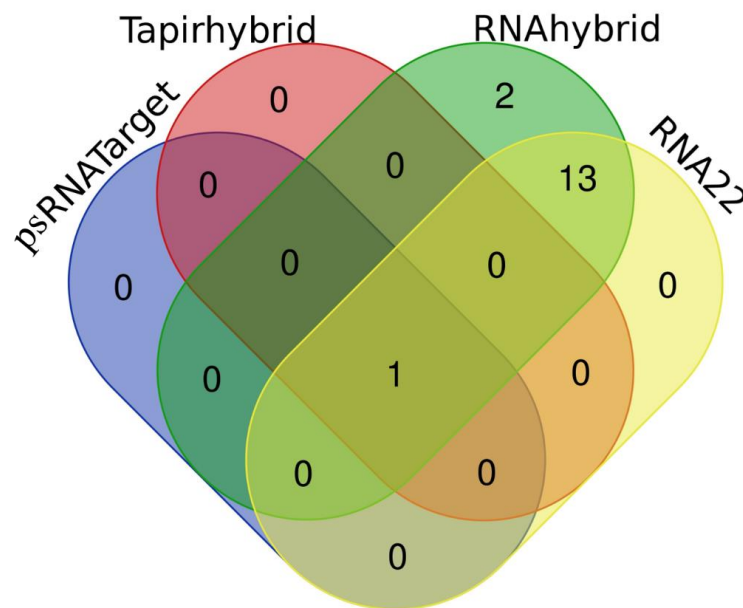




Supplement 1. Venn diagram representing mutually common binding sites of mature sugarcane miRNAs predicted to potentially target the SCMV genome. The *in silico* prediction was established using computational tools (RNA22, TAPIR, psRNATarget, and RNAhybrid) to identify potential targets of sugarcane-encoded miRNAs. The areas of overlap among computational tools show miRNA binding sites.

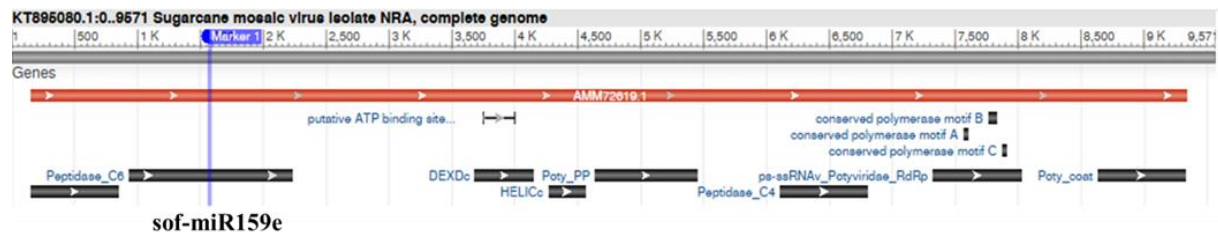
Supplement 2. miRNA target (SCMV isolate NRA, GenBank accession no. KT895080.1) prediction using RNAhybrid algorithm

miRNA	mde	mfe	mfe/mde
sof-miR156	-43.20	-23.90	0.55
sof-miR159a	-44.10	-29.70	0.67
sof-miR159b	-44.10	-29.70	0.67
sof-miR159d	-44.10	-29.70	0.67
sof-miR159e	-40.40	-23.20	0.57
sof-miR159c	-46.70	-24.80	0.53
sof-miR167a	-45.40	-23.80	0.52
sof-miR167b	-45.40	-23.80	0.52
sof-miR168a	-49.99	-25.60	0.51
sof-miR168b	-48.99	-24.40	0.49
sof-miR396	-41.40	-25.70	0.62
sof-miR408a	-50.70	-33.90	0.67
sof-miR408b	-50.70	-33.90	0.67
sof-miR408c	-50.70	-33.90	0.67
sof-miR408d	-50.70	-33.90	0.67
sof-miR408e	-49.20	-27	0.55

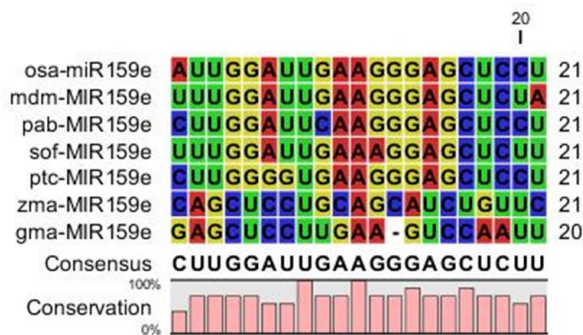
The parameters mde and mfe represent minimum duplex energy and minimum free energy of microRNA/target duplexes, respectively.

Supplement 3. miRNA target (SCMV isolate NRA, GenBank accession no. KT895080.1) prediction using RNA22

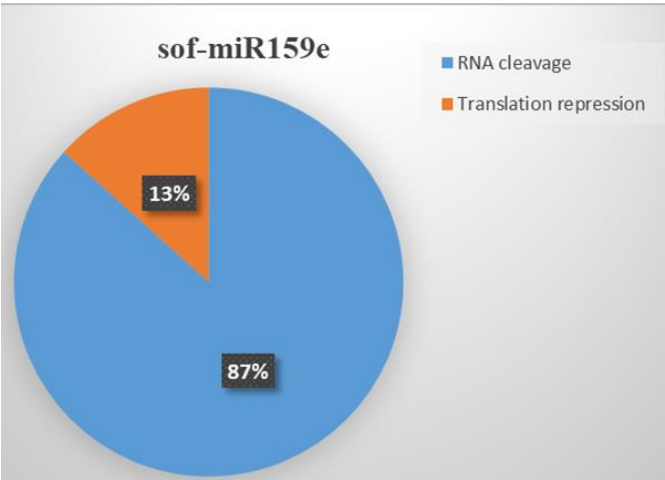
miRNA name	Leftmost position of predicted target site	Folding energy (-Kcal/mol)	Heteroduplex	P value
sof-miR156	4288	-14.10	AGTTGCACT--ATTCTGTCA CACGAGTGAGAGAAGACAGT	1.32E-1
sof-miR159a	734	-15.50	CAGTGGCCTCACATTCA-TCCAGA GTC-TCGAGG--GAAGTTAGGTTT	6.99E-2
sof-miR159b	734	-15.50	CAGTGGCCTCACATTCA-TCCAGA GTC-TCGAGG--GAAGTTAGGTTT	6.99E-2
sof-miR159d	734	-15.50	CAGTGGCCTCACATTCA-TCCAGA GTC-TCGAGG--GAAGTTAGGTTT	6.99E-2
sof-miR396	946	-13.80	TCAATCTAGAAGAATGTGGAA GTCAAGTTCTTTTCGACACCTT	2.9E-1
sof-miR408a	2418	-12.90	GTTA-AGAACCAAGGCATTGCAG CGGTCCCTT--CTCCGTCACGTC	1.2E-1
sof-miR408b	2418	-12.90	GTTA-AGAACCAAGGCATTGCAG CGGTCCCTT--CTCCGTCACGTC	1.2E-1
sof-miR408c	2418	-12.90	GTTA-AGAACCAAGGCATTGCAG CGGTCCCTT--CTCCGTCACGTC	1.2E-1
sof-miR408d	2418	-12.90	GTTA-AGAACCAAGGCATTGCAG CGGTCCCTT--CTCCGTCACGTC	1.2E-1
sof-miR396	2632	-12.00	AAGAGC-TGATAGCTGAGGGA GTCAAGTTCTTTTCGACACCTT	2.69E-1
sof-miR408e	2856	-14.50	CTAATATCAGATTTAGTGCAG CGGTCCCTTCTCAGTCACGTC	3.9E-1
sof-miR167a	4234	-12.10	TAGTATATGTTGCAAGCTACA GTCTAGTACGACCGTCGAAGT	6.88E-2
sof-miR167b	4234	-12.10	TAGTATATGTTGCAAGCTACA GTCTAGTACGACCGTCGAAGT	6.88E-2
sof-miR156	4288	-14.10	AGTTGCACT--ATTCTGTCA CACGAGTGAGAGAAGACAGT	1.32E-1
sof-miR159a	5429	-12.00	GAACGCTCC-TTTAATACAAC GTCTCGAGGGAAGTTAGGTTT	3.03E-1
sof-miR159b	5429	-12.00	GAACGCTCC-TTTAATACAAC GTCTCGAGGGAAGTTAGGTTT	3.03E-1
sof-miR159d	5429	-12.00	GAACGCTCC-TTTAATACAAC GTCTCGAGGGAAGTTAGGTTT	3.03E-1
sof-miR159c	5429	-12.00	GAACGCTCC-TTTAATACAAC TCCTCGAGGGAAGTTAGGTTT	3.03E-1
sof-miR408a	5539	-21.80	ACCAGGGAAGAACAAGCGCAG CGGTCCCTT-CTCCGTCACGTC	1.78E-1
sof-miR408b	5539	-21.80	ACCAGGGAAGAACAAGCGCAG CGGTCCCTT-CTCCGTCACGTC	1.78E-1
sof-miR408c	5539	-21.80	ACCAGGGAAGAACAAGCGCAG CGGTCCCTT-CTCCGTCACGTC	1.78E-1
sof-miR408d	5539	-21.80	ACCAGGGAAGAACAAGCGCAG CGGTCCCTT-CTCCGTCACGTC	1.78E-1
sof-miR408e	5539	-21.80	ACCAGGGAAGAACAAGCGCAG CGGTCCCTT-CTCAGTCACGTC	1.78E-1
sof-miR159a	8206	-12.20	CGTGGCTTCTGGAATGCAAC GTCTCGAGGGAAGTTAGGTTT	1.86E-1
sof-miR159b	8206	-12.20	CGTGGCTTCTGGAATGCAAC GTCTCGAGGGAAGTTAGGTTT	1.86E-1
sof-miR159d	8206	-12.20	CGTGGCTTCTGGAATGCAAC GTCTCGAGGGAAGTTAGGTTT	1.86E-1
sof-miR159e	8206	-12.20	CGTGGCTTCTGGAATGCAAC TTCTCGAGGAAAGTTAGGTTT	1.86E-1
sof-miR159c	8206	-12.20	CGTGGCTTCTGGAATGCAAC TCCTCGAGGGAAGTTAGGTTT	1.86E-1
sof-miR408a	8400	-14.10	GCT--GGAACAGTCGATGCAG CGGTCCCTTCTCCGTCACGTC	3.76E-1
sof-miR408b	8400	-14.10	GCT--GGAACAGTCGATGCAG CGGTCCCTTCTCCGTCACGTC	3.76E-1
sof-miR408c	8400	-14.10	GCT--GGAACAGTCGATGCAG CGGTCCCTTCTCCGTCACGTC	3.76E-1
sof-miR408d	8400	-14.10	GCT--GGAACAGTCGATGCAG CGGTCCCTTCTCCGTCACGTC	3.76E-1
sof-miR408e	8400	-19.10	GCT--GGAACAGTCGATGCAG	3.76E-1



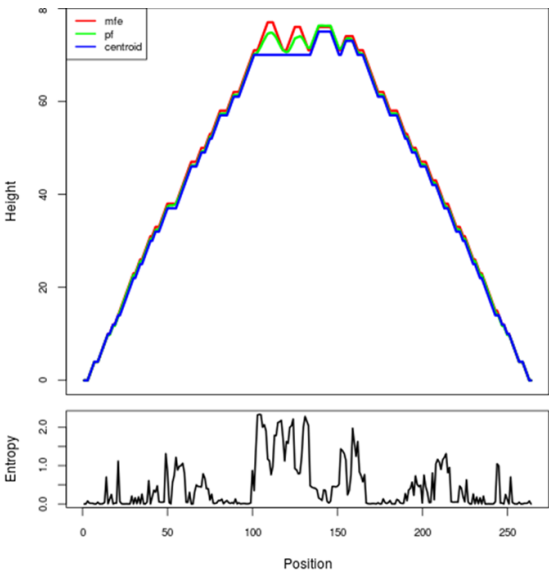
Supplement 4. The position of the sof-miR159e-genome binding site is shown by a blue marker on the SCMV genome.



Supplement 5. Sequence alignment of the mature miR159e in seven plant species. osa-MIR159e (*Oryza sativa*), mdm-MIR159e (*Malus domestica*), pab-MIR159e (*Picea abies*), sof-MIR159e (*Saccharum officinarum*), ptc-MIR159e (*Populus trichocarpa*), zma-MIR159e (*Zea mays*), gma-MIR159e (*Glycine max*).



Supplement 7. The inhibition type (RNA cleavage/translation repression) of sof-miR159e-mediated viral RNA genome regulation.



Supplement 6. MFE structure, the thermodynamic ensemble of RNA structures, the centroid structure, and the positional entropy for each position.