

O-MB-14

IDENTIFICATION OF POLYMORPHISM ON SIMPLE SEQUENCE REPEATS MARKERS ASSOCIATED WITH BROWN PLANTHOPPER RESISTANCE GENES IN TWENTY RICE GENOTYPES AND THEIR GENETIC RELATIONSHIP

Nono Carsono^{1*}, Yessikha V. Barus⁴, Santika Sari⁵, Winny D. Widarmi⁵, Danar Dono², Yayan Sumekar³, and Murdaningsih H.K¹

¹ Staff, Lab of Plant Biotechnology and Breeding, Faculty of Agriculture, Universitas Padjadjaran, Jatinangor, Bandung – Sumedang 45363. E-mail: ncarsono@unpad.ac.id (Author for correspondence).

² Staff, Lab of Entomology, Faculty of Agriculture, Universitas Padjadjaran, Jatinangor, Bandung – Sumedang 45363.

³ Staff, Lab of Weed Science, Faculty of Agriculture, Universitas Padjadjaran, Jatinangor, Bandung – Sumedang 45363.

⁴ Student, Agrotechnology Study Program, Faculty of Agriculture, Universitas Padjadjaran, Jatinangor, Bandung – Sumedang 45363.

⁵ Student, Master Program in Plant Breeding, Faculty of Agriculture, Universitas Padjadjaran, Jatinangor, Bandung – Sumedang 45363.

ABSTRACT

Brown planthopper is one of the most destructive insect pest of rice in Indonesia and other Asian countries. Pyramiding some brown planthopper resistance genes is a valuable approach to create more durable resistance against the pest. The objective of this study was to identify polymorphisms of Brown Planthopper Resistance genes (*Bph*) on 20 genotypes of rice, and to obtain genetic relationship among genotypes tested. The experiment was conducted from June to September 2012 at Green House and Laboratory of Plant Analysis and Biotechnology, Faculty of Agriculture, Universitas Padjadjaran, Jatinangor. Twenty genotypes were analyzed, and two of them were used as check varieties. Simple Sequence Repeat (SSR) markers were applied to detect *Bph3*, *Bph4*, *Qbph3*, and *Qbph4* genes. Polymorphic levels were analyzed by calculating PIC (*Polymorphic Information Content*). The grouping of rice genotypes were done based on principal components analysis (PCA) of SSR data, and the genetic relationship based on the presence of *Bph* genes was estimated using UPGMA (*Unweighted Pair Group With Arithmetic mean*). Results showed that RM313, RM8072, RM8213, RM5953, RM586, and RM589 markers were polymorphic. Rice genotypes PTB 33, Diah Suci, Cibogo, Cisantana, Digul, Ciharang, Inpari 13, Inpari 10, and Memberamo had *Bph3*, *Qbph3*, *Bph4*, and *Qbph4*. Meanwhile *Bph3*, *Qbph3*, and *Bph4* were supposed to be belonged by IR 64, Aek Sibundong, Batang Gadis, IR 66, and Mekongga. Kalimas and Tukat Penatu had *Bph3*, *Qbph3*, dan *Qbph4*. IR 74 had *Bph3* and *Qbph3*, and Fatmawati had *Bph3* and *Bph4*. UPGMA clustering resulted in two main clusters, in which the first cluster consisted of 2 subclusters. PTB-33 was closely related with Memberamo, Tukat Penatu, Digul, Diah Suci, and Kalimas. The SSR markers used in this study were proven to be valuable in molecular detection of *Bph* genes and in estimating genetic relationships of rice genotypes. PTB-33 was a good donor of resistance genes, as well as Memberamo, Tukat Penatu, Digul, Diah Suci, and Kalimas which were identified as promising donors in rice breeding resistance to brown planthopper.

Key words : *Bph* gene, Brown Planthopper, Genetic relationship, SSR markers.

INTRODUCTION

Indonesia and the other Asian countries are currently facing problems in securing supplies of rice. One reason of the decline in rice production is the brown planthoppers (BPH; *Nilaparvata lugens* Stal.) pests. BPH is a global threat because not only attacking rice crops in Indonesia, but also attacking rice crops in China, Thailand, Vietnam, India, Bangladesh, Malaysia, Philippines, Japan, and Korea (Baehaki, 2007). Interesting phenomenon in the interaction between the rice varieties to brown planthopper is the appearance of biotype, the