

UNIVERSITI PUTRA MALAYSIA

GENETIC DIVERGENCE OF RICE GENOTYPES RESISTANT TO BACTERIAL BLIGHT REVEALED BY QUANTITATIVE TRAITS AND MOLECULAR MARKERS

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Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfilment of the requirement for the Degree of Master of Science

January 2013

DEDICATION

THIS THESIS IS SPECIALLY DEDICATED

TO

MY PARENTS AND MY BELOVED FAMILY



Abstract of thesis Presented to the Senate of Universiti Putra Malaysia in the fulfilment of the Requirement for the Degree of Master of Science

GENETIC DIVERGENCE OF RICE GENOTYPES RESISTANT TO BACTERIAL BLIGHT REVEALED BY QUANTITATIVE TRAITS AND MOLECULAR MARKERS

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January 2013

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Globally, bacterial blight (BB) (*Xanthomonas oryzae pv oryzae*) of rice is one of the major diseases that impedes rice production to large extent. The strategy of utilizing BB resistant major genes, solely or in combination, continues to be the most fruitful way for controlling this disease. Genetic diversity plays pivotal role in crop improvement. Molecular markers along with quantitative traits have shown their efficacy in the assessment of genetic diversity. Information regarding genetic diversity among the BB resistant genotypes is currently not available adequately in Malaysia. Forty-one rice genotypes obtained from International Rice Research Institute (IRRI), Malaysian Agricultural Research and Development Institute (MARDI) and Bangladesh Rice Research Institute (BRRI) were evaluated at Field 2, Universiti Putra Malaysia. The aims of this study were to determine genetic diversity as well as selection of best genotypes using morphological, physiological traits, and simple sequence repeats (SSR) and inter simple sequence repeats (ISSR) markers. In this study, significant variation was observed among the genotypes for growth, physiological and yield traits. It was also found in the

present study, that yield per hill, total number of spikelets per panicle and number of filled grains per panicle had high heritability and genetic advance which are regarded as important for trait selection by the scientists. Cluster analyses based on morphological and physiological traits grouped 41 rice genotypes into six and seven groups respectively. The first four principal components (PCs) from principal component analysis (PCA) based on morphological traits showed 70.80% of total variation while the first three PCs showed 66.60% based on physiological traits. The genetic diversity of the 41 rice genotypes was evaluated with 26 SSR and 20 ISSR markers. A total of 88 alleles and 310 polymorphic loci were detected across the 26 SSR markers and 20 ISSR markers respectively. Cluster analysis based on SSR markers and ISSR markers divided 41 rice genotypes into seven and 11 groups respectively including several sub-clusters. First three PCA from SSR analysis indicated 70.99% of total variation while 37.28% of total variation was found from ISSR analysis. Analysis of molecular variance from SSR analysis expressed 67% variation within populations on the contrary, it was 84% from ISSR markers analysis. The Mantel test revealed positive correlation between quantitative traits and molecular markers. The results of the present study recommended some genotypes for future breeding based on quantitative traits, and SSR and ISSR markers analyses. It is expected that the genotypic combinations could produce bacterial blight resistant and high yielding genotypes. The recommended genotypes for crossing are as follows: MR185 with IRBB5, MR185 with BR28, IRBB4 with Bahagia, MR253 with MR185, MR232 with Purbachi and MR185 with MR232.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Master Sains

PENCAPAHAN GENETIK GENOTIP PADI RINTANG LAYU BAKTERIA BERDASARKANCIRI KUANTITATIF DAN PENANDA MOLEKUL

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Di peringkat global, hawar bakteria (BB) padiadalah salah satu penyakit yang menjadi halangan pengeluaran padi secara besaran. Pendekatan strategik pengunaan gen major rintang BB, secara sepenuhnya atau kombinasi, akan memberikan hasil yang baik bagi mengawal penyakit ini. Kepelbagaian genetik memainkan peranan yang sangat penting dalam memajukan tanaman. Penanda molekul serta ciri kuantitatif telah menunjukkan keberkesanan dalam penilaian kepelbagaian genetik. Di Malaysia, pada masa kini, maklumat berkaitan kepelbagaian genetik dikalangan genotip padi rintang BB adalah tidak mencukupi. Empat puloh satu genotip padi yang diperolehi dari Institut Penyelidikan Padi Antarabangsa (IRRI), Institut Penyelidikan dan Kemajuan Pertanian Malaysia (MARDI) dan Institut Penyelidikan Padi Bangladesh (BRRI) telah dinilai di Ladang 2, Universiti Putra Malaysia. Objektif kajian ini adalah untuk menentukan kepelbagaian genetik dan seterusnya memilih genotip terbaik berdasarkan ciri morfologi, fisiologi, dan penanda SSR dan ISSR.Dalam kajian ini, variasi yang bererti di kalangan genotip telahdidapati bagi ciri pertumbuhan, fisiologi dan hasil. Analisis kluster

berdasarkan ciri morfologi dan fisiologi telah membahagikan 41 genotip padi masingmasing kepada enam dan tujuh kumpulan. Empat PCs yang pertama dari analisis PCA berdasarkan ciri morfologi menunjukkan 70.80% dari jumlah variasi, sementara itu tiga PCs yang pertama menunjukkan 66.60% berdasarkan ciri fisiologi. Kepelbagaian genetik 41 genotip padi tersebut telah dinilai mengunakan 26 penanda SSR dan 20 penanda ISSR. Sejumlah 88 alel dan 310 lokus polimorfik telah diperolehi melalui 26 penanda SSR dan 20 penanda ISSR. Analisis kluster berdasarkan penanda SSR dan ISSR telah mengumpulkan 41 genotip padi tersebut kepada masing-masing tujuh dan11 kumpulan, termasuk beberapa sub-kluster. Tiga PCA yang pertama dari analisis SSR menunjukkan 70.99% dari jumlah variasi, sementara itu 37.28% dari jumlah variasi diperolehi dari analisis ISSR. Analisis varians molekular bagi SSR memberikan 67% variasi di dalam populasi, sebaliknya bagi penanda ISSR adalah 84%. Ujian Mantel menunjukkan korelasi positif antara ciri kuantitatif dan penanda molekul. Hasil kajian ini mengesyorkan beberapa genotip untuk pembiakbakaan masa depan berdasarkan analisis ciri kuantitatif, dan penanda SSR dan ISSR. Genotip yang dicadangkan untuk kacukkan tersebut adalah seperti berikut: MR185 dengan IRBB5, MR185 dengan BR28, IRBB4 dengan Bahagia, MR253 dengan MR185, MR232 dengan Purbachi and MR185 dengan MR232.

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DECLARATION

I declare that the thesis is my original work except for quotations and citations which have been duly acknowledged. I also declare that it has not been previously, and is not concurrently, submitted for any other degree at Univesiti Putra Malaysia or at any other institution.



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