

## DEVELOPMENT OF MOLECULAR MARKERS FOR THE INTROGRESSION OF BROAD SPECTRUM BLAST RESISTANCE GENES INTO RICE GERMPLASM CULTIVATED IN ITALY

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Rice blast, which is caused by the fungus *Magnaporthe grisea*, is the most economically important fungal disease in the world's rice-growing areas. Development of resistant cultivars is considered to be the most effective method against blast. Currently, more than 40 rice blast resistance genes have been identified and over 25 of them have been mapped on the rice genome (Chao et al., 1999, Euphytica 109: 183-190). The resistance in newly released rice cultivars to rice blast can be lost quickly due to the high level of instability in the genome of this fungus (Bonman et al., 1992, Annu Rev Phytopathol 30: 507-528); this problem can be overcome by pyramiding multiple resistance genes each recognizing different sets of *Magnaporthe grisea* isolates into a single cultivar, or deploying rice cultivars with broad spectrum resistance or utilizing both the approaches at the same time.

To our knowledge, no known blast resistance genes have been introgressed into elite Italian rice cultivars and this results in a generalized susceptibility of the cultivated Italian rice germplasm with respect to the rice blast disease. Genetic improvement of blast resistance therefore represents a priority of the rice breeding in Italy.

With this purpose in mind, we have collected rice germplasm bearing several known broad range effective blast resistance genes. PCR-based molecular markers linked to these genes have been developed from published primers or by designing primers in genomic regions tightly associated to the genomic map position of the selected blast resistance genes. Allelic variation of the molecular markers obtained (SSR, CAPS, STS) was evaluated into the donors of the blast resistance genes and within a representative collection of rice germplasm that include cultivated, traditional and of general interest rice genotypes. Polymorphic combinations that could allow both the introgression of the broad spectrum resistances into susceptible genetic background and the pyramiding of resistance genes have been identified, suggesting that the markers identified could represent suitable tools for the breeding of rice blast resistance of Italian rice germplasm.