SCREENING OF CULTIVAR AND WEEDY RICE WITH BIRD PEPPER.

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FAKULTI SAINS DAN TEKNOLOGI
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2008

Screening of cultivar and weedy rice with RAPD primer. /
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Lihat sebelah

SCREENING OF CULTIVAR AND WEEDY RICE WITH RAPD PRIMER

By

Maliza binti Mohktar

A research report submitted in partial fulfillment of
the requirements for the award of the degree of
Bachelor of Science (Biological Sciences)

DEPARTMENT OF BIOLOGICAL SCIENCES
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PENGAKUAN DAN PENGESAHAN LAPORAN PITA I DAN II

Adalah ini diakui dan disahkan bahawa laporan penyelidikan bertajuk: **Screening of Cultivar and Weedy Rice with RAPD Primer** oleh **Maliza binti Mohktar**, No. Matrik: **UK12505** telah diperiksa dan semua pembetulan yang disarankan telah dilakukan. Laporan ini dikemukakan kepada Jabatan Sains Biologi sebagai memenuhi sebahagian daripada keperluan memperolehi **Ijazah Sarjana Muda Sains (Sains Biologi),** Fakulti Sains dan Teknologi, Universiti Malaysia Terengganu.

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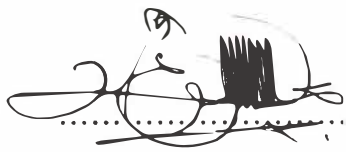
DECLARATION

I, Maliza binti Mohktar, hereby declare that this thesis entitled Screening of Cultivar and Weedy Rice with RAPD Primer is the result of my own research except as cited in the references.

Signature: 

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ABSTRACT

Weedy rice (*Oryza sativa f. spontanea*) is taxonomically classified as the same species as cultivar rice (*Oryza sativa*) but has characterized by seeds strong difference in seeds shattering and dormancy. Weedy rice has serious effect on rice population by causing yield reduction and affects the quality of rice grains. Thus, this study was aimed to develop RAPD marker, which could be used to differentiate cultivar and weedy rice. All together, nine different RAPD primers were used to screen the genomic DNA extracted from cultivar rice (CR) and three different biotypes of weedy rice (WR1, WR2 and WR3). Screening results revealed that two RAPD primers designated A-04 and A-09 produced specific bands that have the potential to be used as marker to discriminate between rice and weedy rice biotypes. Primer A-04 produced a band (750bp) specific to CR, WR2 and WR3, while primer A-09 produced a band (1100bp) specific to CR and WR3. The specific bands produce by primer A-04 in all three biotypes (CR, WR2 and WR3) was successfully cloned into pGEM-T vector. Positive colonies were selected from each biotype and were named as pCR-A04, pWR2-A04 and pWR3-A04 respectively. DNA sequencing of these clones showed that the exact size of clone pCR-A04 was 706bp, while clones pWR2-A04 and pWR3-A04 were 707bp. Homology search in the Genebank databases revealed that all three clones showed significantly amino acid identities of 89% - 95% to retrotransposon protein from various rice cultivars. Multiple alignment of the nucleotide sequences of these clones showed that there were various specific point mutation, which could be used to design SCAR markers specific to each of the biotypes.

ABSTRAK

Padi angin (*Oryza sativa f. spontanea*) boleh diklasifikasikan dalam spesis yang sama seperti padi (*Oryza sativa*) tetapi mempunyai ciri-ciri perbezaan yang ketara dalam penguguran dan kependaman biji benih. Padi angin mengakibatkan kesan yang serius ke atas populasi padi dengan mengurangkan hasil pertanian dan memberi kesan ke atas kualiti biji benih. Oleh itu, kajian ini bertujuan untuk mencipta penanda RAPD di mana ia boleh digunakan untuk membezakan di antara padi dan padi angin. Dengan ini, 9 primer RAPD yang berbeza digunakan untuk menyaring ektrak genomik DNA daripada padi (CR) dan 3 jenis padi angin yang berbeza (WR1, WR2 dan WR3). Keputusan penyaringan menunjukkan bahawa 2 primer RAPD yang dikenali sebagai A-04 dan A-09 menghasilkan jalur yang spesifik yang berpotensi digunakan sebagai penanda untuk mengasingkan di antara padi dan padi angin. Primer A-04 menghasilkan jalur (750bp) yang spesifik untuk CR, WR2 dan WR3, manakala primer A-09 menghasilkan jalur (1100bp) yang spesifik untuk CR dan WR3. Kesemua jalur yang spesifik yang dihasilkan oleh primer A-04 adalah untuk 3 jenis (CR, WR2 dan WR3) telah berjaya diklonkan ke dalam vektor pGEM-T. Koloni yang positif dipilih daripada setiap jenis dan dinamakan sebagai pCR-A04, pWR2-A04 dan pWR3-A04. Penyusunan DNA bagi ketiga-tiga klon menunjukkan saiz sebenar setiap klon iaitu bagi pCR-A04 ialah 706bp, manakala bagi pWR2-A04 dan pWR3-A04 ialah 707bp. Pencarian homologi tumbuhan di dalam pengkalan data bankgen menunjukkan ketiga-tiga klon mempunyai peratusan identiti asid amino sebanyak 89% - 95% untuk retrotransposon daripada pelbagai jenis padi. Penyusunan susunan nukleotida bagi 3 klon itu menunjukkan bahawa terdapat pelbagai tanda mutasi yang spesifik di mana ia boleh digunakan untuk mereka penanda SCAR yang spesifik untuk setiap jenis.