

Caulimovirus Isolation and DNA Extraction

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1. Introduction

Members of the caulimovirus group (*1*) each have a circular double-stranded DNA genome of approx 8 kbp that is encapsidated in a spherical, naked nucleocapsid of approx 50 nm diameter (**Fig. 1**). Caulimoviruses characteristically produce subcellular inclusion bodies in infected tissues that contain most of the virions found in cells, embedded in an apparently random manner. The host ranges of individual caulimoviruses tend to be restricted to one or a few plant families, and group members are transmitted between plants by aphid vectors. Based on possession of all, or most, of these characteristics, 12 definite, and 3 possible, members of the group have been identified (*2*).

The best-characterized and type member of the caulimoviruses is cauliflower mosaic virus (CaMV), from which the group name derives. The complete nucleotide sequence of at least eight different CaMV isolates (*3–10*), and that of four other caulimoviruses (*11–14*) has been determined. The organization of viral genes (**Fig. 1**) is mostly conserved in sequenced caulimoviruses, but one member, cassava vein mosaic virus (CVMV), is somewhat different from the others (*14*). Replication of caulimoviruses involves alternation of genomes as DNA and RNA forms, progeny virion DNA being generated by reverse transcription of a terminally redundant, genome-length RNA utilizing a virus-encoded polymerase. This feature is shared by another group of plant DNA viruses, the badnaviruses, and by animal hepatitis B viruses. Such viruses have been termed pararetroviruses to distinguish them from animal retroviruses, which package an RNA form of the genome derived by transcription of an integrated provirus. Sequence homologies in putative coding regions of different caulimoviruses are relatively low. One short sequence is conserved among