Supplemental Information

Table S1 Preliminary evaluation of hpPSTVd transgenic lines by PSTVdinfection assay.

Transgene	Trsngenic line No.	3-wpi	4-wpi	5-wpi
	24	8/10 ^a	9/10	NT
hpPSTVd-ΔTLE	32	8/10	8/10	NT
	141	7/10	7/10	NT
Empty control		8/10	10/10	NT
hpPSTVd-ΔP	71b	0/20	3/20	6/20
	82	0/20	1/20	3/20
Empty control		0/20	2/20	8/20
hpPSTVd-TL	144	0/20	17/20	NT
	85	0/20	10/20	NT
	173	1/15	11/15	NT
Empty control		7/20	14/20	NT
hpPSTVd-P-uppo	54	4/20	15/20	16/20
	122	14/20	19/20	19/20
	141	11/20	12/20	17/20
	161	14/20	18/20	20/20
Empty control		17/20	18/20	19/20
hpPSTVd-CCR-uppo	65	18/20	18/20	19/20
	114	13/20	18/20	19/20
	12	13/20	17/20	20/20
	131	14/20	19/20	19/20
Empty control		17/20	18/20	19/20
hpPSTVd-CCR-dopo	81	14/20	14/20	15/20
Empty control		17/20	18/20	19/20
hpPSTVd-257a	24	3/10	9/10	10/10
	25	1/10	5/10	7/10
	22	NT ^b	NT	NT
	60	7/10	9/10	10/10
Empty control		10/10	10/10	10/10

^a Number of plants infected/inoculated

^b Not tested

Table S2 Challenge inoculation assay of transgenic *N. benthamiana* lines expressing hpPSTVd-257a by TCDVd for analyzing cross protection against related viroid.

Transgene	Transgenic line (promoter)	3-wpi ^a	4-wpi	5-wpi
hpPSTVd·257a	24 (CaMV-35S)	10/10 ^b	10/10	10/10
npi 01 vu.207a	25 (CaMV-35S)	10/10	10/10	10/10
Empty vector	(CaMV-35S)	10/10	10/10	10/10

^a weeks post inoculation.

^b Number of plants infected/inoculated

 Table S3
 List of oligonucleotides used in this study for preparing the IR constructs.

Name	RE site addition	Sequence	Product	
intFW ^a	Aatll	GC <u>GACGTC</u> CTACAGGGTAAATTCTAGT TTTTC	CAT1 introp	
intRV ^a	HindIII	GC <u>GACGTC</u> CTACAGGGTAAATTCTAGT TTTTC	CATTINUON	
tPSTVd sFW ^a	Bg/II GCAGATCTGGTTCCTGTGGTTCACAC			
tPSTVd sRV ^a	Aatll	GC <u>GACGTC</u> ACCAACTGCGGTTCCAAG	hpPSTVd:ΔTLE	
tPSTVd aFW ^a	HindIII	GC <u>AAGCTT</u> ACCAACTGCGGTTCCAAG	and hpPSTVd:∆P	
tPSTVd aRV ^a	Kpnl	CT <u>GGTACC</u> GGTTCCTGTGGTTCACAC		
TL sFPBg	Bg/II	GC <u>AGATCT</u> CTTCGGGGCGAGGGTG		
TL sRPA	Aatll	GC <u>GACGTC</u> CTCAGGAGGTCAGGTGTG	- hpPSTVd:∆TL	
TL aFPH	HindIII	GCAAGCTTCTCAGGAGGTCAGGTGTG		
TL aRPK	Kpnl	CT <u>GGTACC</u> CTTCGGGGCGAGGGTG		
P Suppo FPBg	Bg/II	TT <u>AGATCT</u> CAGAAAAGAAAAAAGAAGG		
P Suppo RPA	Aatll	GC <u>GACGTC</u> CGAGCCGCCTTCTTTTTC	hpPSTVd·Puppo	
P Auppo FPA	HindIII	GC <u>GACGTC</u> CGAGCCGCCTTCTTTTTC		
P Auppo RPK	Kpnl	CT <u>GGTACC</u> CAGAAAAGAAAAAAAAGAAGG		
CCR Suppo FPBg	Bg/II	TT <u>AGATCT</u> GAGGAGCGCTTCAGGGATC CCCGGGG		
CCR Suppo RPA	Aatll	GC <u>GACGTC</u> TTTTGCCAGTTCGCTCCAG GTTTCCCCG	hpPSTVd:CCRup	
CCR Auppo FPA	HindIII	GC <u>GACGTC</u> TTTTGCCAGTTCGCTCCAG GTTTCCCCG	ро	
CCR Auppo RPK	Kpnl	CT <u>GGTACC</u> GAGGAGCGCTTCAGGGAT CCCCGGGG		
CCR Sdopo FPBg	Bg/II	TT <u>AGATCT</u> TGCGCTGTCGCTTCGGCTA CTACCCGG		
CCR Sdopo RPA	Aatll	GC <u>GACGTC</u> GGAGCTTCAGTTGTTTCCA CCGGG	hpPSTVd:CCRdo	
CCR Adopo FPA	HindIII GC <u>GACGTC</u> GGAGCTTCAGTTGTTTCCA CCGGG		ро	
CCR Adopo RPK	Kpnl	CT <u>GGTACC</u> TGCGCTGTCGCTTCGGCTA CTACCCGG		

siR257a BamHI, KpnI	TT <u>GGATCC</u> CACCGGGTAGTAGCCGAA GCGACAGCGCAAAGGGGGCGAGTTTC CTCGCCCCCTTTGCGCTGTCGCTTCGG CAACTACCCGGTG <u>GGTACC</u> TT	hpPSTVd:257a
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^a Kasai et al., ¹

Underlined nucleotides denote restriction endonuclease site.

Small lettered nucleotides denote the linker sequence.



Figure S1 Gel-blot hybridization analysis of PSTVd-sRNA. The arrows indicate the PSTVd-sRNA of 21 – 24-nts. The amount of PSTVd-sRNA produced by the various transgenic lines was quantified. The relative expression levels of PSTVdsRNA were variable depending on the lines. *Lane 82* hpPSTVd: Δ P-82, *lane 85* hpPSTVd:TL-85, *lane 24* hpPSTVd:257a-24, *lane 25* hpPSTVd:257a-25 and *lane PSTVd* PSTVd inoculated plant. The numbers below each lane represent the µg of RNA charged per lane.

Figure S1 (Sano)

	35 70
PSTVd-I:	5'- UGACCUCCUGAGCAGAAAAGAAAAAAAGAAGGCGGCU-3'
	XX
PSTVd-RG1:	5'- UGACCUCCUGA <u>CAAGAAAAGAAAAAAAGAAGGC</u> GGCU-3'
	35 70

Figure S2 Sequence identity between the PSTVd-I used to construct the IR expressing hpPSTVd:Puppo and the corresponding region of the PSTVd-RG1 isolate. The underlined nucleotides represent the amiR46 sequence¹. The two mismatches are shown by X in the region. The numerical numbers on both sides of the sequence indicate the corresponding nucleotides in genomic sequences of PSTVd-I and PSTVd-RG1.

Figure S2 (Sano)





Figure S3 Diagrammatic representation of steps involved in the preparation of the hairpin constructs derived from the various regions of PSTVd. The arrows inside the box indicate the direction of PSTVd sequence used. The IR sequence of the PSTVd is separated by (a) an intron for hpPSTVd:∆TLE, hpPSTVd:∆P and hpPSTVd:TL; while a small sequence was used as spacer for (b) hpPSTVd:Puppo, hpPSTVd:CCRuppo, hpPSTVd:CCRdopo; and, (c) si257a, respectively. The whole construct was inserted between the promoter (either CaMV-35S or CoMYV) and the Tn (nopaline synthase terminator) sequence of the vector pIG121.

Figure S3 (Sano)



Figure S4 The steps involved in the production of transgenic lines and in the subsequent generation of the T3 lines are shown schematically.

Figure S4 (Sano)

Supplemental information References

 Kasai, A., Sano, T. & Harada, T. Scion on a Stock Producing siRNAs of Potato Spindle Tuber Viroid (PSTVd) Attenuates Accumulation of the Viroid. *PLoS One* 8, e57736 (2013).