

NOTE: **Characterization of a *Peanut mottle virus** Isolate
Infecting Peanut in Israel**

S. Spiegel,** I. Sobolev, A. Dombrovsky, A. Gera, B. Raccach, Y. Tam,
Y. Beckelman, L. Feigelson, V. Holdengreber and Y. Antignus†

Peanut mottle virus (PeMoV) was identified for the first time in Israel in peanut plants expressing mottle symptoms. Particle morphology, biological properties and serology suggested that this virus belongs to the genus *Potyvirus*. The characteristics of the Israeli (IL) PeMoV were compared with those of previously reported isolates. Using RT-PCR, a 1393-bp fragment consisting of the helper component – proteinase (HC-Pro) and a 988-bp product containing the coat protein (CP) were amplified, cloned and sequenced. Comparison of the HC-Pro sequences for PeMoV-IL and PeMoV-M (reported previously), showed 98% homology at the amino acid (aa) level. The aa sequence homology of the entire CP of isolate IL and six other PeMoV isolates ranged from 92% to 98%. A phylogenetic analysis carried out using the CP nucleotide sequence data indicated close similarity between PeMoV-IL and an Australian isolate and between two M isolates. The conserved KITC and CCC motifs in the HC-Pro were replaced by KVSC and ASC, respectively, in PeMoV-IL as in strain M. The DAG motif in the CP was replaced by DAA in the PeMoV isolates including IL. These results prompted the examination of aphid transmissibility of PeMoV-IL which were low and variable among experiments. These results differ from a previous report showing high aphid transmission of PeMoV.

KEY WORDS: Aphid transmission; groundnut; helper component; *Potyvirus*.

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†Dept. of Plant Pathology and Weed Research, ARO, Bet Dagan 50250, Israel **Corresponding author [e-mail: spiegels@volcani.agri.gov.il].