Full-length sequence of Egyptian potato leafroll virus (PLRV) isolate

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ABSTRACT

Potato leafroll virus (PLRV) was isolated from Egyptian fields of potato. Overlapped reverse transcribed PCR products were amplified on the basis of polysomal RNA extracted from PLRV-infected Physalis floridana plants. These products were cloned and sequenced. Sequence reactions indicated that the Egyptian isolate of PLRV contains 5883 nucleotides. The sequence destination analysis between PLRV isolated from Egypt and the isolates of Scotland, Netherlands, Canada and Australia indicated 98.1, 97.9, 97.5 and 93.5% similarity, respectively. The comparison between the open reading frames of the Egyptian isolate and the Scottish isolate of PLRV indicated that ORF1 showed the highest degree (98.7%) of similarity, while ORF7 showed the lowest degree (97.1%) of similarity when compared to the corresponding frames. ORF0, ORF2, ORF3, ORF4, ORF5 and ORF6 showed 98.3%, 98.5%, 97.8%, 98.3%, 97.8% and 97.4% similarity, respectively, when compared to their responding frames of PLRV isolated from Scotland.

Key Words: *PLRV, full length sequence RT-PCR.*

INTRODUCTION

Potato leafroll virus (PLRV), a type member of poleroviruses (D'Arcy and Mayo, 1997), infects potatoes worldwide. Due to infection, potato plants show yellowing and rolling symptoms on the foliage part of the plants. Infected tubers show necrotic legions in the phloem tissue. The viral host range is restricted to members of family *Solanacae*. PLRV is transmitted via green peach aphids (*Myzus persicae*) in a circulative manner without any evidence for propagation in its invertebrate vector (Eskandari *et al.*, 1979). It is restricted to the phloem tissue of the infected plants (Harrison, 1984). PLRV particles are isometric with a diameter of 22-25 nm. It contains 30% of single stranded RNA with a molecular weight of ~5.9 kb and has positive sense properties (Mayo *et al.*, 1989). The viral genome is covalently linked to a 7.2 kDa protein (VPg) at its 5' start and not polyadenelated at the 3'end (Mayo *et al.*, 1982). The RNA codes for at least 8 open reading frames (ORFs) that are located in two clusters of genes and separated by 197 nucleotides (nt) of noncoding sequences. The first cluster is preceded by 174 nt of noncoding sequences, while the second cluster is followed by 141 nt of noncoding sequences (Mayo *et al.*, 1989). The first gene cluster is translated directly from genomic RNA to produce ORF0 with Mr of 28 kDa and responsible for the symptom development