**Molecular Diversity of *Cucurbit aphid-borne yellows virus* (CABYV) Infecting Cucurbits**

**in Thailand**

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**Abstract**

Field surveys and sample collection were conducted during February 2012 -August 2013. A total of 244 cucurbit leaves with yellowing symptom and weeds were collected from 15 provinces in Thailand. Initial screening by one-step RT-PCR using degenerate primers Luteo-CPF and Luteo-CPR found that 160 samples (~65%) were infected by polerovirus with incidence of infection in bottle gourd, bittergourd, cucumber, luffa, melon, pumpkin and wax gourd. In addition, polerovirus was detected in several weeds, *i.e*., begger-ticks, goat weed, ivy gourd and spiny amaranth. Of 160 detected samples, 80 samples from different cucurbit plants and locations were selected for further identification. The amplified PCR product of approximately 600 bp-coat protein (*CP*) gene from 80 samples was cloned and sequenced. The *CP* sequences of polerovirus from 80 samples were aligned and compared with other *CP* sequences from GenBank and the phylogenetic trees were constructed. The results indicated that 3 distinct sequence types of polerovirus were found in relation to yellowing disease in cucurbit plants and they were identified to be *Cucurbit aphid borne yellows virus* (CABYV), *Suakwa aphid-borne yellows virus* (SABYV) and *Melon aphid-borne yellows virus* (MABYV). CABYV was the most common polerovirus found in cucurbit plants with 74% infection incidence. MABYV and SABYV were rarely found with an incidence of 8% and 2%, respectively. According to comparison of nucleotide sequences of *CP* gene, CABYV isolates shared 94-100% nucleotide identity among the TH- group and 94-97% identity with China, Japan, Philippines and Taiwan, respectively. SABYV isolates shared 93-100% nucleotide identity among the TH- group and 90-93 % nucleotide identity with Philippines and Taiwan. MABYV isolates were divided into 2 groups. The first group from Central and North shared 98-99% nucleotide identity among them and 86 % nucleotide identity with China and Taiwan. The second group from Northeast shared 98% nucleotide identity among them and with China and Taiwan. CABYV is the most predominate species found in Thailand. Whereas, the occurrence of SABYV was observed in moderate level and MABYV was observed in the lowest level.