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SCAR (Sequence Characterized Amplified Region) Analysis for *Pi-b* and *Pi-ta* genes on 28 Genotypes of Rice

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ABSTRACT

Evaluation to blast disease (Pyricularia grisea) resistance was carried out by using two SCAR (Sequence Characterized Amplified Region) markers of Pi-b and Pi-ta blast resistance genes, and spray-inoculation method with 10 races of P. grisea on 28 paddy genotypes, that consisted six wild genotypes of rice. The results revealed that among 28 paddy genotypes, fifteen genotypes carrying both genes including Oryza rufipogon; six genotypes carrying Pi-b genes including O. alta, two genotypes carrying Pi-ta gene, and five genotypes did not possess both gene including O. glumaepatula, O. officinalis, O. latifolia, and O. malapuzhaensis. Based on infection intensity, the evaluated genotypes were vary in responses to different ten races of P. grisea, indicated that the evaluated genotypes were vary in carrying Pi genes. Analysis in detail indicated that existence of Pi-ta gene associated with lower infection intensity caused by P. grisea race 063 C.

Keywords: SCAR markers, rice blast resistance, Pyricularia grisea

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 of them have recently been mapped by using Restriction Fragments Length Polymorphism (RFLP) markers (Yu *et al*., 1996; Nakamura *et al*., 1997). Wang *et al.* (1999) has successfully isolated and characterized *Pi-b* 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 Pib 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 (Lee, 1995).

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 seven differential varieties, 27 races of *P. grisea* have been identified in Indonesia (Amir, *et al*., 2000), but there is not available information, whether the resistance to each of these races controlled by specific *Pi* gene or not. The dominant *Pi-b* gene confers high resistance to most Japanese blast race. However, in Indonesia, this gene has not been identified yet particularly which fungus race this gene conferred to and which varieties carrying the gene. Mc Couch *et al*. (1994) indicated that *Pi-ta* gene located at chromosome 9 or 12.

In order to evaluate the existence of *Pi-b* and *Pi-ta* genes in cultivated rice in Indonesia along with wild species of rice, molecular analysis by utilizing *Pi*-b and *Pi-ta* SCAR (Sequence Characterized Amplified Region) markers, and spray-inoculation method were conducted to 22 cultivated rice and 6 wild species.

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