**Supplementary Table 2:**

Sequence stretches localized in the 5´-UTR or ORF1 of carmovirus genomes with complementarity to their 3´-CITEs.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Carmovirus** | **5´-UTR** | **3´-CITE** | **5´-UTR**  | **5´-ORF**  | **interaction** |
| **MNSV** | 84 nt | ISS | UAGCCG (10) (+)AUCGGU | UUAGCCA (121) (+)AAUCGGU | both |
| **PSNV** | 134 nt | PTE | GUUGG (14) (+)CGGUU  | GCCGG (171) (+/-)CGGUU | UTR |
| **CarMV** | 70 nt | PTE | UGGCGG (9) (+) ACCGUC | GGUAGC (139) (+) CCGUCG  | UTR |
| **GaMV** | 42 nt | PTE | CGCCAA (9) (+) GCGGUU | GUUGG (96) (+) CGGUU | UTR |
| **PFBV** | 32 nt | PTE | UCUGG (21) (+)AGACC | gCUGGCAGG (99)(+)aGACCGUCU | ORF |

The length of the 5´-UTR and the shape of the 3´-CITE are indicated (second and third column). Only carmoviruses with proposed/determined 3´-CITEs are shown, excluding TCV, for which 5´-3´ interaction has been shown to occur directly through ribosomes ([Stupina et al., 2011](#_ENREF_52)) and viruses of the genus *Pelarspovirus* ([Scheets et al., 2015](#_ENREF_49)), previously classified as carmoviruses. Nucleotides of the 5´-UTR (column 4) or the ORF1 (column 5) complementary to the 3´-CITE (lower line) are shown. The number in brackets indicates the location of the first complementary nucleotide in the 5´end sequence (upper line). The (+) or (+/-) indicate the possibility of these nucleotides being unpaired, based on the structure prediction by Mfold. The last column indicates which of these two sequence stretches has been predicted ([Simon and Miller, 2013](#_ENREF_51)) or shown (for SCV ([Chattopadhyay et al., 2011](#_ENREF_5))) to be involved in 5´-3´ interaction. Pea stem necrosis virus (PSNV); Carnation mottle virus (CarMV); galinsoga mosaic virus (GaMV); pelargonium flower break virus (PFBV).