

MARKER-ASSISTED PYRAMIDING OF BLAST RESISTANCE GENES BY FORWARD AND BACKGROUND SELECTION IN A JAPONICA ELITE RICE CULTIVAR

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Rice blast, caused by *Magnaporthe oryzae*, is the most important rice fungal diseases worldwide. The pyramiding of blast resistance *Pi* genes, coupled to

molecular marker-assisted backcrossing (MABC), should provide broad spectrum and potentially durable resistance while limiting the donor genome in the background of an elite cultivar. Here we applied this procedure, coupled to foreground and background selections based on KASPar assay, to introgress four *Pi* genes (*Piz*, *Pib*, *Pita*, and *Pik*) into a renowned *japonica* Italian rice variety highly susceptible to blast. Up to 95.4% of the recurrent genome was recovered. Interestingly, we also obtained several lines where three *Pi* genes were stacked, with high recovery percentage levels: three *Pi* genes (*Piz* + *Pib* + *Pita* and *Pib* + *Pik* + *Pita*) were present in two lines with 95.45% and 91.30% recovery percentage, respectively, and a reduced number of heterozygous alleles. Phenotyping analyses confirmed the effectiveness of the pyramided lines against multivirulent strains of the fungal pathogen. In conclusion, blast resistant *japonica* lines were developed that could be also useful as blast resistance donors in future breeding programs related to *japonica* rice.