

Table S1 Viral sequences identified by high-throughput sequencing analysis

Library name	Contig number	Closest related virus	Consensus length (nt)	Total read count	Average coverage	Best match (GenBank accession)	aa identity (%)	Cover region	Genus
WD-FZ	contig_539	White clover cryptic virus 2 (WCCV2), RNA1	2,434	29,310	1, 809	White clover cryptic virus 2 RNA1 (NC_021094)	77	complete <i>RdRp</i> gene	<i>Betapartitivirus</i>
	contig_24	Cannabis cryptic virus (CanCV), RNA2	2,244	11,393	755	Cannabis cryptic virus, RNA2 (NC_031130)	72	complete <i>cp</i> gene	
	contig_341	Currant latent virus (CuLV)	6,712	247,068	5, 465	Currant latent virus, RNA1 (NC_029038)	75	complete RNA1 polyprotein gene	<i>Cheravirus</i>
	contig_62		2,270	114,114	7, 402	Currant latent virus, RNA2 (KC935375)	75	partial RNA2 polyprotein gene	
	contig_30	Aconite virus A (AcVA)	5,428	1,166,397	31, 210	Aconite virus A (MN944106)	72	nearly complete <i>RdRp</i> gene	<i>Carlavirus</i>
	contig_15, 527	Cucumber mosaic virus (CMV)	3,371	1,810,218	75, 124	Cucumber mosaic virus RNA1 (LC593244)	98	almost complete RNA1	<i>Cucumovirus</i>
	contig_61		3,053	699,777	30, 895	Cucumber mosaic virus RNA2 (LC593245)	99	almost complete RNA2	
	contig_82		2,217	3,575,260	184, 183	Cucumber mosaic virus RNA3 (LC593246)	98	almost complete RNA3	
	contig_1317	Apple stem grooving virus (ASGV)	6,509	24,272	540	Apple stem grooving virus (KU947036)	97	almost complete genome	<i>Capillovirus</i>
	contig_6, 287	Tulip breaking virus (TBV)	9,479	2,188,397	135, 266	Tulip breaking virus (MH886517)	56	almost complete genome	<i>Potyvirus</i>
ZY-FZ	contig_1, 934	Cucumber mosaic virus (CMV)	2,856	1,975,751	89,806	Cucumber mosaic virus RNA1 (KC527787)	99	almost complete RNA1	<i>Cucumovirus</i>
	contig_362		2,963	256,569	4,082	Cucumber mosaic virus RNA2 (KC52769)	100	almost complete RNA2	
	contig_352		2,207	2,568,895	107,037	Cucumber mosaic virus RNA3 (EF216865)	98	almost complete RNA3	
	contig_31	Chilli veinal mottle virus	7,930	545,473	6, 852	chilli veinal mottle virus isolate	98	nearly complete	<i>Potyvirus</i>

isolate (ChiVMV)					(MT974520)	genome		
contig_5, 396		8,894	2,895,365	65,803	tomato spotted wilt orthotospovirus segment L (MF805766)	99	almost complete genome	
contig_8, 094	Tomato spotted wilt orthotospovirus (TSWV)	2,985	947,758	37,910	tomato spotted wilt orthotospovirus segment S (HQ402595)	99	almost complete genome	<i>Orthotospovirus</i>
contig_617		4,840	589,258	13,392	tomato spotted wilt orthotospovirus segment M (JF960236)	99	almost complete genome	
contig_986	Tobacco vein distorting virus (TVDV)	2,418	8,637	148	tobacco vein distorting virus (EF529624)	88	complete <i>RTD</i> gene	<i>Polerovirus</i>
contig_943	Potato leafroll virus (PLRV)	2157	5,768	94	potato leafroll virus (NC_001747)	88	partial <i>RTD</i> gene	<i>Polerovirus</i>

Table S2 Identity of the RNA1 and RNA2 encoded polyproteins between CuLV-YWDi and other cheraviruses

CuLV-YWDi	CULV	ALSV	CRLV	AVB	StPV
RNA1	(KT692952)	(AB030940)	(MK952187)	(MK153131)	(OP328251)
	75.7%	66.4%	63%	33.8%	27.6%
CuLV-YWDi	CuLV	ALSV	(MK952188)	AVB	StPV
RNA2	(KT692953)	(AB030941)	CRLY	(MK153132)	(OP328252)
	74.7%	68.7%	65.5%	22.9%	22.6%

Table S3 Primers used for detection the viruses infecting *Aconitum carmichaelii*

Virus	Primer name*	Primer sequence (5'-3')	Size (nt)	Tm (°C)
AcoPV-1	FZPoF8659	TTGAGGCAGATTAGCTCCAAGC	532	57
	FZPoR9191	TATTGCGTAAGGCTGCTGCCTTC		
AcoBPV-1	WCCV2R2F1464	ACACAGCTCCAAGCGTTCTTGTC	494	58
	WCCV2R1R1931	TTCGGACATGCCAGGAACAGC		
CuLV-YWDi	CuLVR1F61	TTCGTTTCCCAACTCTGCTACC	665	55
	CuLVR1R725	AACAACGCCACGTGGCATATCG		
AcoAV-1	FZAVF1900	ATGATTCCCAGTGGCTCTCTC	1100	57
	FZAVR3000	TGTAGTCCACGCTGCATATGC		
AcVA	AcVAF109	ATATCGTAGCCCACTTGAGG	905	55
	AcVAR994	TGCAAGTTGTGGCTTCGAACC		
	AcVAF201	ACTATGCACTTGAGGCTCATG	714bp	55
	AcVAR914	TAACGTGGTGAGCGAATTTGC		
CMV	CMVCPuF	TCTCATGGATGCTTCTCCGCG	880	55
	CMVCPuR	CCGTAAGCTGGATGGACAACC		
ASGV	ASGVF5431	TCTGGAAGAAGGTGCACCAAACG	918	56
	ASGVR6326	TGCAAGACCGCGACCAAATTTG		
ChiVMV	ChiVMVdF	GGATAGAGCTGARCARCCAG	920	57
	ChiVMVdR	CTTTGAAGCCCATATCTTGGC		
TSWV	TSWVMF1829	TGATAAGTAGATAGAGAGCAAGC	503	55
	TSWVMR2332	TGAAGTATAGCTCATGGACC		
TVDV	TVDVdF	ATGGTGACTCTGAAGGATCCTGC	534	57
	TVDVdR	TGGTCAACATACGCTTCGTCAGTG		
PLRV	PLRV-CP-F	ATGAGTACGGTCGTGGTTAAAG	600	57
	PLRV-CP-R	ATGGTGACTCTGAAGGATCCTGC		
AcLV	AcLVdF	AGTTCAACGAAGGTCTCAAAGG	971	54
	AcLVdR	TCTCTGGTTAATTCAGGTCCATTGC		

* F: Forward primer; R: Reverse primer; primers of AcVAF201 and AcVAR914 were used to detection AcVA in *A. carmichaelii* seedlings.

Table S4 Single or mixed viral-infection rates in *Aconitum carmichaelii* detected by RT-PCR

Viral viruses	Numbers of virus-positive sample	Detection rate (%)
1 virus	9	6.3
2 viruses	19	13.4
3 viruses	34	23.9
4 viruses	40	28.2
5 viruses	22	15.5
6 viruses	6	4.2
7 viruses	2	1.4
No virus	10	7.0
Total	142	

Note: A total of 132 in 142 samples were virus-positive

Table S5 Viruses involved in single or mixed infection in *Aconitum carmichaelii*

order	viruses	Single or mixed viral-infection types	Positive numbers	Detection rate (%)
1	1 virus	AcoPV-1	4	2.8
2	1 virus	CuLV	2	1.4
3	1 virus	CMV	1	0.7
4	1 virus	TSWV	1	0.7
5	1 virus	TVDV	1	0.7
6	2 viruses	AcoPV-1+CMV	8	5.6
7	2 viruses	ACVA+CMV	6	4.2
8	2 viruses	AcoAV-1+CMV	2	1.4
9	2 viruses	CuLV +CMV	1	0.7
10	2 viruses	ACVA+ASGV	1	0.7
11	2 viruses	AcoPV-1+TVDV	1	0.7
12	3 viruses	AcoPV-1+ACVA+CMV	12	8.5
13	3 viruses	AcoAV-1+ACVA+CMV	7	4.9
14	3 viruses	AcoBPV-1+ACVA+CMV	4	2.8
15	3 viruses	AcoPV-1+CMV+TVDV	2	1.4
16	3 viruses	AcoPV-1+AcoAV-1+CMV	2	1.4
17	3 viruses	CuLV +ACVA+CMV	2	1.4
18	3 viruses	AcoPV-1+TSWV+TVDV	1	0.7
19	3 viruses	AcoPV-1+CMV+TSWV	1	0.7
20	3 viruses	AcoAV-1+CMV+ChiVMV	1	0.7
21	3 viruses	AcoBPV-1+CuLV +AcoAV-1	1	0.7
22	3 viruses	AcoPV-1+AcoAV-1+ACVA	1	0.7
23	4 viruses	AcoPV-1+AcoBPV-1+ACVA+CMV	8	5.6
24	4 viruses	AcoPV-1+AcoAV-1+ACVA+CMV	8	5.6
25	4 viruses	AcoPV-1+CuLV +ACVA+CMV	7	4.9
26	4 viruses	AcoPV-1+ACVA+CMV+ASGV	4	2.8
27	4 viruses	AcoBPV-1+AcoAV-1+ACVA+CMV	3	2.1

28	4 viruses	AcoBPV-1+ACVA+CMV+ASGV	2	1.4
29	4 viruses	CuLV +ACVA+CMV+ASGV	2	1.4
30	4 viruses	AcoPV-1+CMV+TVDV+PLRV	1	0.7
31	4 viruses	AcoPV-1+AcoBPV-1+TSWV+TVDV	1	0.7
32	4 viruses	CuLV +AcoAV-1+ACVA+CMV	1	0.7
33	4 viruses	AcoPV-1+AcoAV-1+ACVA+ASGV	1	0.7
34	4 viruses	AcoBPV-1+CuLV +ACVA+CMV	2	1.4
35	5 viruses	AcoPV-1+AcoBPV-1+AcoAV-1+ACVA+CMV	5	3.5
36	5 viruses	AcoPV-1+CuLV +AcoAV-1+ACVA+CMV	3	2.1
37	5 viruses	AcoPV-1+CuLV +ACVA+CMV+ASGV	3	2.1
38	5 viruses	AcoPV-1+AcoAV-1+ACVA+CMV+ASGV	3	2.1
39	5 viruses	AcoPV-1+AcoBPV-1+CuLV +ACVA+CMV	2	1.4
40	5 viruses	AcoBPV-1+CuLV +ACVA+CMV+ASGV	2	1.4
41	5 viruses	AcoPV-1+AcoAV-1+CMV+TSWV+PLRV	1	0.7
42	5 viruses	AcoPV-1+AcoBPV-1+ACVA+CMV+ASGV	1	0.7
43	5 viruses	AcoPV-1+AcoAV-1+ACVA+CMV+ChiVMV	1	0.7
44	5 viruses	CuLV +AcoAV-1+ACVA+CMV+ChiVMV	1	0.7
45	6 viruses	AcoPV-1+AcoBPV-1+CuLV +ACVA+CMV+ASGV	3	2.1
46	6 viruses	AcoPV-1+AcoBPV-1+CuLV +AcoAV-1+ACVA+ CMV	1	0.7
47	6 viruses	AcoPV-1+CuLV +AcoAV-1+ACVA+CMV+ASGV	1	0.7
48	6 viruses	AcoBPV-1+CuLV +AcoAV-1+ACVA+ CMV+ASGV	1	0.7
49	7 viruses	AcoPV-1+AcoBPV-1+ CuLV +AcoAV-1+AcVA+CMV+ASGV	2	1.4
	No virus		10	7.0
total			142	

Table S6 Primers used for amplification of the complete nucleotide sequence of AcoPV-1

Primer name*	Primer sequence (5'-3')	Size (nt)	T _m (°C)	Note
PotyvirusF98	AAGCACACATAAGCACAATGGCG	1603	58	
PotyvirusR1701	ACATTCGGATTTCTCCTGATTACG			
PotyvirusF1588	TTCAAATGGCGCCAGCGCGC			
PotyvirusR3167	AGCTGCAACAAGACACACATCAC	1579	58	
PotyvirusF3099	AAGAAGCGCAATGGCAGATCTC			
PotyvirusR4555	TTCAGGCCAAAATCAACAACCGC			
PotyvirusF4442	GATACCAACAAGTGGAATCAC	1544	58	
PotyvirusR5986	TTACTGAGTCGATGTCCAGCTC			
PotyvirusF5845	ACTTTTGACGGTATGTGATCC			
PotyvirusR7459	TCATTGAGCCATTCCACACTCC	1614	58	
PotyvirusF7305	AGCATTGAATATGAAGGCAGCAGTC			
PotyvirusR8772	ATCCTACTGTGCATGTGTTGCTC			
PotyvirusF8659	TTGAGGCAGATTAGCTCCAAGC	532	58	
PotyvirusR9191	TATTGCGTAAGGCTGCTGCCTTC			
PotyvirusF8971	AATGCACAACCCACACTAAGGC			
		~540	58	For 3'-end

Vial9 (PCR)	GACCACGCGTATCGATGTCGAC			
Vial8 (RT)	GACCACGCGTATCGATGTCGACTTTTTTTTTTTTTTTT			
	V (V = A, C or G)			
PotyvirusR224	ATGTTGGATTTCGTAGTTGGCAATAGC	~220	65	For 5'
PotyvirusR386	TTCTTGAGAGCCGCATCCTGGGCCTC	~380	60	RACE

* F: Forward primer; R: Reverse primer

Table S7 Primers used for amplification of the complete nucleotide sequence of CuLV-YWDi

Primer name*	Primer sequence (5'-3')	Size (nt)	Tm (°C)	Segment	Note
CheravirusR1R191	ACATGTGTCCTCTGGAGAGGAG	~190	58		
CheravirusR1R232	ATACGCATTGACCTCTGGAGAGAGGC	~220	62		For 5' RACE
CheravirusR1F61	TTCGTTTCCCAACTCTGCTACC				
CheravirusR1R725	AACAACGCCACGTGGCATATCG	660	58		
CheravirusR1F550	ATCAACGCAGACAGGCTCTGC				
CheravirusR1R2033	AAGGCATCCATCCAGCTAACC	1471	58		
CheravirusR1F1901	AGGTGCAAAAAGAAACGGTTGTGC	1592	58		
CheravirusR1R3493	AACATATACAGGGCAAACCTTGATC				
CheravirusR1F3320	TGCATCATTTCCCTCAATTCGAGGC	1729	58	RNA1	
CheravirusR1R5031	ATGTGCCAATCTCCAGGAGATCC				
CheravirusR1F4798	ATGCTGAGTCGCTAGTTATGCAG				
CheravirusR1R6334	TGTGAGACCACCCAATCTGTAG	1537	58		
Vial9 (PCR)	GACCACGCGTATCGATGTCGAC				
Vial8 (RT)	GACCACGCGTATCGATGTCGACTTTT TTTTTTTTTTTV (V = A, C or G)	~400	56		For 3'-end
CheravirusR1F6179	TGGTCTCTATGCAGTTTAAAGCTCG				
CheravirusR2R178	ACAGGATTCAACCAACCGCTGGTGGC	~200			For 5' RACE
CheravirusR2F150	ACTTCCCTCCCTTCTTCTAAC				
CheravirusR2R480	TCATCTTTGGCCAAGTAGGTGG	330	54		
CheravirusR1F362	AATGCTGGCACGTCTCCGTGC				
CheravirusR1R2012	AGACGGTGTCCCATTCTACTAGC	1652	58		
CheravirusR2F1846	TCTACACCTTCCCTTCAATAGTTG				
CheravirusR2R3120	ATGATTAGCACGGACCCAAAGTTG	1274	58	RNA2	
CheravirusR2F2767	ATGTGGTTGCGCACCTATCGAGTTGC				
Vial9 (PCR)	GACCACGCGTATCGATGTCGAC				
Vial8 (RT)	GACCACGCGTATCGATGTCGACTTTT TTTTTTTTTTTV (V = A, C or G)	~400	60		For 3'-end

* F: Forward primer; R: Reverse primer

Table S8 Primers used for amplification of the complete nucleotide sequence of AcoBPV-1

Primer name*	Primer sequence (5'-3')	Size (nt)	Tm (°C)	Segment	Note
BetapartitivirusR1R200	AGTAGAATCAAGAACAGCAGTGGGATCAC	~200	62		For 5' RACE
BetapartitivirusR1F23	ACATTCGTCTCCAGTATCAAGC	2072	58		
BetapartitivirusR1R2094	TTGCTAGATCAGGCATTCCATC				
Vial9 (PCR)	GACCACGCGTATCGATGTCGAC			RNA1	
Vial8 (RT)	GACCACGCGTATCGATGTCGACTTTTTTTTTT TTTTTTV (V = A, C or G)				For 3'-end
BetapartitivirusR1F2007	TCTCACTATAAACCAGACGTTTCGC	~400	60		
BetapartitivirusR2R233	TGAAGAATCAGTACGAGCAGCAGTATTGG	~250	62		For 5' RACE
BetapartitivirusR2F80	TCTAACGATGTCTACCTCATCTAC	1852	58		
BetapartitivirusR1R1931	TTCGGACATGCCAGGAACAGC				
BetapartitivirusR2F1815	ATGACTCCAATCACTCCTGTGAATG			RNA2	
Vial9 (PCR)	GACCACGCGTATCGATGTCGAC	~400	56		For 3'-end
Vial8 (RT)	GACCACGCGTATCGATGTCGACTTTTTTTTTT TTTTTTV (V = A, C or G)				

* F: Forward primer; R: Reverse primer

Table S9 Primers used for amplification of the complete nucleotide sequence of AcVA-YWDi

Primer name*	Primer sequence (5'-3')	Size (nt)	Tm (°C)	Note
AcVAR148	TACCTATCGACGGCTGTGGCAGAG	~150	62	For 5' RACE
AcVAF27	AGATAAGAGCTGAACATACACGAC	1543	58	
AcVAR1569	AGCAATGTGACTTCACTAGCAGC			
AcVAF1462	TACTGCTGGGACAAGCTATGGC	1504	58	
AcVAR2965	TACATCTATCCTCACAAAGCTCTC			
AcVAF2851	ACCTAGTGCTGTGCCTATGGAC	1524	58	
AcVAR4374	TCAGCACTACAACCAGTGAGCTC			
AcVAF4257	ATTATTGGCCGACTGCCGTGC	1413	58	
AcVAR5670	AGGAAAGTGAACAACATATTGGCC			
AcVAF5410	TGTCGCTTTGCACCTTACATGC	1461	58	
AcVAR6871	AGGTCACAAGAGTTACCACGTC			
AcVAF6785	ATTACGTAAGCACTGCGTGCC	1482	58	
AcVAR8267	ATTCAAACACGTCGAAAGCAGC			
AcVAF7900	ACAACTTGCGAGGCGACACCAC			
Vial9 (PCR)	GACCACGCGTATCGATGTCGAC	~950	58	For 3'-end
Vial8 (RT)	GACCACGCGTATCGATGTCGACTTTTTTTTTTTTTT (V = A, C or G)			

* F: Forward primer; R: Reverse primer