

**PB-37**

## **Development of Molecular Markers for Downy Mildew Resistance in Maize Population**

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### **[Introduction]**

Maize (*Zea mays*) is C4 plant and 3 major crops for mankind in the world. However, several diseases infection of maize are considered as a one of huge problems for maize production. Downy mildew (DM) caused by *Peronosclerospora* and *Sclerospora* species is the most destructive diseases for maize crops in the lowland tropics, especially in tropical Asian countries. In Asia, DM is the most important biotic stress in maize. Despite efforts toward the development of DM resistant cultivars or seed treatment with metalaxyl fungicide, DM still emerges in localized areas as a severe pathogen.

### **[Materials and Methods]**

On the basis of previous study, *ZmBak1* which was known as DM resistant gene candidate at B73, Ki11 was isolated. After PCR analysis, 3 SNP markers were developed specific to DM infected Ki11 were developed using High Resolution Melt (HRM).

A total of 200 F<sub>7</sub> population were screened for DM incidence (%) and determined genotype using 3 SNP markers.

### **[Result and Discussion]**

After DM resistance screening at mid-April to June, early September to October in Cambodia, Ki11 was determined as a resistance cultivar comparison to B73. A total of 200 B73 × Ki11 F<sub>7</sub> population was evaluated for DM incidence. Among population, 186 lines were determined as susceptible (>50%) plants, and eventually, 9 lines were determined as resistance (<25%) plants.

Previous study, Bak1 might be involved DM resistance mechanism. Full length, 2212 bp, Bak1 gene was isolated using GRMZM2G121565 sequence information. A total of 26 SNP and 116 bp of InDel fragment were identified. Eventually, 3 SNP markers (150 bp, 92 bp, 93 bp) were determined as a DM resistance molecular marker. B73 × Ki11 population was analyzed using 3 SNP marker. The results will be discussed.

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