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SCAR (Sequence Characterized Amplified Region) Analysis for Blast Resistant Evaluation on 12 Genotypes of Rice

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ABSTRACT

Resistance evaluation to blast disease (Pyricularia grisea) on 12 paddy genotypes was carried out in the green house by using spray inoculated method with race 033 and 041 of P. grisea , and SCAR (Sequence Characterized Amplified Region) marker by using Pib primer pairs. The results revealed that among 12 paddy genotypes were classified into six resistance groups. The first group comprised two genotypes (Jatiluhur and Asahan) having three resistance genes. The second group comprised two genotypes (Oryza malampuzhaensis and O. punctata) having two resistance genes against race 033 and 041. The third group had one resistance gene against race 033, comprised one genotype (Way Rarem). The fourth group comprised one genotype (Danau Tempe) having two resistance genes against 041 race and Pib. The fifth group comprised three genotypes (Kalimutu, Maninjau and Laut Tawar) having two resistance genes against race 033 and Pib. The sixth group comprised two genotypes (Kencana Bali and Cirata) having no resistance gene to blast race 033 and 041, and Pib. These results indicated that Pib gene did not confer resistance to race 033 and 041 of Pyricularia grisea. Resistance to race 033 and 041 might be controlled by different resistant gene.

Key words : SCAR, Blast resistant, Rice

INTRODUCTION

Rice blast, caused by the fungal pathogen *Pyricularia grisea*, is the most serious disease for upland. However, recently it has been reported that the pathogen also infest irrigated rice (Amir *et al.*, 2000). The fungus attacks leaves during early growth stages, develops lesions that are followed by premature leaf senescence of infected tissues, especially in case of heavy infections. After heading, the pathogen infects the panicles or the neck, giving high lost of yield. The use of resistant cultivars is the most effective means on controlling the diseases, however, the useful life span of many cultivars is only few years, due to breakdown of the resistance in the face of high pathogen variability of the fungus (Kiyosawa, 1982).

The genes conferring resistance to rice blast has been studied extensively. So far at least 30 resistance loci have been identified in rice (Inukai *et al.*, 1994), and several loci have recently been mapped by using Restriction Fragments Length Polymorphism (RFLP) markers (Yu *et al.*, 1996; Nakamura *et al.*, 1997). Wang *et al.* (1999) was successfully isolated and characterized *Pib* gene, one of the genes conferring resistance to rice blast disease, by using map-based cloning strategy. The availability of information regarding the complete sequence of *Pib* gene leads to the possibility of developing specific primers to mark the *Pi-b* gene. These markers are classified as Sequence Characterized Amplification Region (SCAR) markers, which offer advantage on accuracy over RAPD markers, since the primer consist of more than 20 bases, and simplicity over RFLP markers. Detection of SCAR markers does not need laborious steps of blotting, hybridization and detection (Sobir, 2000).

Resistance to blast diseases in rice is conferred by R-genes that named as *Pi* genes (Ou, 1985). The *Pi* genes act as major gene, which recognize specific rice blast race, following gene-for-gene hypothesis (Ebron *et al.*, 2002). To date 25 *Pi* genes have been identified already (Fukuta *et al.*, 2002), located in several loci on rice genome (Wang *et al.*,1999). To date, based on reactions pattern to 7 differential varieties, in Indonesia have been identified 27 races of *P. grisea* (Amir *et al.*, 2000), but was not available information, wheather resistance to each of these races controlled by specific

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