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First Report of *Peanut stunt virus* on *Glycine max* in Korea

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Peanut stunt virus (PSV) is a member of the genus *Cucumovirus* in the family Bromoviridae. Other members of the genus are its type member *Cucumber mosaic virus* (CMV) and *Tomato aspermy virus* (TAV). PSV like other cucumoviruses has a tripartite genome of positive strand RNAs, designated RNA1, RNA2 and RNA3, in other decreasing size. PSV is an economically important pathogen and occurs worldwide in legume plants. Since PSV was first described in the United States in 1966, many strains of PSV have been characterized. In Korea, there has been previous record on PSV infection of peanut, black locust, red goosefoot and white clover (The Korean Society of Plant Pathology, 2009). In Sangju County of South Korea in 2005, a PSV (PSV-K1) was first detected using RT-PCR from naturally infected soybean showing yellow mosaic on the leaves and virus particles were isolated from these infected leaves (Fig. 1A). Purified virus preparations were revealed the presence of small isometric virions of 28 nm in diameter (Fig. 1B).

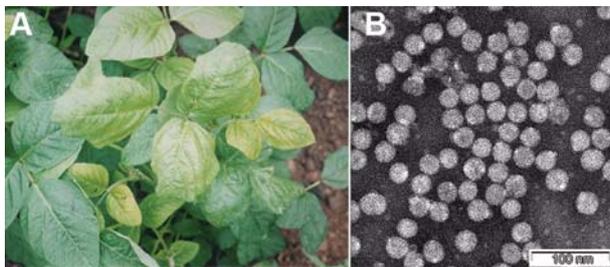


Fig. 1. (A) PSV-K1-infected soybean plants showing yellow mosaic symptom. (B) Electron micrograph showing purified particles of *Peanut stunt virus* (PSV)-K1 from Soybean. Bar represents 100 nm, respectively.

The nucleotide sequence of full-length RNA3 from PSV strain K1 was determined. PSV-K1 RNA3 is 2089 nucleotides (nt) organized into two putative ORFs and 5'- and 3'-untranslated regions (UTRs) of 52 and 229nt, respectively. Two large open reading frames (ORFs) encoded a putative movement protein (MP) (nt 53–925) and a coat protein (CP) (nt 1183–1860) predicted to be a 31-kDa protein (P31) and a 25-kDa protein (P25), respectively. ORF3a (MP) is separated from the next ORF3b (CP) by an IR non-coding region (internal region) 257nt in length (nt 926–1182).

Multiple sequence alignments were generated using DNAMAN 7.0 (Lynnon Biosoft, Quebec, Canada) on the basis of complete nucleotide sequences of PSV RNA3, and a phylogenetic tree was constructed by the neighbor-joining algorithm (Fig. 2). Bootstrap analysis was performed with 1,000 replicates. The resulting tree of RNA3 revealed that PSV-K1 RNA3 is more closely related to that of PSV-ER (94.6%) than to those of other cucumoviruses. Percent nucleotide sequence identities of RNA3 from PSV-K1 ranged from 58.7 to 94.6% with RNA3 sequences of members of the genus *Cucumovirus*. PSV was first divided into two subgroups based on a wide range of comparative analyses, including serology, competition hybridization and sequence comparison (Hu et al., 1997).

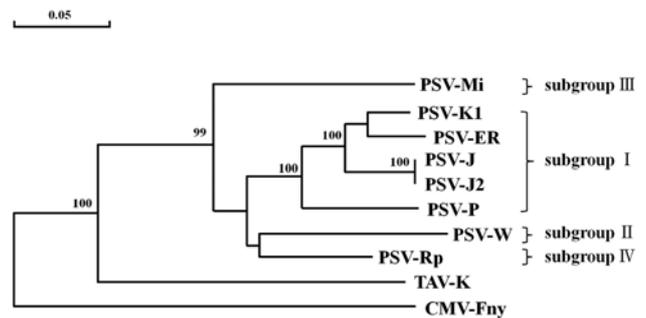


Fig. 2. Phylogenetic analysis of PSV RNA3 nucleotide sequences of Cucumoviruses. Numbers on nodes indicate bootstrap values. The bar corresponds to a 5% difference.

Recently, the complete nucleotide (nt) sequence of PSV-Mi and PSV-Rp strain was determined, and based on nt sequence diversity, the establishment of a subgroup and was proposed (Yan et al., 2005 and Kiss et al., 2008).

Phylogenetic analyses of PSV-K1 show clearly that this strain is related to representatives of subgroup containing PSV-ER. Based on these data, we conclude that PSV is closely related to PSV-ER strain from cowpea and it is the first report of PSV on soybean in Korea.

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