

Siriporn Korinsak 2009: Marker-Assisted Pyramiding Bacterial Blight Resistance Genes (*xa5*, *Xa21*, *xa33(t)*, *Xa34(t)* and *qBB11*) in Rice.  
Master of Science (Agricultural Research and Development), Major Field: Agricultural Research and Development, Interdisciplinary Graduate Program.  
Thesis Advisor: Mr. Theerayut Toojinda, Ph.D. 134 pages.

Bacterial Blight (BB) caused by *Xanthomonas oryzae pv. oryzae* (*Xoo*) is one of the most serious diseases in rice production world wide. Utilization of resistant varieties is considered to be the most effective method to control this disease. Three resistance genes, *xa5*, *xa33(t)* and *Xa34(t)* were identified in rice cultivars IR62266, Ba7 and Pin Kaset, respectively in this study. These cultivars and a KDML105 introgression line carrying the *Xa21* and *qBB11* were used as the BB resistance donors to construct the pyramiding population. Marker-Assisted Selection (MAS) was carried out to pyramid five BB resistance genes including *xa5*, *Xa21*, *xa33(t)*, *Xa34(t)* and *qBB11* into indica rice genetic background. Pyramiding lines carrying the combination of two, three and four resistance genes were tested for BB resistance against six BB isolates, TB0304, TXO16, TXO34, TXO37, TXO107 and TXO133. The pyramided lines having more than single gene showed broader resistance spectrum and higher level of resistance than parental lines with single gene. *xa5* was the most effective, followed by *Xa34(t)*, *xa33(t)* and *Xa21*. The two new identified resistance genes *xa33(t)* and *Xa34(t)* and closely their liked markers will be useful information to improve broad-spectrum BB resistance in Thai rice breeding programs through MAS. Furthermore, the pyramided lines obtained in this study can be used as genetic resources of BB resistance in breeding programs.

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