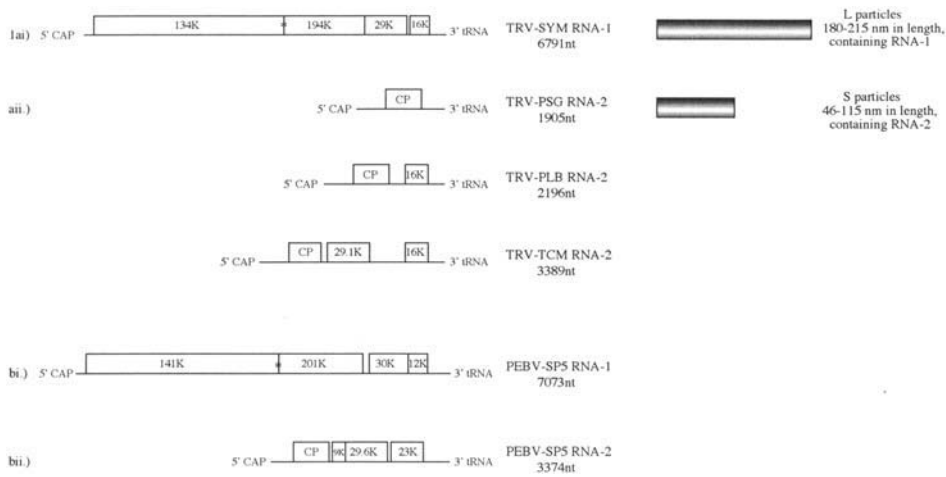

Fig. 1. Tobravirus structure and genome organization. (ai) Genome organization of RNA-1 of TRV isolate SYM. (aii) Genome organization of RNA-2 of various TRV isolates. (bi and bii) Genome organization of RNA-1 and RNA-2 of PEBV isolate SP5. RNA is shown as a horizontal line and the positions of the open reading frames (ORFs) are indicated by boxes. The numbers inside the boxes are the approximate mol wt in kDa of the proteins encoded by each ORF. The coat protein ORF is denoted by CP. The position of the readthrough termination codon on RNA-1 is indicated by an asterisk.

with the TMV 126- and 183-kDa replicase proteins. The third ORF on TRV RNA-1 encodes a 29-kDa protein that has homology with the TMV 30-kDa movement protein. Unlike TMV, the 3' proximal ORF on TRV RNA-1 does not encode the CP, but encodes a cysteine-rich 16-kDa protein. Although the function of this protein is not yet known, it is thought that in PEBV the equivalent 12-kDa protein may have a role in virus multiplication (S. A. MacFarlane, personal communication).

The TRV 29- and 16-kDa proteins are coded by RNA-1, but they are not translated directly from the genomic RNA and are expressed from individual subgenomic RNA species that are 3' coterminal with RNA-1 ***(11)***. TRV RNA-1 also has the potential to code for a 59-kDa protein by translation of an internal ORF. This ORF initiates at an AUG codon present 87 nucleotides downstream of the termination codon for the 134-kDa protein and terminates at the stop codon for the 194-kDa protein. This protein has not been detected; however, plants transformed with the equivalent readthrough regions of PEBV and TMV have been found to be resistant to subsequent infections with the same viruses ***(12,13)***.