

Supplementary materilas

Supplementary Table S1. Correlation analysis between disease incidence and leaf colour value in five fields

Disease Incidence	G norm		VI_green	
	R ²	p-value	R ²	p-value
BrYV%	0.09	0.63	0.10	0.606
TuMV%	0.01	0.882	0.01	0.899
Virus	0.33	0.31	0.49	0.191

Supplementary Table S2. Full-length nucleotide sequences of 21 BrYV isolates, 55 TuYV isolates and 4 outgroup species (BWYV, BMYV, ToYV and PLRV) analyzed in this study.

Host	Location	Virus isolate	Accession number
<i>Cicer arietinum</i>	Australia	TuYV-MK111	MT586573
<i>Cicer arietinum</i>	Australia	TuYV-5510	MT586572
<i>Brassica napus</i>	Australia	TuYV-5514b	MT586576
<i>Lens culinaris</i>	Australia	TuYV-L31_4	MT586574
<i>Pisum sativum</i>	Australia	TuYV-P6_2	MT586575
<i>Cicer arietinum</i>	Australia	TuYV-1740	MT586571
<i>Brassica oleracea</i>	Australia	TuYV-MJ11-2	LR584025
<i>Cicer arietinum</i>	Australia	TuYV-YK12-1	LR584027
<i>Brassica napus</i>	Australia	TuYV-MK107	MT586590
<i>Brassica napus</i>	Australia	TuYV-C2016a	MT586585
<i>Lens culinaris</i>	Australia	TuYV-MK113	MT586589
<i>Brassica napus</i>	Australia	TuYV-MK102	MT586577
<i>Sinapis arvensis</i>	Australia	TuYV-5248	MT586581
<i>Brassica napus</i>	Australia	TuYV-MK104	MT586578
<i>Pisum sativum</i>	Australia	TuYV-P5_8	MT586586
<i>Cicer arietinum</i>	Australia	TuYV-BL13-1	LR584020
<i>Brassica napus</i>	Australia	TuYV-BG12-1	LR584019
<i>Brassica napus</i>	Australia	TuYV-C21A	MT586582
<i>Pisum sativum</i>	Australia	TuYV-MK109	MT586579
<i>Brassica napus</i>	Australia	TuYV-5512b	MT586580
<i>Brassica napus</i>	Australia	TuYV-WA-1_Canola	LR584021
<i>Brassica napus</i>	Australia	TuYV-MK106	MT586584
<i>Pisum sativum</i>	Australia	TuYV-MK103	MT586583
<i>Brassica napus</i>	Australia	TuYV-5509	MT586587
<i>Brassica napus</i>	Australia	TuYV-C2016b	MT586588
<i>Raphanus raphanistrum</i>	Australia	TuYV-MJ11-3	LR584026
<i>Brassica napus</i>	Australia	TuYV-C20A	MT586597
<i>Brassica oleracea</i>	Australia	TuYV-MJ11-1	LR584024
<i>Beta vulgaris</i>	Australia	TuYV-Br12	MT586598
<i>Brassica napus</i>	Australia	TuYV-5514a	MT586594
<i>Brassica napus</i>	Australia	TuYV-5513	MT586592
<i>Brassica napus</i>	Australia	TuYV-5512a	MT586593
<i>Brassica napus</i>	Australia	TuYV-5414	MT586591
<i>Brassica napus</i>	Australia	TuYV-MK105	MT586595
<i>Diuris pendunculata</i>	Australia	TuYV-WA-1	JQ862472
<i>Cicer arietinum</i>	Australia	TuYV-5511	MT586596
<i>Chinese cabbage</i>	China	BrYV-C-Haidian	KF015269
<i>Raphanus sativus</i>	China	BrYV-CR	JN015068
<i>Brassica napus</i>	China	BrYV-BJS	HQ388351
<i>Brassica napus</i>	China	BrYV-China	KY310572

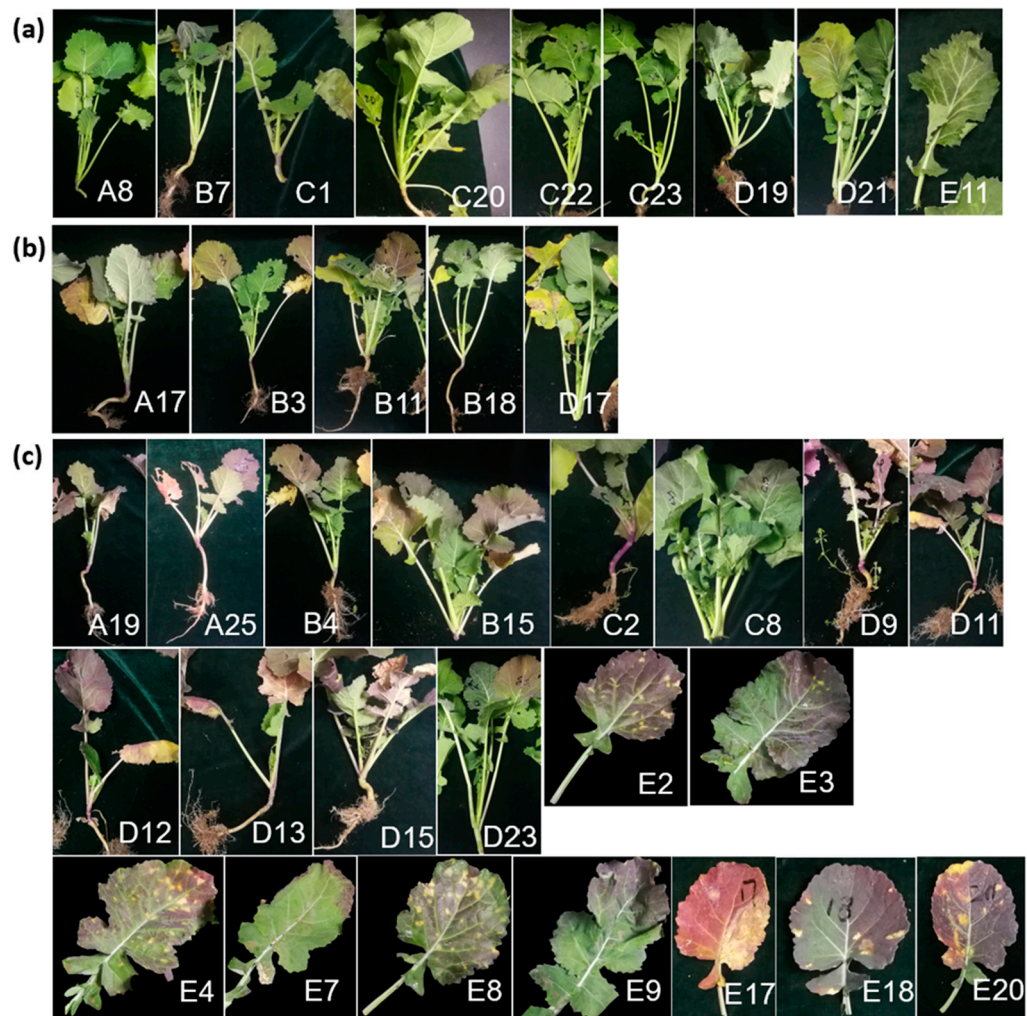
<i>Brassica napus</i>	China	BrYV-ABJ	NC_016038
<i>Nicotiana tabacum</i>	China	BrYV-Anhui	MF314820
<i>Brassica campestris</i>	China	BrYV-AJS	HQ388350
<i>Nicotiana tabacum</i>	China	BrYV-NtabQJ	MK057527
<i>Nicotiana tabacum</i>	China	TuYV-Anhui	KR706247
<i>Nicotiana tabacum</i>	China	ToYV-Shandong	MK751486
<i>Brassica napus</i>	China	BrYV-Inc	ON804808
<i>Brassica napus</i>	China	BrYV-BBJ	HQ388349
<i>Brassica napus</i>	China	BrYV-814NJLH	ON804809
<i>Brassica napus</i>	China	BrYV-NJ13	ON804810
<i>Arachis pintoi</i>	Colombia	TuYV-Pintoi-VarA	KU726090
<i>Arachis pintoi</i>	Colombia	TuYV-Pintoi-VarB	KU726091
<i>Lactuca sativa</i>	France	TuYV-FL1	NC003743
<i>Pisum sativum</i>	Germany	TuYV-Salzlandkreis-2_16	MN497803
<i>Pisum sativum</i>	Germany	TuYV-Kreis_Stormarn_16	MN497808
<i>Pisum sativum</i>	Germany	TuYV_Landkreis_Meissen_17	MN497810
<i>Pisum sativum</i>	Germany	TuYV-Muenster_17	MN497806
<i>Pisum sativum</i>	Germany	TuYV-Muenster_18	MN497807
<i>Pisum sativum</i>	Germany	TuYV-Salzlandkreis-2_18	MN497804
<i>Pisum sativum</i>	Germany	TuYV-Salzlandkreis-1_18	MN497802
<i>Pisum sativum</i>	Germany	TuYV-JKI_29344	MK450520
<i>Pisum sativum</i>	Germany	TuYV-Landkreis_Meissen_18	MN497811
<i>Pisum sativum</i>	Germany	TuYV-Salzlandkreis-1_17	MN497801
<i>Raphanus raphanistrum</i>	Germany	TuYV-JKI_29345	MK450519
<i>Pisum sativum</i>	Germany	TuYV-Muenster_16	MN497805
<i>Pisum sativum</i>	Germany	TuYV-Salzlandkreis-1_16	MN497800
<i>Pisum sativum</i>	Germany	TuYV-Landkreis_Meissen_16	MN497809
<i>Raphanus sativus</i>	Japan	BrYV-R3b	LC428363
<i>Brassica rapa</i>	Japan	BrYV-CC1	LC428358
<i>Brassica oleracea</i>	Japan	BrYV-CD9	LC428362
<i>Sinapis alba</i>	Japan	BrYV-WN1	LC428359
<i>Brassica rapa</i>	Japan	BrYV-TO3	LC428360
<i>Raphanus sativus</i>	Japan	BrYV-R40	LC428365
<i>Raphanus sativus</i>	Japan	BrYV-RT8	LC428364
<i>Brassica napus</i>	Japan	BrYV-NAP	LC428361
<i>Brassica oleracea</i>	South_Africa	TuYV-Bo10/12	KU198395
<i>Chinese cabbage</i>	South_Korea	BrYV-CS	KF923236
<i>Beta vulgaris</i>	USA	BWYV	NC_004756
<i>Solanum tuberosum</i>	USA	PLRV	NC_001747
<i>Beta vulgaris</i>	USA	BMVYV	NC_003491

Supplementary Table S3: Genetic distances calculated within groups of BrYV and TuYV isolates

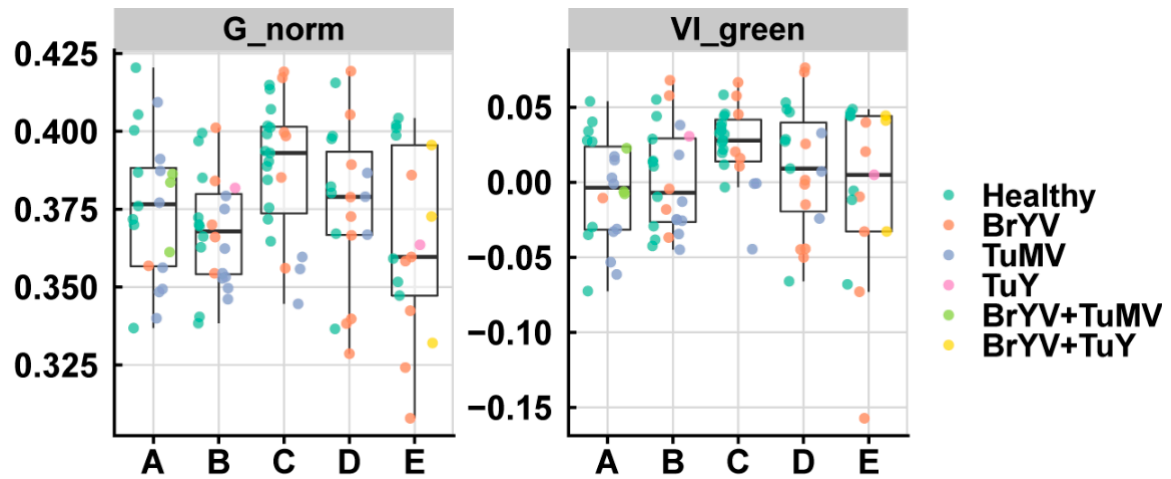
Method	P-distance
Overall mean distance	0.092
Within groups mean distance: BrYV	0.049
Within groups mean distance: TuYV	0.047
Between groups mean distance: BrYV vs TuYV	0.0031
Net between groups mean distance: BrYV vs TuYV	0.0021

Supplementary Table S4. The primer sequences used in this study

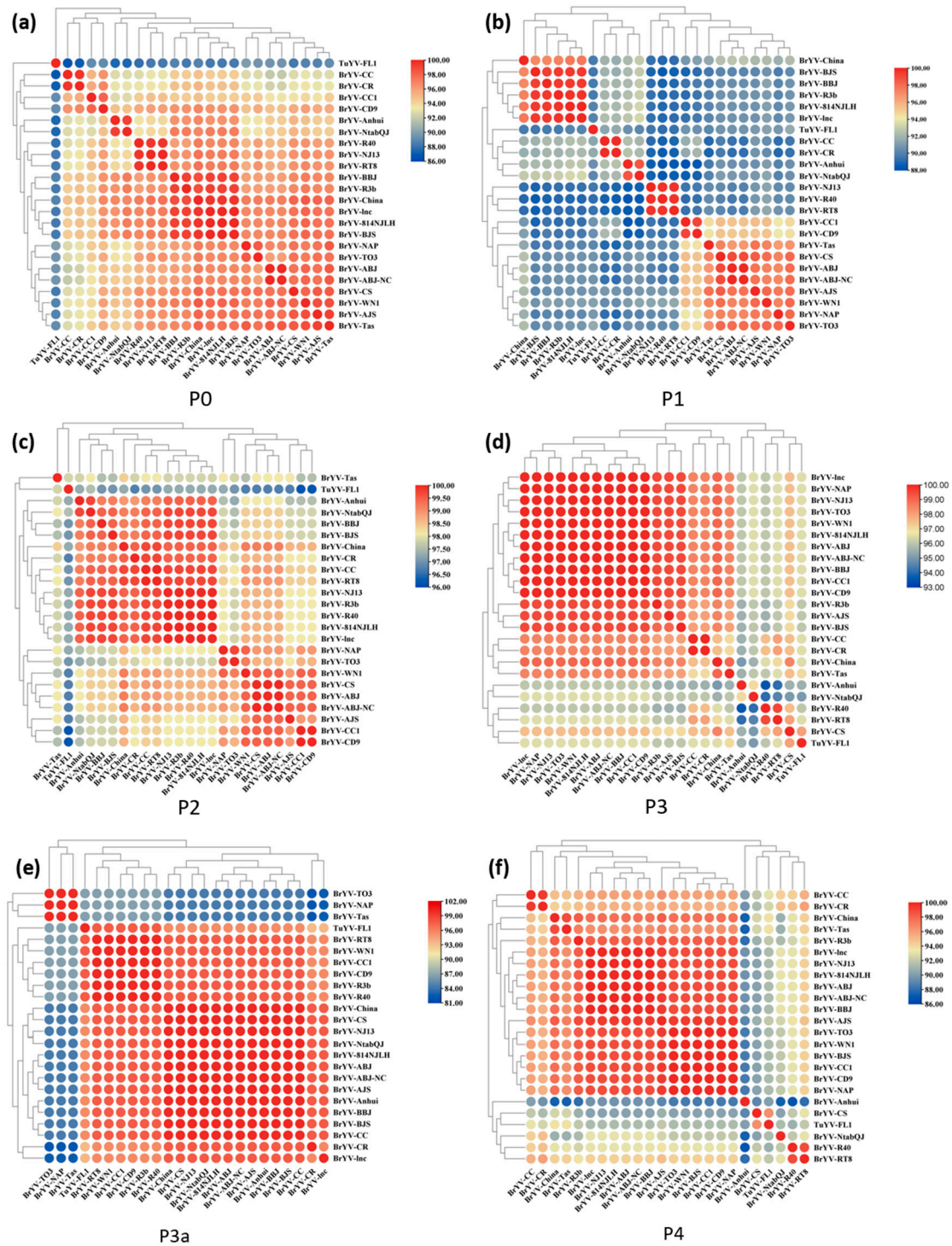
Primer name	Sequence (5' → 3')	Reference
BrYV 1F	AGAAAAGAAACCAGGAGGGAATC	In this study
BrYV 1R	AATGTTCTCCTCGGGTTGC	In this study
BrYV 2F	CCCCGAAGCAGAACTAAAGA	In this study
BrYV 2R	GGAAATCAAGCCCAACTCCA	In this study
BrYV 3F	AGCGTGGACAGATCGTGATA	In this study
BrYV 3R	GAGTGCCGTAGGGATTTCTC	In this study
CABYV AR 2299	ACTACATGGTCACTAGCCTCCG	In this study
CABYV AR 2911	AACAATCAACCTCGCTCACG	In this study
BWYV ST9 2017	ACTGTCTGAGTAAAGCGGCAA	In this study
BWYV ST9 2449	CCGGTGTATACGAGACTGGC	In this study
GMMV-2201	AGTGGGACCATTAGCCTCG	In this study
GMMV-2900	ATATGCCCTGGGATTCGTG	In this study
TuMV-F	TGGCTGATTACGAAGTACG	Wei <i>et al.</i> , 2013
TuMV-R	CTGCCTAAATGTGGGTTTGG	Wei <i>et al.</i> , 2013
TuYV-F	AAGAGGCTTGCCCTTCCTG	Zhang <i>et al.</i> , 2016
TuYV-R	AACCAAATCCGGTGTTGGAT	Zhang <i>et al.</i> , 2016
BrYA484F	TACTTGGACTAGAGATGCTGAAAG	Zhang <i>et al.</i> , 2016
BrY761R	AGACCGAAGAGCTGAAAAGG	Zhang <i>et al.</i> , 2016
BrYB88F	CCTCCACCCAAAACAAGTAT	Zhang <i>et al.</i> , 2016
BrYC257F	CGAGTTTCCGTACTTGTTG	Zhang <i>et al.</i> , 2016
CMV-F	TGTCCRACYGTBAGTAGGGT	Zhang <i>et al.</i> , 2021
CMV-R	CGAAGAAACCTAGGAGATGG	Zhang <i>et al.</i> , 2021
CABYV-2715	GACTGCTCCGGTTTTGACTGG	Shang <i>et al.</i> , 2008
CABYV-4100	CGTCTACCTATTTCTGGGT	Shang <i>et al.</i> , 2008



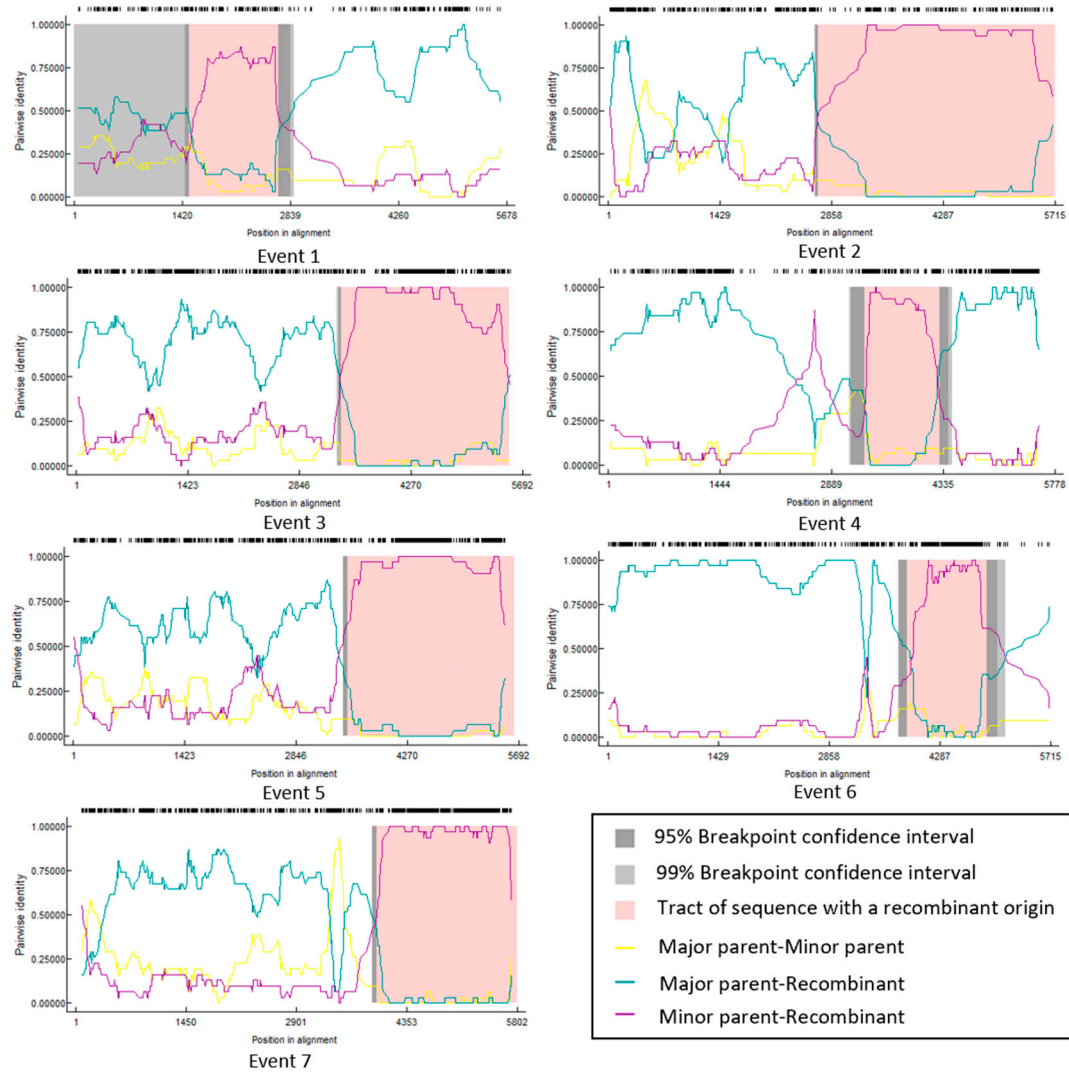
Supplementary Figure S1. Three types of plants with different symptoms after BrYV infecting in field on oilseed rape. (a) displayed the type I plants. These plants exhibited no significant symptoms. (b) was the BrYV infected plants with yellowing leaves in type II. (c) showed the type III BrYV positive plants with remarkable red or purple leaves. The block capitals A, B, C, D and E indicated different samples collected from corresponding fields.



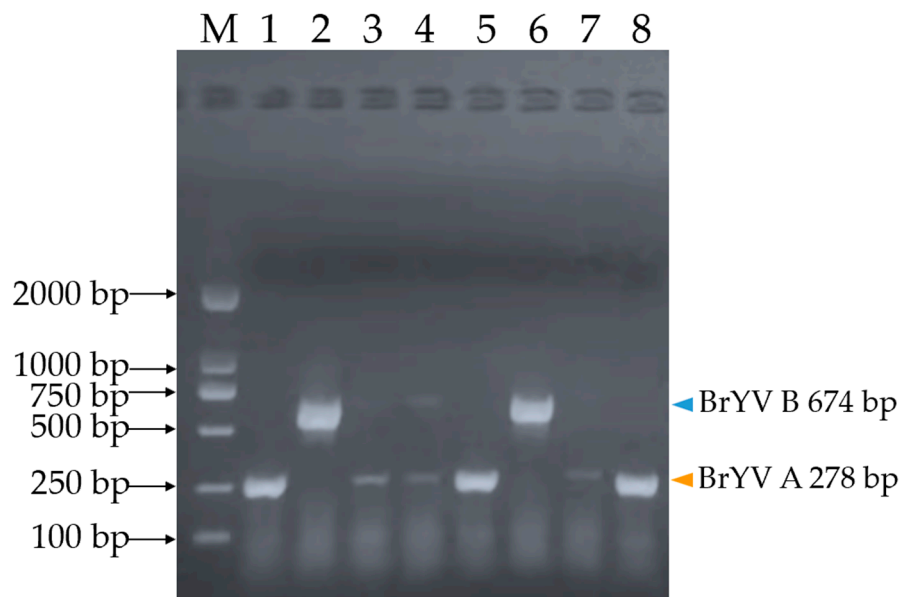
Supplementary Figure S2. The distribution of the leaf color value in five fields. Leaf color values were estimated by G_norm (left) or VI_green (right) parameters. Blue dots indicate healthy plant leaf color values. Orange, cornflowerblue and purple dots suggest the color value of BrYV, TuMV and TuYV infected plant, respectively. Green and yellow dots represent the leaf color values of co-infection of BrYV and TuMV, and BrYV and TuYV, respectively. The block capitals A, B, C, D and E indicated five sampling fields.



Supplementary Figure S3. Pairwise analysis of BrYV coding proteins. The matrix displayed pairwise amino acid identity among different BrYV and TuYV isolates in (a) P0 protein (RNA silencing suppressor), (b) P1 protein, (c) P2 protein, (d) P3 coat protein, (e) P3a protein and (f) P4 movement protein. All virus isolates information and GenBank accession numbers were depicted in Table S3. The phylogenetic trees based on aligned amino acid sequence of BrYV and TuYV. The identity of each amino acid pairwise was indicated by colored dot.



Supplementary Figure S4. The RDP method plots of 7 recombinants among BrYV and TuYV isolates. The detailed information of the seven recombinants was introduced in Table 3. For each recombinant event, the left and right boundaries of the pink area indicated the inferred recombination breakpoint locations. The dark grey and grey areas marked 95% and 99% breakpoint confidence interval, respectively. The x, y axes supplied particular location in the relevant recombinant sequence and the pairwise identity of major parent-minor parent (yellow line), major parent-recombinant (green line) and minor parent-recombinant (purple line). Vertical lines above the plot illustrated positions of the variable nucleotide sites.



Supplementary Figure S5. The electrophoretogram of RT-PCR analysis against BrYV. Lane M: DNA marker indicated PCR products size ranging from 100 bp to 2000 bp; Lane 1 and 2 were BrYV-A and BrYV-B plasmid control, respectively; Lane 3, 4 and 5 were samples from Chuxiong in Yunnan province; Lane 6, 7 and 8 were samples from Changshun in Guizhou province. The orange triangle with the length of 278 bp suggested BrYV A test band which was amplified by primer pairs of BrYA484F and BrY761R. The blue triangle at around 674 bp indicated BrYV B test band which was detected by BrYB88F and BrY761R.