

Siripar Korinsak 2010: Identification of Blast Resistance QTLs in Two Rice RIL Populations and Marker Assisted Selection for Pyramiding of Four QTLs in RD6 Rice Variety. Master of Science (Plant Breeding), Major Field: Plant Breeding, Interdisciplinary Graduate Program. Thesis Advisor: Mr. Theerayut Toojinda, Ph.D. 73 pages.

Blast disease, caused by the fungus, *Pyricularia grisea* Sacc, is the most destructive diseases in rice worldwide. To improve durable and broad spectrum resistance in rice, understanding the host-pathogen interaction is required. In this study, the blast strains B71, B88, B124, B151, B161, B209, B248 and B259 derived from sexual recombinations of B1-2 and TH16 were used to demonstrate the arising of new virulence strains that cause a change of the virulence spectrum in rice varieties. Recombinant strains B71, B124, B151, B161 and B248 had shown more virulence than the parental strains on the tested rice varieties. The strain B124 is the most aggressive strain with broader virulence spectrum. The blast strain B1-2, reported to overcome the broad spectrum resistant QTL of Jao Hom Nin (JHN) rice variety, was used to identify its corresponding resistance QTL using two rice mapping populations derived from crosses of KDML105 x JHN and IR57514 x KDML105. Four QTLs, qBL1<sub>IR</sub>, qBL2<sub>KD</sub>, qBL6<sub>IR</sub> and qBL8<sub>KD</sub> were identified on chromosomes 1, 2, 6 and 8 respectively. The qBL1<sub>IR</sub> and qBL6<sub>IR</sub> mapped to RM495-RM84 and GT11-RM564 intervals respectively are associated with the infection efficiency. The qBL2<sub>KD</sub> and qBL8<sub>KD</sub> mapped to RM213-RM208 and RM310-RM72 intervals respectively are associated with the extension of lesion size. Four QTLs, qBL1<sub>JHN</sub>, qBL2<sub>IR64</sub>, qBL11<sub>JHN</sub> and qBL12<sub>Azu</sub>, for blast resistance were pyramided into Thai glutinous rice variety RD6 using marker assisted selection (MAS). The introgression lines carrying combinations of QTLs showed lower level of infection and broader resistance spectrum than the original RD6, especially the introgression lines carrying the qBL11<sub>JHN</sub>. The information of genetic variation of blast fungus, mapping locations of resistance genes and their closely linked markers will be useful for blast resistance rice breeding program in the future.

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