



Natural variation of rice blast resistance gene *Pi-d2*

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ABSTRACT. Studying natural variation in rice resistance genes of cultivated and wild rice relatives can predict resistance stability to rice blast fungus. In the present study, the protein coding regions of the rice *R* gene *Pi-d2* in 35 rice accessions, including *Oryza sativa* L. subsp. *indica* Kato (Aus), *indica* (IND), temperate *japonica* (TEJ), tropical *japonica* (TRJ), *aromatic* (ARO); subgroups of *Oryza sativa*; 6 accessions of wild rice varieties; *O. nivara*; and *O. rufipogon* were analyzed. A total of 13

nucleotide differences were found in the open reading frames (ORFs) of *Pi-d2*. Translation of these ORFs revealed 9 variants; 3 were novel *Pi-d2* variants. Variants H2 and H5 were identified in accessions of cultivated rice and *O. nivara*, H1, H3, H4, H6, and H8 were only identified in cultivated rice. H2 and H5 were the common types of IND and *O. nivara*, H8 was the common type of TRJ and AUS, H6 was the specific type of AUS, and H3 was the specific type of ARO. H7 and H9 were specific haplotypes of *O. nivara* and *O. rufipogon*, respectively. These findings demonstrate that *Pi-d2* variants are useful indicators for each subgroup, and *Pi-d2* is an ancient gene that predates speciation of rice subgroups.

Key words: Resistance gene; Natural variation; Blast disease; *Oryza sativa*; *Pi-d2*