No. 1 from gene *1A*

```
1     TGGATGCGTC CTGTGCCCGA GGGTATTGTT TATTCTGTCG GTTATAATGA ACGCGGTTTA
61    GGTCCGAAGT CTGATGGAGA GCTTTACATT GTCAATAGTG AATGCGTGAT CTGTAACAGT
121   GAATCTTTAT CCACTGTCAC GCGTTCTCTT CAAGCTCCAA CCGGGACCAT TAGTCAAGTT
181   GACGGAGTTG CTGGTTGTGG GAAAACCACG GCAATTAAAT CCATTTTTGA GCCGTCCACT
241   GACATGATCG TTACCGCGAA CAAGAAGTCC GCCCAA
```

No. 2 from gene *2A*

```
1     TGTCCAACGC CAACCATCGC GATTCCTCCG GATTTAAACC GTGCTACTGA TCGTGTTGAT
61    ATCAATTTAG TTCAATCCAT TTGTGACTCG ACTCTGCCCA CTCGTAGTAT TACGACGACT
121   CTTTTCATCA AGTGTTCGTC GAAAGTGCAG ACTATTCTAT AGATCTGGAT CATGTTAGAC
181   TTCGACAGTC TGATCTTATT GCAAAAATTC CAGATTCAGG GCATATGATA CCGGTTCTGA
241   ACACCGGGAG CGGTCACAAG AGAGTAGGTA CAACGAA
```

No. 3 from gene *2B*

```
1     TGGCTCGTAT GGTGGAGGCG AAGAAGCAGA GACGAAGGTC TCACAAACAG AATCGACGGG
61    AACGAGGTCA CAAAAGTCCC AGCGAGAGAG CGCGTTCAAA TCTCAGACTA TTCCGCTTCC
121   TACCGTTCTA TCAAGTGGAT GGTTCGGAAC TGACAGGGTC ATGCCGCCAT GTGAACGTGG
181   CGGAGTTACC CGAGTCTGAG GCCTCTCGTT TAGAGTTATC GGCGGAAGAC CATGATTTTG
241   ACGATACAGA TTGGTTCGC
```

No. 4 from gene *3A*

```
1     AAAGACCCTT CAGCATCAGT GGAAACTGTT CGAGTAACAG CACATAACAC TTGAGGGACA
61    CTCATGTATC CTTTTGAGCA TAATTCACCA ACATCATATC CAGACTTAAA GAAGGAAGCA
121   ATACGACCGT GGGTTACTTC GGGAACGAGG GGCCGGACTG AAATAGCATT ATCAGCGCGC
181   ATCCAATGAT GCCGGCCTAG GTCACACTCA GTAGCCATTT TCTTAATGGC TTCAGGGCT
```

No. 5 from gene *CP*

```
1     TTTACGGACT GTCACCCACA CGGTAGAATC AAATTTCGGC AAAGGATTAA CTCGAATTTG
61    AATGCGCGAA ACAAGCTTCT TATCATATTC CGTGACTGAA TCAGGTAGTA ACAACCTTTT
121   ACCGTAATAA GACCCACGGT CTATTTTTGG TGGCTTTAGG GTAATAGATG TGAACGTGTA
181   CCCAGGTCTA CAGCGTTCAC TCCCTACAAA G
```

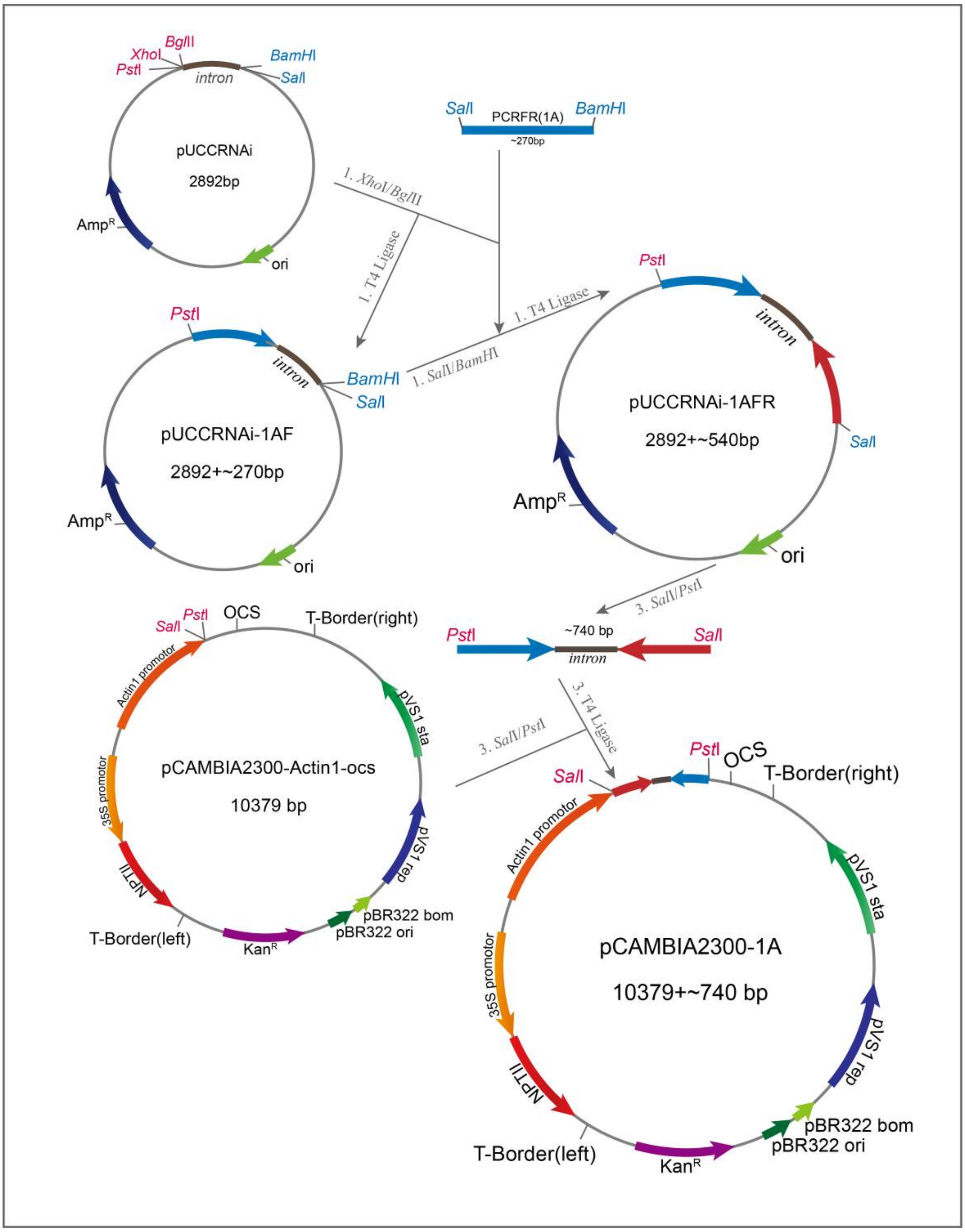
Appendix A Selected fragment sequences of CMV genes.

Appendix B Oligonucleotides used for PCR amplification and plasmid construction

No.	Primer	Applications	Sequence (5'-3')[1]	Tm (˚C)
1	1AF	Insertion of CMV 1A fragment into pUCCRNAi vector	ATTGTCGACTGGATGCGTCCTGTGC	60
2	1AR		ATCGGATCCTTGGGCGGACTTCTTG	60
3	2AF	Insertion of CMV 2A fragment into pUCCRNAi vector	AATGTCGACTGTCCAACGCCAACC	60
4	2AR		AGGGGATCCTTCGTTGTACCTACTC	60
5	2BF	Insertion of CMV 2B fragment into pUCCRNAi vector	ATTGTCGACTGGCTCGTATGGTGGA	60
6	2BR		GAGGGATCCGCGAACCAATCTGTAT	60
7	3AF	Insertion of CMV 3A fragment into pUCCRNAi vector	ATAGTCGACAGCCCTGAAGCCATTA	60
8	3AR		AGAGGATCCAAAGACCCTTCAGCAT	60
9	CPF	Insertion of CMV CP fragment into pUCCRNAi vector	ATTGTCGACCTTTGTAGGGAGTGA	60
10	CPR		ATCGGATCCTTTACGGACTGTCA	60
11	M13+	Vector Primer of pUCCRNAi, use for screening positive clone	AGGGTTTTCCCAGTCACG	60
12	M13-		GTGTGAAATTGTTATCCGCTC	60
13	Actin1PF	Vector primer of pCMBIA-2300-Actin1-ocs, use for screening putative transformants	CCTCAGCATTGTTCATCGGTAGTT	59
14	IntronR	Vector primer of pCMBIA-2300-Actin1-ocs, use for screening putative transformants and detect pre-ihpRNA expression	TGTGTCACTCAAAACCAGATAAAC	59
15	NptIIF	Internal primers of NptII gene, use for screening putative transformants	GATACCGTAAAGCACGAGGAA	59
16	NptIIR		TGACTGGGCACAACAGACAAT	59
17	D1AF	Internal primers of pCMBIA2300-1A , use for detecting pre-ihpRNA[2] expression	TGGATGCGTCCTGTGC	58
18	D2AF	Internal primers of pCMBIA2300-2A , use for detecting pre-ihpRNA expression	TGTCCAACGCCAACC	58
19	D2BF	Internal primers of pCMBIA2300-2B , use for detecting pre-ihpRNA expression	TGGCTCGTATGGTGGA	58
20	D3AF	Internal primers of pCMBIA2300-3A , use for detecting pre-ihpRNA expression	AGCCCTGAAGCCATTA	58
21	DCPF	Internal primers of pCMBIA2300-CP, use for detecting pre-ihpRNA expression	CTTTGTAGGGAGTGA	58
22	ActinF	Internal primers of actin gene, for RT-PCR	ACTGTCCCTATCTATGAAGGTTATGC	60
23	ActinR		GAAACAGACAGGACACTCGCACT	60
24	QCPF	Internal primers of CMV CP gene, for Quantitative RT-PCR	TTCACATCTATTACCCTAAAGCCAC	60
25	QCPR	Internal primers of CMV CP gene, for Quantitative RT-PCR	AGATGGCGGCAACGGATA	60
26	QActinF	Internal primers of *actin* gene, for Quantitative RT-PCR	GGTCCTCTTCCAGCCATCC	60
27	QActinR	Internal primers of *actin* gene, for Quantitative RT-PCR	CCACTGAGCACAATGTTACCG	60

[1] Restriction sites introduced into the primer sequences are underlined.

2 pre-ihpRNA: sequence expected to fold to produce the ihpRNA structure



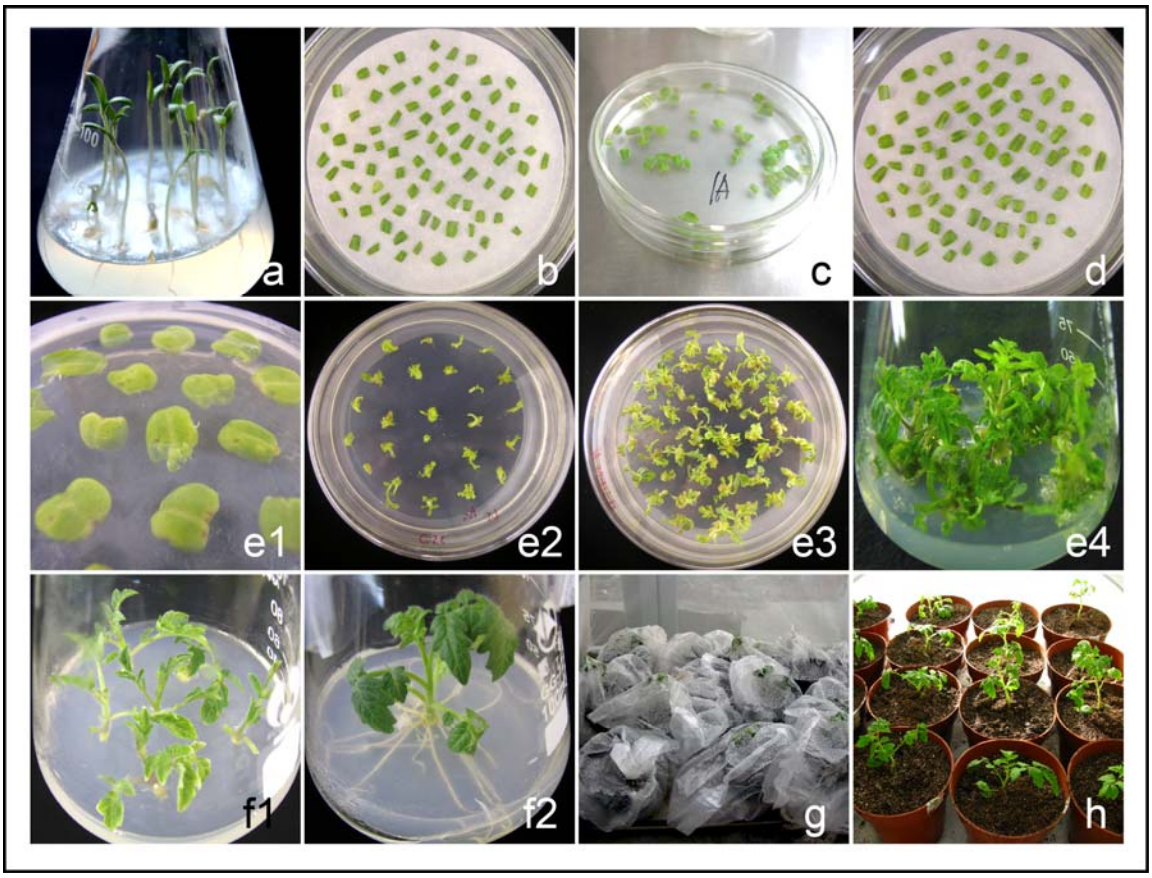
Appendix C Construction of the plant ihpRNA expression vector.

This graphic take the plasmid pCAMBIA2300-1A as a sample. Other vectors contruction process are follwed as this flow diagram.

Appendix D Media used for tomato transformation

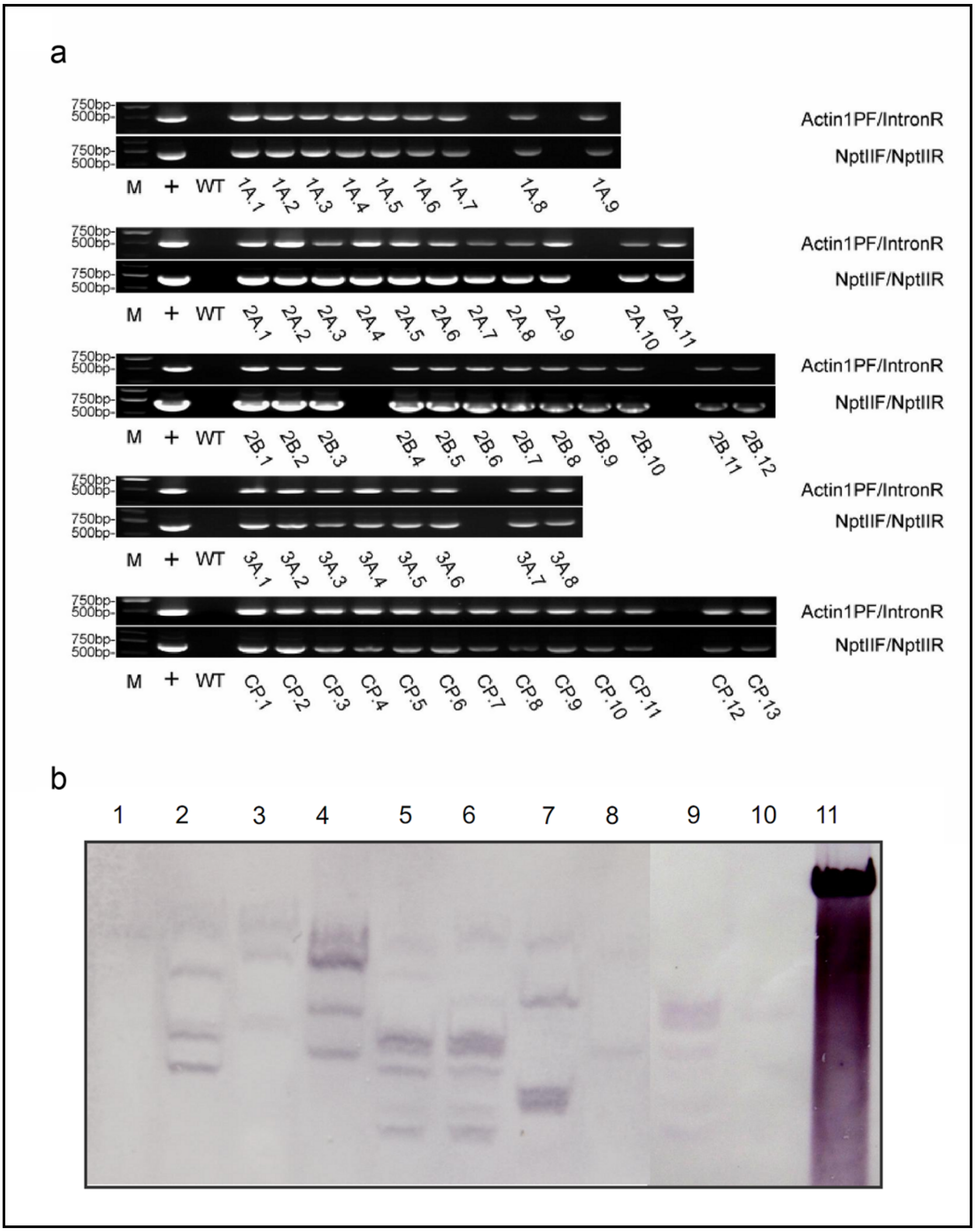
Medium	Medium composition (per liter)[a]	pH
1/2MS	1/2MS +15 g sucrose +6.5 g agar	5.8
Medium A	MS +30 g sucrose	5.8
Medium B	MS +30 g sucrose +6.5 g agar +1 mg ZT	5.8
Medium Base	MS +20 g sucrose +6.5 g agar +100 mg inositol +0.5 mg folic acid	6.0
Medium C	Medium Base +2 mg ZT +100 mg Kan +200 mg Tim	6.0
Medium C1	Medium Base +1 mg ZT +80 mg Kan +200 mg Tim	6.0
Medium C2	Medium Base +0.5 mg ZT +1.5 mg IAA +80 mg Kan+ 200 mg Tim	6.0
Medium D	Medium Base +2 mg IBA +200 mgTim	6.0

[a]MS, MS salts with Gamborg's Vitamins (Sigma M0404); ZT, Trans-Zeatin-Riboside (Sigma Z3541); Kan, Kanamycin; Tim, Timentin; IAA, 3-Indoleacetic acid (Sigma); IBA, Indolebutyric acid (Sigma).



Appendix E Transgenic tomato plantlets obtained by *Agrobacterium tumefaciens*-mediated transformation.

a Seedling; **b** prepared cotyledons and pre-incubation; **c** invasion with *Agrobacterium tumefaciens*; **d** co-cultivation; **e1-4** Screening Kan^R shoots; **e**1 Kan^R buds were induced in medium C; **e2** and **e3**. Kan^R buds were transferred to medium C1; **e4** Kan^R shoots were formed from buds in medium C2; **f1** and **f2** Rooting of Kan^R shoots in medium D; **g** maintain humidity by wraping bags containing plants in soil and; **h** regenerated plants transferred to the pot.



Appendix F Molecular characterization of transgenic tomato plants.

a Polymerase chain reaction (PCR) analysis of putative T0 transgenic plants using primer pairs of Actin1PF/IntronR and NptIIF/NptIIR. The DNA from wild-type plants (lane WT) and different T0 transgenic plants were used as templates (PCR-positive plants were numbered accordingly). M, 2 kb DNA marker; +, plasmid pCAMBIA2300-1A as templates.
b Southern blot analysis of EcoRV-digested genomic DNA for checking transgene copy number using the NptII gene as a probe. DNA from plasmid pCAMBIA2300-1A (lane 11) and different transgenic (Lanes 1-2, T01A.1~2; Lanes 3-4, T02A. 1~2; Lanes 5-6, T02B.1~2; Lanes 7-8, T03A.1~2; Lanes 9-10, T0CP.1~2) were used as templates.

Appendix G Screening CMV-resistance in T1 transgenic plants.

Labeled T1 plants, such as T11A.1, indicate T1 = T1 generation, 1A~CP = transgenic plants corresponding target genes; .1 = number of T0 transgenic lines. WT, wild-type tomato variety “Moneymaker” without transgenes.

Appendix H CMV resistance of the transgenic plants estimated by statistical data of disease indexes

A. Statistical data of T0 Transgenic plants disease indexes

T0 Transgenic plant	N	Subset for alpha = .05	
		1	2
1A	9	9.0902	
3A	8	10.9788	
CP	13	11.7047	
2B	12	12.2972	
2A	11	12.9012	
WT	20		91.8889
Sig.		.359	1.000

a Uses Harmonic Mean Sample Size = 11.167.

B. Statistical data of T1 Transgenic plants disease indexes

T1 Transgenic plant	N	Subset for alpha = .05	
		1	2
2B	15	10.5382	
1A	14	10.5480	
2A	15	15.1149	
CP	12	16.5230	
3A	10	18.0741	
WT	20		91.8889
Sig.		.223	1.000

a Uses Harmonic Mean Sample Size = 13.696.

C. Statistical data of T0 grafted-plants disease indexes

T0 Grafted scion	N	Subset for alpha = .05	
		1	2
2B	7	9.3386	
2A	8	10.6500	
3A	6	12.2233	
CP	10	18.8140	
1A	6	21.7600	
WT	20		93.3335
Sig.		.161	1.000

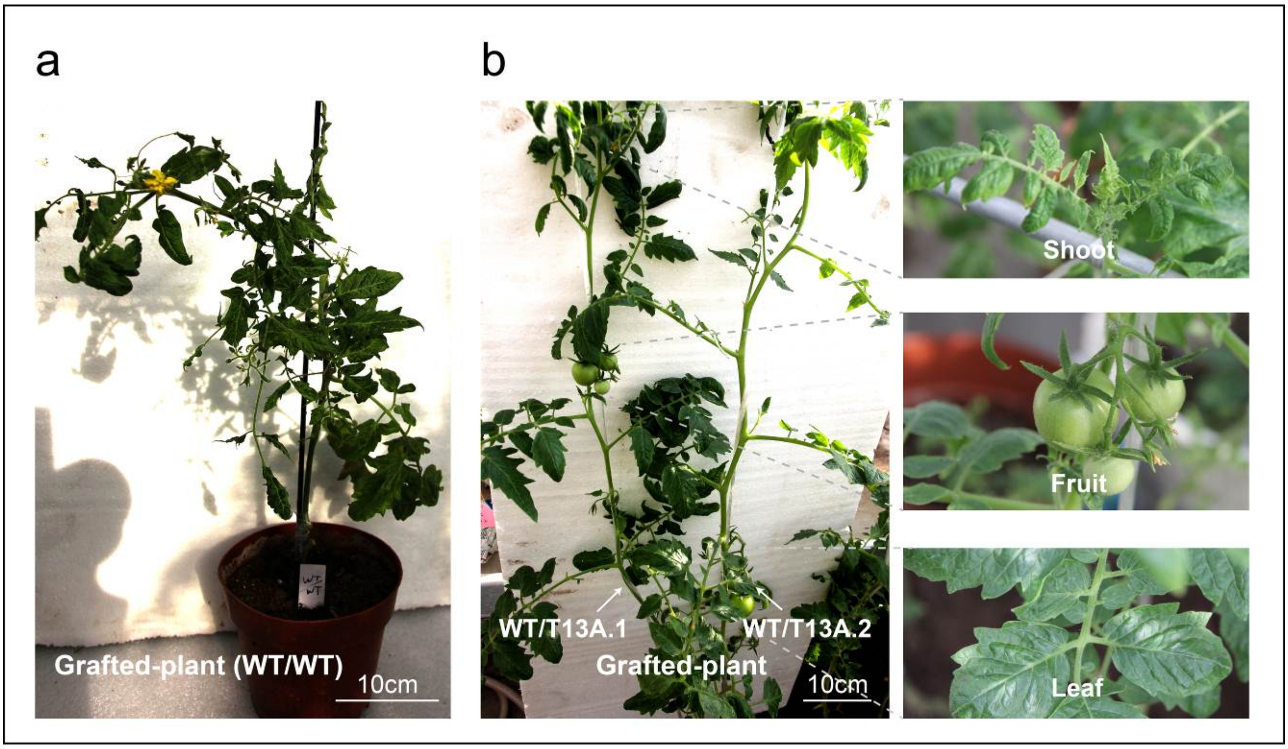
a Uses Harmonic Mean Sample Size = 7.987.

D. Statistical data of T1 grafted-plants disease indexes

T1 Grafted scion	N	Subset for alpha = .05	
		1	2
3A	5	7.0360	
1A	5	8.4820	
CP	5	9.0740	
2A	5	9.7420	
2B	5	16.1100	
WT	20		93.3335
Sig.		.146	1.000

a Uses Harmonic Mean Sample Size = 5.714.

The letters 1 and 2 indicate significant differences ($P<0.05$) between means with in each sample with Duncan's multiple rangetest.



Appendix I Durability of CMV-resistance in grafted plants.

a WT/WT, non-transgenic Moneymaker self-grafting. **b** Effect three months after grafting and post-inoculation. This photograph shows grafted plants whose rootstocks were T13A.1 (left) and T13A.2 (right) as representative examples.