

Sompong Chankaew 2009: Inheritance of Resistance to Cercospora Leaf Spot Disease in Mungbean (*Vigna radiata* (L.) Wilczek). Master of Science (Plant Breeding), Major Field: Plant Breeding, Interdisciplinary Graduate Program. Thesis Advisor: Professor Peerasak Srinives, Ph.D. 53 pages.

Cercospora leaf spot (CLS) caused by the fungus *Cercospora canescens* is a serious disease in mungbean, causing yield lost of up to 50 %. Information on inheritance of resistance to the disease is useful in breeding cultivars resistance to CLS. This disease usually outbreaks in rainy seasons or under high humidity condition and thus limited the progress in breeding for the resistance. Molecular marker linking to the gene controlling the resistance, if available, can help selection and advance the generation year - round. Microsatellite or simple sequence repeat (SSR) markers are widely used in plant genetics and breeding and thus used in this study. The mapping population was developed from a cross between the susceptible cultivar Kamphaeng Saen (P<sub>1</sub>) and a highly resistance mungbean line V4718 (P<sub>2</sub>). The population of P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub> and F<sub>2,3</sub> were evaluated for reaction to CLS in the field at the Tropical Vegetable Research and Development Center of Kasetsart University, Kamphaeng Saen Campus. The results showed that the resistance is controlled by a major dominant gene.

Sixty-nine SSR markers were found polymorphic among the two parents and thus employed to construct a mungbean partial genetic linkage map using the program JoinMap ver. 3.0. The quantitative trait loci (QTLs) associating with CLS resistance was also determined. The linked markers at the minimum LOD score of 7.0 and maximum distance of 50.0 cM of Kosambi function were clustered. The partial linkage map comprised 55 markers in 11 linkage groups, covering approximately 854.8 cM. There were 14 unlinked markers. The QTL analysis using WinQTLcart 2.5 program revealed 1 major QTL (*qCLS*) linking to CLS resistance gene. It was located between the markers CEDG117 and VR393 on linkage group 3. The QTL can explain as high as 77.3 % of phenotypic variation.

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