

IDENTIFICATION OF BLAST RESISTANCE LOCI IN JAPONICA RICE THROUGH GENOME WIDE ASSOCIATION STUDY (GWAS)

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The fungus *Pyricularia oryzae*, is the causal agent of rice blast, which represents the most damaging fungal disease of rice worldwide. The vast majority of the rice varieties cultivated in Europe and several other temperate regions are from moderately to severely susceptible to blast, making the identification of resistant sources in temperate *japonica* rices a priority. In the present work, a Genome Wide Association Study (GWAS) for

rice blast resistance was carried-out on a germplasm collection of 311 temperate/tropical *japonica* and *indica* rice accessions adapted to temperate conditions and subjected to genotyping by sequencing to yield 37,423 SNP markers. The panel was evaluated for blast resistance in field conditions for two years, under the disease pressure of the natural blast population, and in growth chamber, using a mixture of three diverse fungal strains. A total of 11 accessions showed high levels of resistance when tested in the two conditions (field and growth chamber), and therefore represent potential donors of resistance genes harbored in rice genotypes adapted to temperate conditions. A general higher level of blast resistance was observed in tropical *japonica* and *indica* with respect to temperate *japonica* varieties. GWAS identified 14 Marker-Traits Associations (MTAs), 8 of which highlighted under field conditions and 6 under growth chamber screening. Three MTAs were in common among the two phenotyping conditions, while 5 MTAs were specifically detected under field conditions and 3 were specific for the growth chamber inoculation. Comparative analysis of physical/genetic positions of the MTAs highlighted for most of them co-positional relationships with cloned or mapped blast resistance genes or with candidate genes whose functions were compatible for conferring resistance to the blast pathogen. However, for 3 MTAs (BRF10, BRF11–2 and BRGC11–3), no obvious candidate genes or positional relationships with previously identified blast resistance loci were highlighted, raising the possibility that they represent new sources of blast resistance. In conclusion, 14 MTAs for blast resistance were identified using both field and growth chamber screenings of a rice germplasm collection. Haplotype analyses of the 11 accessions showing high levels of resistance in both conditions suggested that such levels of resistance were conferred by different combinations of resistance loci. Consequently, the effective combinations of loci conferring blast resistance identified in the rice accessions will provide useful bases for resistance breeding to blast, while the newly identified blast resistance loci will open the way to their further characterization.