-1611.
- Qiu, Y., Guo, J., Jing, S., Zhu, L. and He, G., 2012. Development and characterization of japonica rice lines carrying the brown planthopper-resistance genes *BPH12* and *BPH6*. *Theoretical and Applied Genetics* 124, 485-494.
- Rabiei, B., Valizadeh, M., Ghareyazie, B., Moghaddam, M. and Ali, A., 2004. Identification of QTLs for rice grain size and shape of Iranian cultivars using SSR markers. *Euphytica* 137, 325-332.
- Ragimekula, N., Varadarajula, N.N., Mallapuram, S.P., Gangimani, G., Reddy, R.K. and Kondreddy, H.R., 2013. Marker assisted selection in disease resistance breeding. *Journal of Plant Breeding and Genetics* 1(2), 90-109.
- Rahman, L., Qiao, Y.L., Jiang, W., Jena, K.K., Chu, S.-h. and Koh, H.-J., 2008. Genetic analysis and high-resolution mapping of two rice brown planthopper resistant genes, *Bph20* (t) and *Bph21* (t) from An *Oryza Minuta* introgression line, Crop Science Society of Korea. Korean Society Of Crop Science, Korea, pp. 272-273.
- Rahman, M.L., Jiang, W., Chu, S.H., Qiao, Y., Ham, T.-H., Woo, M.-O., Lee, J., Khanam, M.S., Chin, J.-H. and Jeung, J.-U., 2009. High-resolution mapping of two rice brown planthopper resistance genes, *Bph20* (t) and *Bph21* (t), originating from *Oryza minuta*. *Theoretical and Applied Genetics* 119, 1237-1246.
- Ram, T., Deen, R., Gautam, S., Ramesh, K., Rao, Y. and Brar, D., 2010. Identification of new genes for Brown Planthopper resistance in rice introgressed from *O. glaberrima* and *O. minuta*. *Rice Genetics Newsletter* 25, 67.
- Ramaila, M., Mahlangu, S. and du Toit, D., 2013. Agricultural productivity in South Africa: Literature review. Directorate: Economic Services Production Economics Unit. Retrieved.
- Ren, X., Wang, X., Yuan, H., Weng, Q., Zhu, L. and He, G., 2004. Mapping quantitative trait loci and expressed sequence tags related to brown planthopper resistance in rice. *Plant Breeding* 123, 342-348.

- Renganayaki, K., Fritz, A.K., Sadasivam, S., Pammi, S., Harrington, S.E., McCouch, S.R., Kumar, S.M. and Reddy, A.S., 2002. Mapping and Progress toward Map-Based Cloning of Brown Planthopper Biotype-4 Resistance Gene Introgressed from into Cultivated Rice. *Crop Science* 42, 2112-2117.
- Roy, S., Banerjee, A., Bhattacharya, S., Pattanayak, A. and Bansal, K.C., 2013. Omics-based approaches for rice improvement. *OMICS Applications in Crop Science*, 1.
- Rustgi, S., Shafqat, M.N., Kumar, N., Baenziger, P.S., Ali, M.L., Dweikat, I., Campbell, B.T. and Gill, K.S., 2013. Genetic dissection of yield and its component traits using high-density composite map of wheat chromosome 3A: Bridging gaps between QTLs and underlying genes. *PloS One* 8, e70526.
- Saha, P., Dasgupta, I. and Das, S., 2006. A novel approach for developing resistance in rice against phloem limited viruses by antagonizing the phloem feeding hemipteran vectors. *Plant Molecular Biology* 62, 735-752.
- Saito, A., Yano, M. and Kishimoto, N., 1991. QTL mapping for the paste viscosity characteristics in rice. *Japan Breeding* 41, 665-670.
- Salvi, S. and Tuberosa, R., 2005. To clone or not to clone plant QTLs: present and future challenges. *Trends in Plant Science* 10, 297-304.
- Sandhu, S., Colombo, C., Bastos, C.n.R. and Siqueira, W.J., 2003. DNA tagging of blast resistant gene (s) in three Brazilian rice cultivars. *Genetics and Molecular Biology* 26, 473-476.
- Sangha, J.S., Chen, Y.H., Palchamy, K., Jahn, G.C., Maheswaran, M., Adalla, C.B. and Leung, H., 2008. Categories and inheritance of resistance to *Nilaparvata lugens* (Hemiptera: Delphacidae) in mutants of Indica Rice 'IR64'. *Journal of Economic Entomology* 101, 575-583.
- SAS, I., 2003. SAS version 9.1. SAS institute Cary, North Carolina, USA.
- Savary, S., Horgan, F., Willocquet, L. and Heong, K., 2012. A review of principles for sustainable pest management in rice. *Crop Protection* 32, 54-63.
- Sax, K., 1923. The association of size differences with seed-coat pattern and pigmentation in *Phaseolus vulgaris*. *Genetics* 8, 552.
- Saxena, R. and Barrion, A., 1987. Biotypes of insect pests of agricultural crops. *Insect Science* 8, 5.
- Saxena, R. and Pathak, M., 1979. Factors governing susceptibility and resistance of certain rice varieties to the brown planthopper. *Brown Planthopper: Threat to Rice Production in Asia*, 303-317.
- Schrodi, S.J., Mukherjee, S., Shan, Y., Tromp, G., Sninsky, J.J., Callear, A.P., Carter, T.C., Ye, Z., Haines, J.L. and Brilliant, M.H., 2014. Genetic-based

prediction of disease traits: prediction is very difficult, especially about the future. *Applied Genetic Epidemiology* 5, 162.

- Senguttuvan, T., Gopalan, M. and Chelliah, S., 1991. Impact of resistance mechanisms in rice against the brown planthopper, *Nilaparvata lugens* Stål (Homoptera: Delphacidae). *Crop Protection* 10, 125-128.
- Sharma, A., Namdeo, A. and Mahadik, K., 2008. Molecular markers: new prospects in plant genome analysis. *Pharmacognosy Reviews* 2.
- Sharma, H.C., 2008. Biotechnological approaches for pest management and ecological sustainability, CRC Press.
- Sharma, P., Ketipearachchi, Y., Murata, K., Torii, A., Takumi, S., Mori, N. and Nakamura, C., 2003. RFLP/AFLP mapping of a brown planthopper (*Nilaparvata lugens* Stall) resistance gene *Bph1* in rice. *Euphytica* 129, 109-117.
- Sharma, P., Torii, A., Takumi, S., Mori, N. and Nakamura, C., 2004. Marker-assisted pyramiding of brown planthopper (*Nilaparvata lugens* Stal) resistance genes *Bph1* and *Bph2* on rice chromosome 12. *Hereditas* 140, 61-69.
- Sidhu, G. and Khush, G., 1978. Genetic analysis of brown planthopper resistance in twenty varieties of rice, *Oryza saliva* L. *Theoretical and Applied Genetics* 53, 199-203.
- Skov, E. and Wellendorf, H., 1992. Application of RAPD for high density genome mapping and search for linkage to QTL in Norway spruce (*Picea abies*), International Conference on the Plant Genome, Plant Genome I.
- Soller, M. and Beckmann, J., 1983. Genetic polymorphism in varietal identification and genetic improvement. *Theoretical and Applied Genetics* 67, 25-33.
- Sonah, H., Deshmukh, R.K., Sharma, A., Singh, V.P., Gupta, D.K., Gacche, R.N., Rana, J.C., Singh, N.K. and Sharma, T.R., 2011. Genome-wide distribution and organization of microsatellites in plants: an insight into marker development in *Brachypodium*. *Plos One* 6, e21298.
- Soundararajan, R., Kadirvel, P., Gunathilagaraj, K. and Maheswaran, M., 2004. Mapping of quantitative trait loci associated with resistance to brown planthopper in rice by means of a doubled haploid population. *Crop Science* 44, 2214-2220.
- Steele, K., Price, A., Shashidhar, H. and Witcombe, J., 2006. Marker-assisted selection to introgress rice QTLs controlling root traits into an Indian upland rice variety. *Theoretical and Applied Genetics* 112, 208-221.
- Stuber, C. and Moll, R., 1972. Frequency changes of isozyme alleles in a selection experiment for grain yield in maize (*Zea mays* L.). *Crop Science* 12, 337-340.

- Su, C.-C., Cheng, X.-N., Zhai, H.-Q. and Wan, J., 2002. Detection and analysis of QTL for resistance to the brown planthopper, *Nilaparvata lugens* (Stal), in rice (*Oryza sativa* L.), using backcross inbred lines. *Yi chuan xue bao= Acta Genetica Sinica* 29, 332-338.
- Su, C., Wan, J., Zhai, H., Wang, C., Sun, L., Yasui, H. and Yoshimura, A., 2005. A new locus for resistance to brown planthopper identified in the indica rice variety DV85. *Plant breeding* 124, 93-95.
- Su, C., Zhai, H., Wang, C., Sun, L. and Wan, J., 2006. SSR Mapping of Brown Planthopper Resistance Gene *Bph9* in Kaharamana, an *Indica* Rice (*Oryza sativa* L.). *Acta Genetica Sinica* 33, 262-268.
- Suh, J., Yang, S., Jeung, J., Pamplona, A., Kim, J., Lee, J., Hong, H., Yang, C., Kim, Y. and Jena, 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.
- Sun, J., Zhang, Y., Ge, C. and Hong, X., 2011. Mining and characterization of sequence tagged microsatellites from the brown planthopper *Nilaparvata lugens*. *Journal of Insect Science* 11, 1-11.
- Sun, L.-H., Wang, C.-M., Su, C.-C., Liu, Y.-Q., Zhai, H.-Q. and Wan, J.-M., 2006. Mapping and marker-assisted selection of a brown planthopper resistance gene *bph2* in rice (*Oryza sativa* L.). *Acta Genetica Sinica* 33, 717-723.
- Sun, L., Liu, Y., Jiang, L., Su, C., Wang, C., Zhai, H. and Wan, J., 2007. Identification of quantitative trait loci associated with resistance to brown planthopper in the indica rice cultivar Col. 5 Thailand. *Hereditas* 144, 48-52.
- Sun, L., Su, C., Wang, C., Zhai, H. and Wan, J., 2005a. Mapping of a major resistance gene to the brown planthopper in the rice cultivar Rathu Heenati. *Breeding Science* 55, 391-396.
- Sun, L., Su, C., Wang, C., Zhai, H. and Wan, J., 2005b. Mapping of a major resistance gene to the brown planthopper in the rice cultivar Rathu Heenati. *Breeding Science* 55, 391.
- Sundaram, R., Naveenkumar, B., Biradar, S., Balachandran, S., Mishra, B., IlyasAhmed, M., Viraktamath, B., Ramesha, M. and Sarma, N., 2008. Identification of informative SSR markers capable of distinguishing hybrid rice parental lines and their utilization in seed purity assessment. *Euphytica* 163, 215-224.
- Suseela Gomathi, K., 2002. Identification of genetic locus associated with resistance to brown planthopper. Tamil Nadu Agricultural University.

- Takeda, S. and Matsuoka, M., 2008. Genetic approaches to crop improvement: responding to environmental and population changes. *Nature Reviews Genetics* 9, 444-457.
- Tan, S. and Wu, S., 2012. Genome wide analysis of nucleotide-binding site disease resistance genes in *Brachypodium distachyon*. *Comparative and Functional Genomics* 2012.
- Vaughan, D.A., Kadowaki, K.-i., Kaga, A. and Tomooka, N., 2005. On the phylogeny and biogeography of the genus *Oryza*. *Breeding Science* 55, 113-122.
- Vaughan, D.A., Morishima, H. and Kadowaki, K., 2003. Diversity in the *Oryza* genus. *Current Opinion in Plant Biology* 6, 139-146.
- Vipin, C.A., Luckett, D.J., Harper, J.D., Ash, G.J., Kilian, A., Ellwood, S.R., Phan, H.T. and Raman, H., 2013. Construction of integrated linkage map of a recombinant inbred line population of white lupin (*Lupinus albus* L.). *Breeding Science* 63, 292.
- Vos, P., Hogers, R., Bleeker, M., Reijmans, M., Van de Lee, T., Hornes, M., Friters, A., Pot, J., Paleman, J. and Kuiper, M., 1995. AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Research* 23, 4407-4414.
- Wan, B., Zha, Z., Li, J., Xia, M., Du, X., Lin, Y. and Yin, D., 2014. Development of elite rice restorer lines in the genetic background of R022 possessing tolerance to brown planthopper, stem borer, leaf folder and herbicide through marker-assisted breeding. *Euphytica* 195, 129-142.
- Wang, C.-S., Tseng, T.-H. and Lin, C.-Y., 2002. Rice biotech research at the Taiwan Agricultural Research Institute. *Asia-Pacific Biotech News* 6, 950-956.
- Wang, C., Qi, H., Pan, H., Li, J., Fan, Y., Zhang, Q. and Zhao, K., 2005. EST-markers flanking the rice bacterial blight resistance gene *Xa23* and their application in marker-assisted selection. *Scientia Agricultura Sinica* 38, 1996-2001.
- Wang, J., Li, H., Zhang, L., Li, C. and Meng, L., 2014. QTL IciMapping v4.0.1.0 Institute of Crop Sciences, CAAS, Beijing, China and Crop Research Informatics Laboratory, CIMMYT, Apdo., Mexico, DF, Mexico.
- Wang, Y., Guo, H., Li, H., Zhang, H. and Miao, X., 2012. Identification of transcription factors potential related to brown planthopper resistance in rice via microarray expression profiling. *BMC Genomics* 13, 687.
- Williams, J., Kubelik, A., Livak, K., Rafalski, J. and Tingey, S., 1990. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Research* 18, 6531-6535.
- Wu, H., Liu, Y., He, J., Liu, Y., Jiang, L., Liu, L., Wang, C., Cheng, X. and Wan, J., 2014. Fine mapping of brown planthopper (*Nilaparvata lugens* Stal)

resistance gene *Bph28 (t)* in rice (*Oryza sativa* L.). *Molecular Breeding* 33, 909-918.

- Wu, Y., Ko, P., Lee, W., Wei, F., Kuo, S., Ho, S., Hour, A., Hsing, Y. and Lin, Y., 2010. Comparative analyses of linkage maps and segregation distortion of two F₂ populations derived from japonica crossed with indica rice. *Hereditas* 147, 225-236.
- Xanthopoulou, A., Ganopoulos, I., Tsaballa, A., Nianiou-Obeidat, I., Kalivas, A., Tsaftaris, A. and Madesis, P., 2014. Summer squash identification by high-resolution-melting (HRM) analysis using gene-based EST-SSR molecular markers. *Plant Molecular Biology Reporter* 32, 395-405.
- Xu, J., Liu, L., Xu, Y., Chen, C., Rong, T., Ali, F., Zhou, S., Wu, F., Liu, Y. and Wang, J., 2013. Development and characterization of simple sequence repeat markers providing genome-wide coverage and high resolution in maize. *DNA Research* 20, 497-509.
- Xu, X., Mei, H., Luo, L., Cheng, X. and Li, Z., 2002. RFLP-facilitated investigation of the quantitative resistance of rice to brown planthopper (*Nilaparvata lugens*). *Theoretical and Applied Genetics* 104, 248-253.
- Xu, Y., Skinner, D.J., Wu, H., Palacios-Rojas, N., Araus, J.L., Yan, J., Gao, S., Warburton, M.L. and Crouch, J.H., 2009. Advances in maize genomics and their value for enhancing genetic gains from breeding. *International Journal of Plant Genomics* 2009.
- Yamasaki, M., Yoshimura, A. and Yasui, H., 2000. Mapping of quantitative trait loci of ovicidal response to brown planthopper (*Nilaparvata lugens* Stal) in rice (*Oryza sativa* L.). *Breeding Science* 50, 291-296.
- Yang, H., Hu, L., Hurek, T. and Reinhold-Hurek, B., 2010. Global characterization of the root transcriptome of a wild species of rice, *Oryza longistaminata*, by deep sequencing. *BMC Genomics* 11, 705.
- Yang, H., Ren, X., Weng, Q., Zhu, L. and He, G., 2002. Molecular mapping and genetic analysis of a rice brown planthopper (*Nilaparvata lugens* Stal) resistance gene. *Hereditas* 136, 39-43.
- Yang, H., You, A., Yang, Z., Zhang, F., He, R., Zhu, L. and He, G., 2004. High-resolution genetic mapping at the *Bph15* locus for brown planthopper resistance in rice (*Oryza sativa* L.). *Theoretical and Applied Genetics* 110, 182-191.
- Yang, L., Li, R., Li, Y., Huang, F., Chen, Y., Huang, S.S., Huang, L., Liu, C., Ma, Z. and Huang, D., 2012. Genetic mapping of *bph20 (t)* and *bph21 (t)* loci conferring brown planthopper resistance to *Nilaparvata lugens* Stal in rice (*Oryza sativa* L.). *Euphytica* 183, 161-171.

- Yara, A., Phi, C., Matsumura, M., Yoshimura, A. and Yasui, H., 2010. Development of near-isogenic lines for *BPH25(t)* and *BPH26 (t)*, which confer resistance to the brown planthopper, *Nilaparvata lugens* (Stal.) in indica rice 'ADR52'. *Breeding Science* 60, 639-647.
- Ye, C., Argayoso, M.A., Redoña, E.D., Sierra, S.N., Laza, M.A., Dilla, C.J., Mo, Y., Thomson, M.J., Chin, J. and Delaviña, C.B., 2012. Mapping QTL for heat tolerance at flowering stage in rice using SNP markers. *Plant Breeding* 131, 33-41.
- Zhang, F., Guo, H., Zheng, H., Zhou, T., Zhou, Y., Wang, S., Fang, R., Qian, W. and Chen, X., 2010. Massively parallel pyrosequencing-based transcriptome analyses of small brown planthopper (*Laodelphax striatellus*), a vector insect transmitting rice stripe virus (RSV). *BMC Genomics* 11, 303.
- Zhang, Q., 2007. Strategies for developing green super rice. *Proceedings of the national Academy of Sciences* 104, 16402-16409.
- Science* 63, 347.
- Zhou, W.C., Kolb, F., Bai, G.H., Domier, L., Boze, L. and Smith, N., 2003. Validation of a major QTL for scab resistance with SSR markers and use of marker-assisted selection in wheat. *Plant Breeding* 122, 40-46.
- Zhu, L., Zhu, C., Wang, Q. and Huang, Z., 2003. Research progress on brown planthopper resistance genes in rice. *Hubei Agricultural Sciences* 1, 19-24.
- Zhu, Q., Zheng, X., Luo, J., Gaut, B.S. and Ge, S., 2007. Multilocus analysis of nucleotide variation of *Oryza sativa* and its wild relatives: severe bottleneck during domestication of rice. *Molecular Biology and Evolution* 24, 875-888.