21

Carmovirus Isolation and RNA Extraction

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1. Introduction

The Carmovirus group is named after *car*nation *mo*ttle virus (CarMV), its type member. Carmoviruses have icosahedral particles about 30 nm in diameter that sediment at 120–130 S. They are also characterized by a monopartite positive-sense, single-stranded RNA genome of M_r 1.4–1.6 × 10^6 and a single capsid protein of M_r 36,000–46,000 ***(1)***.

There is relatively little information on epidemiology and control of the majority of carmoviruses, though some of them, including CarMV, melon necrotic spot (MNSV), or cowpea mottle (CPMoV) viruses, have significant economic importance. A common characteristic of carmoviruses is their relative facility of transmission by mechanical inoculation. Many carmoviruses have been reported to be transmitted to plants through soil, either in the absence of vectors (CarMV or galinsoga mosaic virus, GMV) or by soil-inhabiting fungi (the case of cucumber soil-borne virus, CSBV, and MNSV). For only one member, pelargonium flower break virus (PFEV), transmission facilitated by thrips has been demonstrated.

CarMV is, together with turnip crinkle virus (TCV), the best-studied of carmoviruses. The complete sequence of CarMV consists of 4003 nucleotide residues ***(2)***. CarMV RNA contains a 69-nucleotide 5' leader sequence before the first AUG and a 288-nucleotide 3' untranslated region. Sequence analysis of the CarMV genome revealed the presence of five open reading frames (**Fig. 1**) that could potentially encode proteins of 27 (p27), 86 (p86), 98 (p98), 7 (p7), and 38 (p38) kDa. p86 and p98 would be synthesized from the first AUG by readthrough at two different UAG amber termination codons, respectively. p86 contains the GDD motif characteristic of RNA-dependent RNA polymerases of positive-strand RNA viruses. The sequence coding for the CarMV

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