**Supplementary Table 1:**

Sequence stretches of the 5´-UTR or ORF1 with complementarity to I-shaped 3´-CITEs.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **ISS** | **5´-UTR** | **Genus** | **5´-UTR**  | **5´-ORF**  | **interaction** |
| **MNSV** | 84 nt | Carmovirus | UAGCCG (10) (+) AUCGGU | UUAGCCA (121)(+)AAUCGGU | both |
| **MNeSV** | 122 nt | Tombusvirus | UGACCAG (16) (+) ACUGGUC  | GGUGAUU (171)(+)CCACUGG  | UTR of CIRV  |
| **MWLMV** | 40 nt | Aureusvirus | AACCA (19) (+) UUGGU  | GACCGU (122)(+)UUGGUG  | ? |
| **JCSMV** | 45 nt | Aureusvirus | UUGACCA (8) (+) AACUGGU  | UUGGUU (100)(+)AACUGG | ? |
| **CBV** | 124 nt | Tombusvirus | GUUGU (17) (+)UGGUG  | GAACCA (154)(+) CUUGGU  | ? |

The length of the 5´-UTR and the virus genus are indicated (second and third column). 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 (+) indicates that these nucleotides are unpaired in the structure prediction by Mfold. The last column indicates that besides this study with MNSV, only for the MNeSV ISS, a 5´-3´ interaction with the 5´-UTR of CIRV has been shown to exist ([Nicholson et al., 2010](#_ENREF_36)). Cucumber bulgarian virus (CBV), maize white line mosaic virus (MWLMV), johnsongrass chlorotic stripe mosaic virus (JCSMV).