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Introgression of Bcterial Leaf Blight Resistance Gene from Oryza Minuta J.B. Presl. Ex C. B. Presl. into New Rice Type (Oryza sativa L.)

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ABSTRACT

F_1 Hybrids, backcross progenies, advanced introgression lines (2n=24) and monosomic alien addition lines or MAALs (2n=25) were successfully produced following embryo rescue between an elite new plant type (NPT) breeding line of Oryza sativa (2n=24, AA) and a wild species, O. minuta (2n=48, BBCC). F_1 hybrids performance were intermediate between the parents. The F_1 hybrids had 36 chromosomes indicating having 12 chromosome A from O. sativa and 12 B and 12 C from O. minuta. THE BACK CROSS progenies had different chromosome number indicating abnormal meiosis of the hybrids and back cross progenies. Plant with 2n=24 and 25 chromosomes were obtained in BC_4F_1. The hybrids and backcross progenies were susceptible to bacterial leaf blight (BB). However, several of the 2n=24 plants derived resistant plant to bacterial leaf bligkt race 1 of the Philippines races. The gene is different from introgressed gene intio rice from O. longistaminata (Xa21) and from O. Minuta Acc. 101141.

Key words: Oryza minuta, MAALS, Bacterial leaf blight

INTRODUCTION

Rice is important cereal for one third of the world population. During the last three decades, world rice production has doubled from 257 million tons in 1966 to 563 million tons in 1998. More than 90 percent of rice is produced and consumed in Asia. To meet the growing need of an ever increasing human population, 50% more rice is needed by 2025, hence, rice varieties with higher yield potential are needed to meet the global need. To achieve this, IRRI is exploring a new plant type (NPT) of rice which could increase the yield potential by 20% (Khush, 1995). The NPT has the characteristics of few but all productive tillers, large panicles, 200-250 grains per panicles, sturdier stems, deeper root system, thick and dark green leaves and maturity of 115-120 days. Although major increases in rice production have occurred, several biotic and abiotic stresses limit rice production. Moreover, diseases and insect pest are a continued threat, particularly due to changes in insect biotypes and pathotypes. There is, thus, an urgent need to broaden the rice gene pool and identify new genes for resistance to major diseases and insect pests from diverse sources. Wild species are important reservoir of useful genes for rice improvement (Sitch, 1990; Brar and Khush, 1997).

A number of pathogens and insects attack the rice plants. One of the major rice diseases is bacterial blight (BB). Bacterial blight of rice caused by Xanthomonas oryzae pv. Oryzae is one of the important rice production constraints (Mackill, 1986). It reduces grain yield to varying levels depending upon the stage of the crop affected and degree of susceptibility of cultivar. Losses due to bacterial blight in the tropics are higher than in temperate regions (Mizukami and Wakimoto, 1969) because of the prevalence of more virulent populations of the pathogen (Buddenhagen and Reddy, 1972). Xanthomonas oryzae pv. Oryzae (Xoo) produces bacteriocin like substances on solid media (Mew, 1987). The proteins function as signal molecules which affect host-specific plants responses such as cell division, water soaking (i.e.,filling of the cellular spaces in the leaf mesophyll with water instead of air) and the hypersensitive response. The first evidence for pathogenic specialization was reported in 1979 by Vera-Crus and Mew. They recognized four bacterial groups where interaction was confined to a specific cultivar-isolate combination. "Race" was adopted to classify the bacterial isolates. Each race has specific virulence to

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