16

Ilarvirus Isolation and RNA Extraction

Deyin Guo, Edgar Maiss, and Günter Adam

1. Introduction

The genus *Ilarvirus* belongs to the family *Bromoviridae*, together with three other genera *Bromovirus, Cucumovirus,* and *Alfamovirus* ***(1)***. The ilarvirus genus includes at present 15 approved species and is divided into 10 subgroups according to serological relationships ***(2)***. The members are listed in **Table 1**.

Most of the members of the ilarvirus genus have a wide host range and infect woody plants. They can cause diseases of economical importance in stone fruit trees (*Prunus* spp.), apple, hop, citrus, and rose plants ***(2,3)***. The type member, tobacco streak virus (TSV), however, infects mainly herbaceous plants and causes diseases in tobacco, dahlia, cotton, tomato, asparagus, and some legume species. The chief measure to control ilarviruses is the use of virus-free propagating material, but the healthy plants can become reinfected easily, since many ilarviruses are transmitted by pollen. Engineered resistance may become a promising perspective for the future control of ilarviruses ***(4)***.

The morphology of ilarvirus particles is quasi-isometric, with diameters between 23 and 35 nm. Occasionally, bacilliform particles are visible in the electron microscope (EM) (**Fig. 1A**) with 12–35 nm width and 20–38 nm length ***(2,3)***. The variability in particle size is caused by the encapsidation of the three different-sized RNAs into three separate virions (**Fig. 1A**). The particles are very unstable in plant sap, can be easily deformed, and the virus concentration in leaf tissue is low. This renders ilarviruses difficult to purify in good quality and sufficient quantity, and has led to the sigla of the genus which was derived from *i*sometric *la*bile *r*ingspot viruses.

Ilarviruses possess a tripartite, positive-sense single-stranded RNA genome encapsulated by a coat protein (CP) of approx 25–30 kDa ***(3)***. A schematic drawing of the genome organization and position of the open reading frames is

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