Table 2
Sequence Information Available for Ilarviruses

Virus	RNA segment	Accession no. for sequence[a]
Prunus necrotic ringspot	RNA-3	L 38823 Hammond (6)
Apple mosaic	RNA-3; RNA-4	U15608 (Shier et al., unpublished), L03726 (8); U03857 (9)[b]
Tobacco streak	RNA-3	X00435 (10)
Prune dwarf	RNA-4	L28145 (11)
Citrus variegation	RNA-3	U17389 (7)
Citrus leafrugose	RNA-2; RNA-3	U17726 (5); U17390 (7)
Lilac ring mottle	RNA-3	U17391 (20)

[a]The corresponding references are given in parentheses.
[b]This sequence was published as ApMV sequence, but probably is really PNRSV according to sequence comparisons (*see* **refs. 6** and **8**).

CPs of several ilarviruses and AMV are freely exchangeable in the process of genome activation. For example, the TSV genome can be activated by AMV CP and vice versa, although they have no apparent sequence similarity *(14)*. Obviously, this shared function depends only on the secondary and tertiary structure of the CP and the viral genomic RNAs, which allow the recognition and interaction between the protein and the viral RNA, even in heterologous combinations *(15)*.

2. Materials
2.1. Equipment (see Note 1)

1. Centrifuge for Eppendorf (Netheler-Hinz Gmbh, Hamburg, FRG) tubes.
2. Low-speed centrifuge with swingout rotor.
3. High-speed centrifuge, like Sorval (Newtown, CT).
4. Ultracentrifuge with fixed-angle and swingout rotor.
5. ISCO (Columbus, OH) density gradient fractionator.
6. pH meter.
7. Waring blender.
8. Spectrophotometer.
9. Pipeting devices like Eppendorf pipets.

2.2. Buffers and Reagents

1. Inoculation buffer: 0.03M HEPES buffer, pH 7.5, or standard virus buffer (*see* **item 2**) without mercaptoethanol, but with diethyldithiocarbamate (DIECA) and 2% polyvinylpyrrolidon (PVP), average mol wt 10,000.