

DEVELOPMENT OF MOLECULAR MARKERS FOR THE INTROGRESSION OF BROAD SPECTRUM BLAST RESISTANCE GENES INTO ITALIAN RICE GERMPLASM

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rice, rice blast resistance, PCR-based marker, gene pyramiding

Rice blast, caused by the fungus *Pyricularia grisea* (sexual form *Magnaporthe grisea*), is the most economically important fungal disease in the world's rice-growing areas. Development of resistant cultivars is considered the most effective method to contrast the pathogen. However, cultivars undergo rapid breakdown in their resistance mainly due to the emergence of new pathotypes, due to the high level of instability in the genome of the pathogen (Kiyosawa, 1972; Bonman et al., 1992). More than 40 rice blast resistance genes have been identified and most them have been mapped on the rice genome. In the breeding strategy, the possibility of pyramiding two or more resistance genes into a genotype, is considered a powerful tool to build up broad and durable resistance in a new variety (Francia et al., 2005). Italian rice germplasm is generally characterized by moderate to high sensitivity to blast; in particular, no known blast resistance genes have been introgressed into target varieties and this results in a generalized susceptibility of the cultivated Italian rice germplasm to the pathogen. Molecular assisted breeding is therefore required as major tool to build up new competitive varieties.

In the present work, we have collected a series of 25 rice genotypes bearing 13 known broad range resistance genes, effective against blast. More than twenty-five 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 genes. Allelic variation of the molecular markers obtained (SSR, CAPS, STS, InDel) was evaluated into the donors of the blast resistance genes and within a representative collection of about 90 rice genotypes, including traditional and modern rice varieties, and varieties for special use. Polymorphic combinations allowing both the introgression of the broad spectrum resistances into susceptible genetic background and the pyramiding of resistance genes, have been identified, thus confirming the potential of the identified markers for molecular-assisted breeding. Molecular analyses and genotyping of the rice collection are coupled to pathogenicity assays performed on seedlings in controlled conditions, with three known blast isolates representative of the Italian blast population, and in field conditions to verify the efficacy of the known resistance genes against the actual pathogen pathotypes.

This study acknowledges financial support of the project CEREALAB (Regione Emilia Romagna) and of the EU co-funded project EURIGEN (049 AGRI GEN RES).

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