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Molecular identification of blast resistance and pathogenesis-related genes in various traditional paddy varieties from different divisions of Sabah, East Malaysia

Abstract

Paddy is the staple food of local people in Sabah, but its production is affected by a disturbing disease known as blast, which is caused by fungi (i.e., Magnaporthe grisea and Magnaporthe oryzae) infection. Knowledge regarding distribution of blast-resistant (BR) genes among various Sabah traditional paddy varieties in different divisions of Sabah is not clear; hence, molecular identification of BR genes in Sabah traditional paddies is urgently needed. In this study, genomic DNA was extracted from 21 different Sabah traditional paddy varieties collected from three divisions of Sabah including the West Coast Division (WCD), Sandakan Division (SD), and Interior Division (ID). The presence of 11 BR and 2 pathogenesis-related (PR) genes in their genome was molecularly screened using a PCR approach and validated using direct sequencing. Our results showed that high frequencies of Pib (95.2%), pi-ta (100.0%), and RCC2 (100.0%) genes were obtained in all 21 Sabah traditional paddy varieties screened. Interestingly, one of the paddy varieties from ID of Sabah, PBT23, did not contain the Pib gene but carried the Pita/Pita-2 allele in its genome. Besides, only three paddies (PBT08 and PBT07 from WCD, and PBT23) exhibited the Pik-p gene, and no varieties were found to carry the Pik, Pik-m, Pit, Piz, Piz-t, Pi-ta, Pi9, and wwin2 genes. In conclusion, this study serves as the basis for improvement and effectual management of traditional paddies in different divisions of Sabah towards blast resistance with knowledge of BR or PR genes inherited in their genome.