

# A new jasmine virus C isolate identified by nanopore sequencing is associated to yellow mosaic symptoms of *Jasminum officinale* in Italy

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## **Supplementary Files**

### **Supplementary Table S1.**

Specific primers designed on the genomic sequence of jasmine virus C isolate Bari. The primers were used for RT-PCR initial confirmation on the infected plants, for viral detection in the survey and for sequencing of the 3' end portion (3' end RACE). Non-viral sequences are in italics. Nucleotide positions are on the consensus sequence deposited in GenBank (Acc. nr. OL828237).

### **Supplementary Table S2.**

List of all the viruses cited and used in the elaborations (pairwise matrices, phylogenetic trees, Suppl. Figure S2) with available ICTV official abbreviations. The accession numbers as proteins ID (GenBank) or reference nucleotide genomes are reported.

### **Supplementary Table S3.**

Matrix of pairwise identities of coat proteins amino acid sequences among jasmine virus C isolates and other member species in the *Carlavirus* genus.

### **Supplementary Table S4.**

Matrix of pairwise identities of replicases amino acid sequences among jasmine virus C isolates and other member species in the *Carlavirus* genus.

### **Supplementary Table S5.**

List of the most frequent nucleotide polymorphic sites retrieved in jasmine virus C Bari isolate genomic consensus sequence (produced by Illumina sequencing with an average coverage of 8.81x). Lower and higher frequency values are highlighted in yellow. Amino acid residues changes are reported when a non-synonymous mutation is present in the codon (in red either the nucleotide change and amino acids of a different structural type).

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Graphic representation of InterPro and CCD protein domain searches and annotations, including summary tables described in the genome of jasmine virus C Bari isolate. (A) ORF 1, Replicase domains. (B) ORF 2, Triple Gene Block 1. (C) ORF 3, Triple Gene Block 2. (D) ORF 4, Triple Gene Block 3. (E) ORF 5, Coat Protein. (F) ORF 6, Nucleic Acid Binding protein.

**Supplementary Figure S2.**

Alignment (obtained with Clustal Omega; <https://www.ebi.ac.uk/Tools/msa/clustalo/>) of the nucleic acid binding proteins (ORF6 protein) of JaVC available in GenBank. Amino acid residues of the Bari isolate (from *J. officinale*) that diverge in the position from the almost invariant residues aligned from all the other isolates (from *J. sambac*) are in red. Accession numbers: Yunnan, MH389795; A31 Taiwan, KX364696; Fujian, MH231174; Guangdong, MH389788; Guangxi, MH389789; Hunan, MH389790; Jilin, MH389791; Sichuan, MH389793; Jangsu, MH389792; Shandong, MH389794.

**Supplementary Figure S3.**

Alignment (obtained with Clustal Omega; <https://www.ebi.ac.uk/Tools/msa/clustalo/>) of coat proteins of selected *Carlavirus* members used to calculate the pairwise percentage similarity among aphid-transmitted and whitefly-transmitted species. Melon: melon yellowing-associated virus, MYaV, NC\_038324; cowpea: cowpea mild mottle virus, CPPMV; carya: *Carya illinoensis* carlavirus 1, MW328759; narcissus: Narcissus common latent virus, NCLV, NC\_008266; A-31: jasmine virus C, Taiwan isolate A-31, KX364696; carnation: carnation latent virus, CLV, MN450069; shallot: shallot latent virus, SLV, NC\_003557

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Primer Name	Sequence (5' -> 3')	Position (nt)	Product Size (bp)
<b>Detection</b>			
Jvc_R2_for	5'-GAGCAAAGTGGGACTGATGCCT-3'	2975-2997	164
Jvc_R2_rev	5'-CTCTGATATTCTCTGCAGCCCTT-3'	3116-3138	
Jvc_R3/5_for	5'-CCTCAAACAGGATGCCGGCACTC-3'	7750-7772	213
Jvc_R3/5_rev	5'-GACTGATCAGGCGACCTACTCC-3'	7941-7962	
Jvc_rN3_for	5'-CCGCCGTTGTACATTCCTATCC-3'	268-289	1336
Jvc_r1_REV	5'-AGCACTTTCACCACCAATGCT-G	1582-1603	
<b>3' RACE</b>			
J3'for	5'-GGGCGAAATCCATTTCTAGATG-3'	8249-8270	243
J3' cDNA RACE	5'-GGCCACGCGTCGACTAGTACGTTTTTTTTTTTTTTTTTTN-3'		
J3-RACE Rev (Tag)	5'-GGCCACGCGTCGACTAGTACG-3'		

**Supplementary Table S2.** List of all the viruses cited and used in the elaborations (pairwise matrices, phylogenetic trees, Suppl. Figure S2) with available ICTV official abbreviations. The accession numbers as proteins ID (GenBank) or reference nucleotide genomes are reported.

Abbreviation	Species	Accession number CP	Accession number replicase
AcLV	Aconitum latent virus	BAB56118	NP_116487
ACLSV	Apple chlorotic leafspot virus	AAA42589	AAA42587
AHLV	American hop latent virus	AFI61523	YP_006297586
ASPV	Apple stem pitting virus	BAA04857	BAA04853
AtrMoV	Atractylodes mottle virus	AKZ66618	YP_009508317
BISV	Blueberry scorch virus	NP612812	AAY18403
ButMV	Butterbur mosaic virus	BAI49696	QQX32740
CLV	Carnation latent virus	CAA09306	QJX15400
-	Carya illinoensis carlavirus 1	QQG34676	QQG34672
CVB	Chrysanthemum virus B	CAM35757	CAO78688
CVR	Chrysanthemum virus R	YP009553180	YP_009553176
CoLV	Cole latent virus	QGN03517	QGN03513
CoMMV	Cole mild mosaic virus	QGN03509	QGN03507
CVNV	Coleus vein necrosis virus	ABS89249	EF527260
CPMMV	Cowpea mild mottle virus	ADQ54111	HQ184471
DVS	Daphne virus S	CAF04331	BAU20378
EIVC	Elderberry carlavirus C	YP009224944	YP_009224940
EIVE	Elderberry carlavirus E	ALY33533	YP_009224952
GalLV	Gaillardia latent virus	AHN84515	YP_009022064
GaVA	Garlic virus A	BAA61810	BAA61806
HelVS	Helenium virus S	BAA01248	QQX32728
HNNV	Helleborus net necrosis virus	ACM45983	FJ196835
HLV	Hippeastrum latent virus	AAZ15110	YP_002308447
HpLV	Hop latent virus	BAB13716	AJR19303
HpMV	Hop mosaic virus	ACB32253	YP_001798592
HdCMV	Hydrangea chlorotic mottle virus	ACE78185	YP_002985636
KLV	Kalanchoe latent virus	ACL01038	FJ531634
LNRSV	Ligustrum necrotic ringspot virus	ABW69738	QUP51755
LVA	Ligustrum virus A	AOO96603	YP_009288956
LSV	Lily symptomless virus	CAD56794	QBS17038
MYaV	Melon yellowing-associated virus	NC_038324.1	-
MjMV	Mirabilis jalapa mottle virus	AEQ35304	YP_004901680
NCLV	Narcissus common latent virus	CAC85384	YP_699983
NCLV	Narcissus common latent virus	YP_699987	CAJ43609
OVH	Opuntia virus H	ANH10858	ANH10854
PLV	Passiflora latent virus	ABE97939	QWT83583
PhIVB	Phlox Virus B	ABW05096	YP_001552317
PhIVM	Phlox virus M	YP_009664747	
PhIVS	Phlox virus S	ABP37860	YP_001165301
PVM	Potato virus M	BAA03343	QBL75476
PVM	Potato virus M	ASV70527	-
PVS	Potato virus S	CAI06119	QNN79442
SLV	Shallot latent virus	NC_003557.1	-
-	Stevia carlavirus 1	QQG34563	QQG34559
-	Tagetes carlavirus 1	QQG34557	QQG34553
YLV	Yam latent virus	AJD23369	YP_009134730

Matrix of pairwise identities of coat proteins amino acid sequences among jasmine virus C isolates and other member species in the *Carlavirus* genus.

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Matrix of pairwise identities of replicases amino acid sequences among jasmine virus C isolates and other member species in the *Carlavirus* genus.

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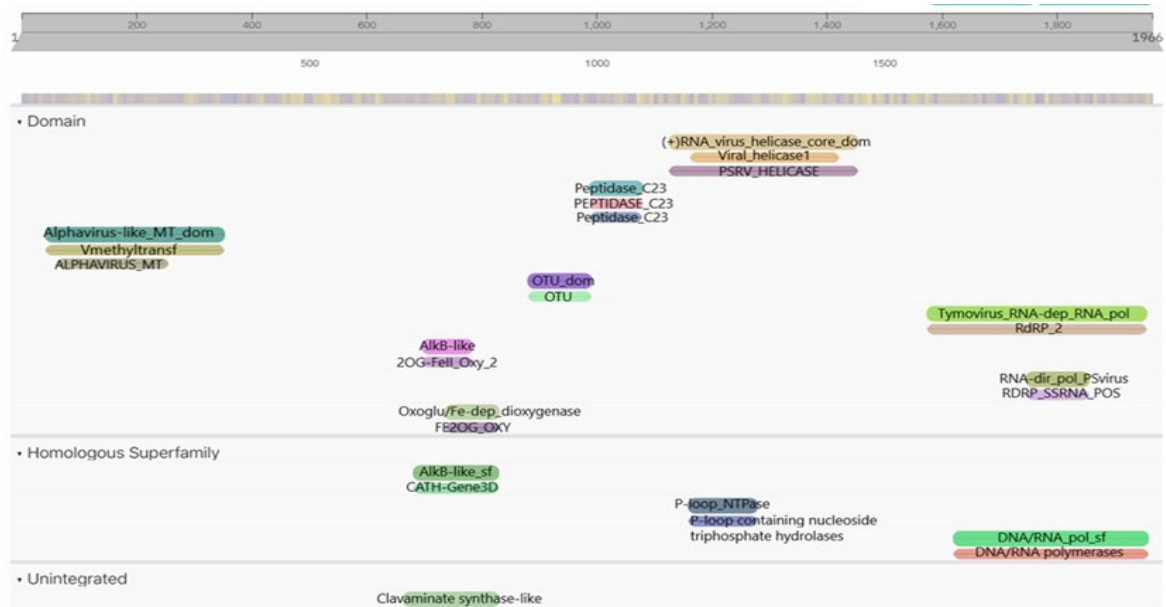
## Supplementary Table S5.

List of the most frequent nucleotide polymorphic sites retrieved in jasmine virus C Bari isolate genomic consensus sequence (produced by Illumina sequencing with an average coverage of 8.81x). Lower and higher frequency values are highlighted in yellow. Amino acidic residues changes are reported when a non-synonymous mutation is present in the codon (in red either the nucleotide change and amino acids of a different structural type).

Name	Gene	Position	Length	Change	Polymorphism Type	Variant Frequency	P-Value	Codon	Amino acid	Changes	
T	ORF1	668	1	C->T	SNP (transition)	19.7%	2.7E-33	GAc	D=D		
G	"	716	1	A->G	SNP (transition)	11.9%	1.8E-26	GTa	V=V		
T	"	941	1	C->T	SNP (transition)	16.7%	1.6E-63	GTc	V=V		
C	"	1001	1	T->C	SNP (transition)	11.7%	3.4E-19	CCt	P=P		
T	"	1052	1	C->T	SNP (transition)	48.6%	2.3E-128	AGc	S=S		
T	"	1250	1	C->T	SNP (transition)	23.2%	2.1E-73	GGc	G=G		
G	"	1525	1	C->G	SNP (transversion)	19.8%	2.3E-50	AcC	T	AgC	S
T	"	1544	1	C->T	SNP (transition)	11.0%	7.5E-25	TTc	F=F		
A	"	1617	1	T->A	SNP (transversion)	13.8%	3.0E-29	tGC	C	aGC	S
G	"	1908	1	A->G	SNP (transition)	25.4%	1.2E-36	aAA	K	gAA	E
G	"	1940	1	A->G	SNP (transition)	10.5%	1.4E-13	AGa	R=R		
A	"	2046	1	G->A	SNP (transition)	10.8%	1.4E-27	TTg	L=L		
T	"	2432	1	C->T	SNP (transition)	17.6%	2.8E-42	GTc	V=V		
A	"	3086	1	T->A	SNP (transversion)	12.4%	1.6E-31	CGt	R=R		
A	"	3242	1	T->A	SNP (transversion)	11.3%	8.7E-22	GTt	V=V		
A	"	3278	1	G->A	SNP (transition)	10.0%	2.1E-12	GAg	E=E		
G	"	3485	1	A->G	SNP (transition)	49.5%	3.9E-139	CTa	L=L		
T	"	3560	1	C->T	SNP (transition)	16.8%	3.3E-34	CAc	H=H		
G	"	3944	1	A->G	SNP (transition)	54.5%	2.1E-150	ACa	T=T		
G	"	4004	1	A->G	SNP (transition)	16.4%	4.5E-27	CGa	R=R		
G	"	4245	1	A->G	SNP (transition)	10.1%	2.8E-20	aTC	I	gTC	V
C	"	4417	1	T->C	SNP (transition)	17.3%	1.4E-40	GtG	V	GcG	A
C	"	4538	1	T->C	SNP (transition)	45.5%	5.4E-81	GGt	G=G		
A	"	4844	1	C->A	SNP (transversion)	13.9%	1.1E-19	GTc	V=V		
C	"	5084	1	T->C	SNP (transition)	14.2%	6.1E-31	GGt	G=G		
C	"	5165	1	T->C	SNP (transition)	36.7%	1.0E-106	TGt	C=C		
C	"	5729	1	T->C	SNP (transition)	11.9%	3.4E-45	ATt	I=I		
C	"	5900	1	T->C	SNP (transition)	18.3%	3.1E-45	GTt	V=V		
G	TGB1	6236	1	A->G	SNP (transition)	29.5%	5.7E-67	CaA	Q	CgA	R
G	TGB1	6366	1	A->G	SNP (transition)	13.7%	7.7E-36	AGa	R=R		
A	TGB3	7145	1	T->A	SNP (transversion)	11.1%	3.1E-10	AtT	I	AaT	N
A	CP	7318	1	T->A	SNP (transversion)	11.5%	1.7E-14	GCt	A=A		

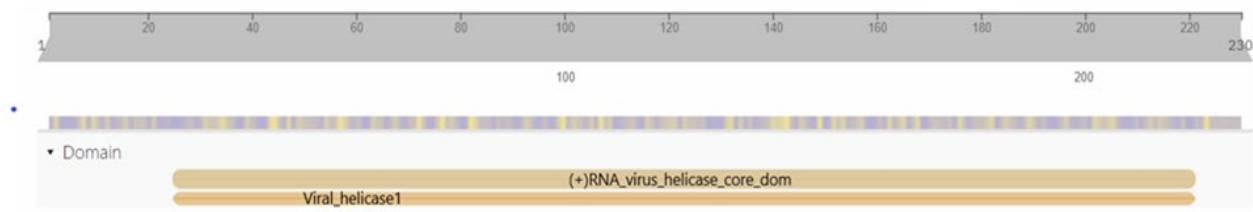
**Supplementary Figure S1.** Graphic representation of InterPro and CCD protein domain searches and annotations, including summary tables described in the genome of jasmine virus C Bari isolate. (A) ORF 1, Replicase domains. (B) ORF 2, Triple Gene Block 1. (C) ORF 3, Triple Gene Block 2. (D) ORF 4, Triple Gene Block 3. (E) ORF 5, Coat Protein. (F) ORF 6, Nucleic Acid Binding protein.

**(A) ORF 1, Replicase domains.**



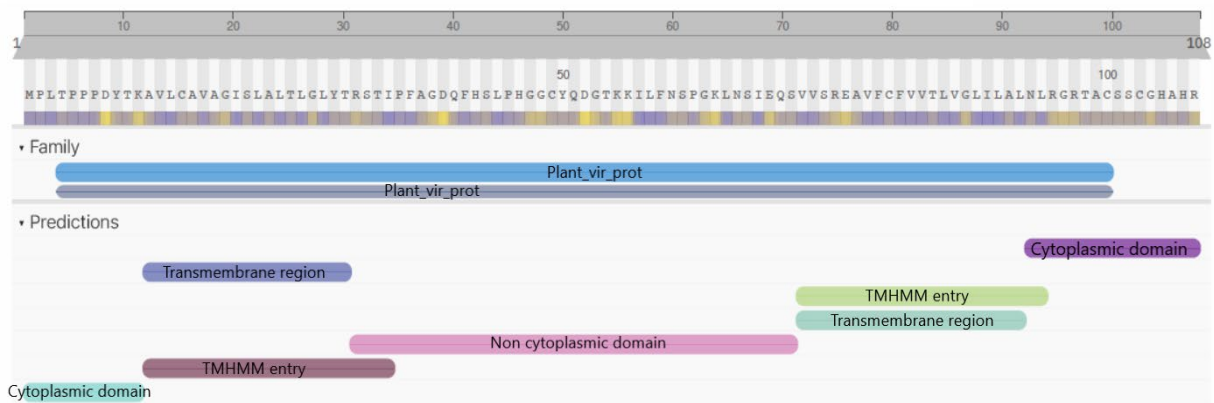
InterPro Name	InterPro ID	InterPro Type	Database	Database ID	Start	End	Length
Alphaviruslike_MT_dom	IPR002588	Domain			43	351	308
Vmethyltransf			Pfam	PF01660	43	351	308
ALPHAVIRUS_MT			PROSITE	PS51743	63	254	191
AlkB-like_sf	IPR037151	homologous superfamily			681	828	147
2OG-Fell_Oxy_2			Pfam	PF13532	698	783	85
CATH-Gene3D				G3DSA:2.60.120.590	681	828	147
Clavaminatase synthase-like		Unintegrated	SUPERFAMILY	SSF51197	690	828	138
Oxoglu/Fe-dep_dioxygenase	IPR005123	Domain			738	829	91
FE2OG_OXY			PROSITE	PS51471	738	829	91
OTU_dom	IPR003323	Domain			882	990	108
OTU			PROSITE	OTU	882	990	108
Peptidase_C23	IPR008041	Domain			989	1079	90
Peptidase_C23			PROSITE	PS51492	989	1079	90
Peptidase_C23			Pfam	PF05379	990	1077	87
(+)RNA_virus_helicase_core_dom	IPR027351	Domain			1138	1460	322
Viral_helicase1			Pfam	PF01443	1164	1420	256
PSRV_HELICASE			PROSITE	PS51657	1138	1460	322
Tymovirus_RNAdep_RNApol	IPR001788	Domain			1576	1955	379
RdRP_2			Pfam	PF00978	1576	1955	379
RNA-dir_pol_Psvirus	IPR007094	Domain			1748	1955	207
RDRP_SSRNA_POS			PROSITE	PS50507	1748	1955	207

**(B) ORF 2, Triple Gene Block 1.**



InterPro Name	InterPro ID	InterPro Type	Database	Database ID	Start	End	Length
(+)RNA_virus_helicase_core_dom	IPR027351	Domain			25	221	196
Viral_helicase1			Pfam	PF01443	25	221	196

### (C) ORF 3, Triple Gene Block 2.



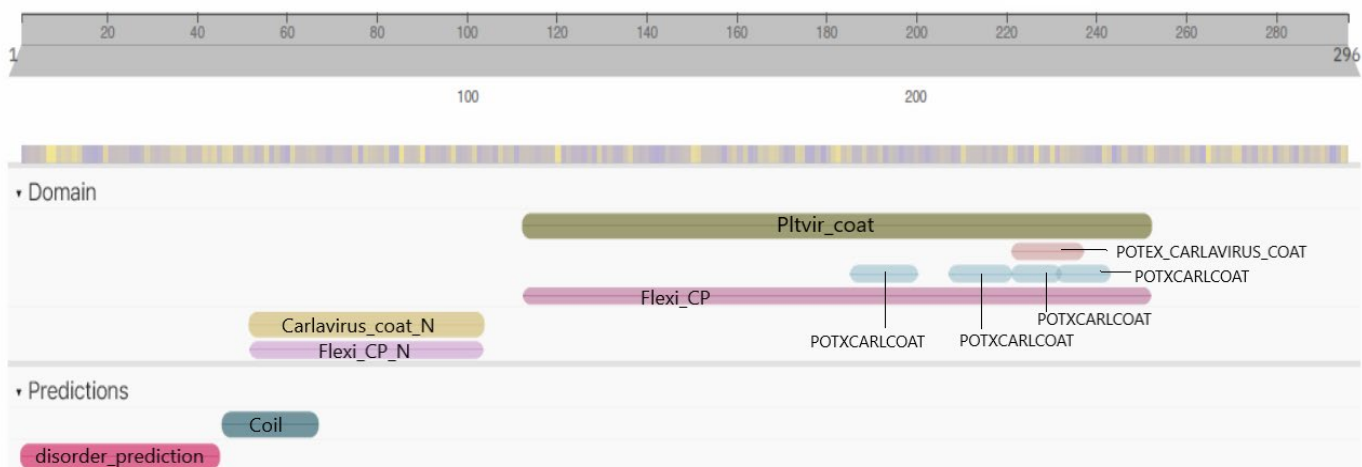
InterPro Name	InterPro ID	InterPro Type	Database	Database ID	Start	End	Length
Cytoplasmic domain			PHOBIUS	CYTOPLASMIC_DOMAIN	1	11	11
Plant_vir_prot	IPR001896	Family			4	99	95
Plant_vir_prot			Pfam	PF01307	4	99	95
Transmembrane region			PHOBIUS	TRANSMEMBRANE	12	30	18
Non cytoplasmic domain			PHOBIUS	NON_CYTOPLASMIC_DOMAIN	31	71	40
TMHMM			TMHMM	TMhelix	72	94	22
Transmembrane region			PHOBIUS	TRANSMEMBRANE	72	92	20
Cytoplasmic domain			PHOBIUS	CYTOPLASMIC_DOMAIN	93	108	15

**(D) ORF 4, Triple Gene Block 3.**



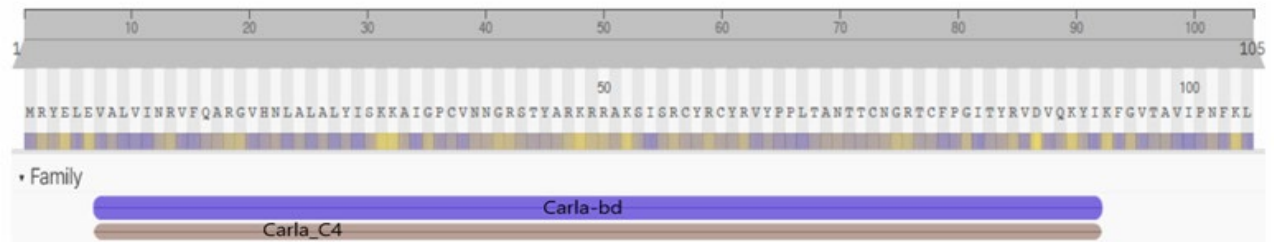
InterPro Name	InterPro ID	InterPro Type	Database	Database ID	Start	End	Length
TGBp3	IPR003411	Family			6	60	54
TGBp3	PF02495		Pfam		6	60	54
Signal peptide H-region			PHOBIUS	SIGNAL_PEPTIDE_H_REGION	6	21	15
Signal Peptide			PHOBIUS	SIGNAL_PEPTIDE	1	28	28
Signal peptide N-region			PHOBIUS	SIGNAL_PEPTIDE_N_REGION	1	5	5
Signal peptide C-region			PHOBIUS	SIGNAL_PEPTIDE_C_REGION	22	28	6
TMHMM			TMhelix	TMHMM	2	24	22
Non cytoplasmic domain			PHOBIUS	NON_CYTOPLASMIC_DOMAIN	29	61	32

**(E) ORF 5, Coat Protein.**



InterPro Name	InterPro ID	InterPro Type	Database	Database ID	Start	End	Length
Disorder_prediction			MOBIDB_LITE	mobidb-lite	1	42	42
Coil	Unintegrated		COILS entry	Coil	46	66	20
Carlavirus_coat_N	IPR013569	Domain			52	103	51
Flexi_CP_N			Pfam	PF08358	52	103	51
Pltvir_coat	IPR000052	Domain			112	252	140
Flexi_CP			Pfam	PF00286	112	252	240
POTXCARLCOAT			PRINTS	PR00232	186	200	14
POTXCARLCOAT			PRINTS	PR00232	208	221	13
POTXCARLCOAT			PRINTS	PR00232	222	232	10
POTXCARLCOAT			PRINTS	PR00232	232	243	11

**(F) ORF 6, Nucleic Acid Binding Protein.**



InterPro Name	InterPro ID	InterPro Type	Database	Database ID	Start	End	Length
Carla-bd	IPR002568	Family			7	92	85
Carla_C4			Pfam	PF01623	7	92	85

## Supplementary Figure S2.

Alignment (obtained with Clustal Omega; <https://www.ebi.ac.uk/Tools/msa/clustalo/>) of the nucleic acid binding proteins (ORF6 protein) of JaVC available in GenBank. Amino acid residues of the Bari isolate (from *J. officinale*) that diverge in the position from the almost invariant residues aligned from all the other isolates (from *J. sambac*) are in red. Accession numbers: Yunnan, MH389795; A31 Taiwan, KX364696; Fujian, MH231174; Guangdong, MH389788; Guangxi, MH389789; Hunan, MH389790; Jilin, MH389791; Sichuan, MH389793; Jangsu, MH389792; Shandong, MH389794.

Bari	MRYELEVALVINRVFQARGVHNLALALYISKKA <b>I</b> GPCVNNGRSTYARKRRRAKSISRCYRC	60
Guangxi	MRYELEVALIINRVFQARGVHNLALALYISKKAAGPCLNNGRSTYARRRRARSISRCYRC	60
Shandong	MRYELEVALVINRVFQARGVHNLALALYISKKA <b>V</b> GPCLNNGRSTYARRRRARSISRCYRC	60
Hunan	MRYELEVALVINRVFQARGVHNLALALYISKKA <b>V</b> GPCLNNGRSTYARRRRARSISRCYRC	60
Jangsu	MRYELEVALVINRVFQARGVHNLALALYISKKA <b>V</b> GPCLNNGRSTYARRRRARSISRCYRC	60
Jilin	MRYELEVALVINRA <b>F</b> QARGVHNLALALYISKKA <b>V</b> GPCVNKGRSTYARRRRATSISRCYRC	60
Fujian	MRYELEVALVINRA <b>F</b> QARGVHNLALALYISKKA <b>V</b> GPVNNGRSTYARKRRARSISRCYRC	60
Sichuan	MRHELEVALAINRVFQARGVHNLALALYISKKA <b>V</b> GPCVNNGRSTYARRRRASSISRCYRC	60
Yunnan	MRYELEVALVINRVFQARGVHDLALALYISKKA <b>V</b> GPCVNNGRSTYARKRRRAKSISRCYRC	60
A31	MRYELEVALVINRVFQARGVHNLALALYISKKA <b>V</b> GPCVNNGRSTYARRRRRAKSISRCYRC	60
Guangdong	MRYELEVALVINRVFQARGVHNLALALYISKKA <b>V</b> GPCVNNGRSTYARRRRRAKSISRCYRC	60
	** :***** ***.*****:***** ** :*:*****:*** *****	
Bari	YRVYPPL <b>T</b> ANT <b>T</b> CNGRTCFFGITYRVDV <b>Q</b> KYIKFGVTA <b>V</b> IPNFKL	105
Guangxi	YRVYPPLSGNTRCDGRTCFFGINYRVDVEEYIKFGVAAAI <b>P</b> NFKL	105
Shandong	YRVYPPLSGNTRCNGRTCFFGINYRVDVEEYIKFGVAAAI <b>P</b> NFEL	105
Hunan	YRVYPPLSGNTRCDGRTCFFGINYRVDVEEYIKFGVAAAI <b>P</b> NFEL	105
Jangsu	YRVYPPLSGNTRCDGRTCFFGINYRVDVEEYIKFGVAAAI <b>P</b> NFKL	105
Jilin	YRVYPPLCGNTRCNGRTCFFGINYRVDVEEYIKFGVAAAI <b>P</b> NFKL	105
Fujian	YRVYPPLCGNTRCNGRTCFFGINYRVDVEKYIKFGVAAAI <b>P</b> NFKL	105
Sichuan	YRVYPPLCGNTRCNGRTCFFGINYRVDVEKYIKFGVAAAI <b>P</b> NFKL	105
Yunnan	YRVYPPLCGNTRCNGRTCFFGINYRVDVEKYIKFGVAAAI <b>P</b> NFKL	105
A31	YRVYPPLCGNTRCNGRTCFFGINYRVDVEKYIKFGVAAAI <b>P</b> NFKL	105
Guangdong	YRVYPPLCGNTRCNGRTCFFGINYRVDVEKYIKFGVAAAI <b>P</b> NFKL	105
	***** .* ** :*****.*****:*****:*.*****:	

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Alignment (obtained with Clustal Omega; <https://www.ebi.ac.uk/Tools/msa/clustalo/>) of coat proteins of selected Carlavirus members used to calculate the pairwise percentage similarity among aphid-transmitted and whitefly-transmitted species. Melon: melon yellowing-associated virus, MYaV, NC\_038324; cowpea: cowpea mild mottle virus, CPPMV; carya : Carya illinoensis carlavirus 1, MW328759; narcissus: Narcissus common latent virus, NCLV, NC\_008266; A-31: jasmine virus C, Taiwan isolate A-31, KX364696; carnation: carnation latent virus, CLV, MN450069; shallot: shallot latent virus, SLV, NC\_003557.

melon	MFSGESNDHFSSRLKKYNEVRKALVSQGKTPEEVKEELDEQVERDRKVFEGRQLAGDTGG	60
cowpea	-----MESVFDLNKLVDSEMAEK----TK-----	20
carya	-----MPQKTESELAAE----AAFAKTAEEA---K-	23
narcissus	-----MSGAFGVDTVSESSLAAQ---KAL--DRAEA-----	26
JaVC_A-31	-----MS-----STSDSSKGK---RPVVIPETQT----	22
JaVC_Bari	-----MS-----STSDDDTKGK---KPVVIPETQT----	22
carnation	-----MPEKRLEEDV-----	10
shallot	-----MT--NEEEEL-----	8
..		
melon	SVVMATEKTEQKTSNPDAKDKGQSSNSKGKVE--EIK---AAQGDISDFQIARLEALKE	114
cowpea	-----TS-----VPKAPDGTALPDIDAE LQKRLDDLRA	48
carya	-----RRAAEMEAKRREDKG--KDV-----ETGQRSGSQTPPEEDKLEVMLEKLID	67
narcissus	-----NQKNADK---L-----KKFAQPESDGSDDASLEQRLNKLRE	60
JaVC_A-31	-----NQPPPER--PAS-----EHADSHNFEADTQEEQLEVRMQKLRQ	58
JaVC_Bari	-----SQPPGR--PAN-----AGADTHNYEADTQEEQLEARMQKLRQ	58
carnation	-----GSQGQTSPPNPPQQHQGEQSVVSGMVSNEVDLRNLQNRVEEA EKFMQRFQXLKE	65
shallot	-----NRVRNLPTRNPGTELEGRSKAV-----NDVGVMEREGFEAVLRSEDRFNKLKE	58
: : *		
melon	WYRANMRPSDVANPLMQSGLKQMEVTDKLEKEDSTNLYSRPALNTLLKWNRAVPVSQNIATA	174
cowpea	FLRKTSASEITNPGFELGRPELKQSTFNSDKHTHIYGKWSIDQLSRIVPKKISNNMATA	108
carya	YRRREYRTSRVTNAGYETGRPLLRTPSNMRGDPNSMYNMLSIDDLYAIKPKAVSNNMATA	127
narcissus	FLRKQRGAIRVTNIGFETGRPTLNLADMRPDPSNPYNRPSIEALATIKPRAVSNNMATT	120
JaVC_A-31	FLKQQQRATQVTNPSFELGRPKLKMLEGVRS DPTNLYNKPTIDQLCAIKPRAISSNMATS	118
JaVC_Bari	FLKQQQRATQVTNPSFELGRPKLKM L DGVRS DPTNLYNKPTIDQLCSIKPRAISSNMATS	118
carnation	FNSQNLTAGELKNGGFESGRPPAKISEHLRGSTANVFTRPSLDALQMMDFKPESNMIVTA	125
shallot	KCIAELSCINVTNCGWESGRPKAQLADSLKGDASNI FTRPSMDALLVRNYAPESNNLATA	118
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melon	EDIAQITSKLESMGVPRERVRDAIFDIVLYAAHNSSSPFQTFEGDIDFRDPKFKSTFSRV	234
cowpea	EEMAKVQITLEGLGVPTHEHVAEVL LQVAIYCKDVSSSFMDS SGTFDWKGGSI----LSD	164
carya	EDMAKIKVSLEALGVPTTEEVSTLVAQAAIYCKDTSSEYMDPRGTFNTSAGAI----SMD	183
narcissus	EDMMRIYTDLEGLGVPTQVQTVVIQAVLFCKDASSVFLDPRGSFEWIGGAI----SAD	176
JaVC_A-31	QDMAAITVAIEALGVPSERIQAVLIQAVAYCKDASSSTYLD PQGVFEWGGGAV---MAD	174
JaVC_Bari	QDMAAITVAIEALGVPSERIQAVLIQAVTYCKDASSSTYLD PQGVFEWGGGAV---MAD	174
carnation	EELAAITAKLEGLGVPTERSAPICWAVARYCANTSTSPYTD PKGVFEFPGGAI----TRD	181
shallot	EELAKISAKVQALGAPEECLA EVFWDICMYCTTAGSSPNVNP KGTISIGGRVV---TRD	174
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melon	SVSSII-KDHSTLRKVCRLFAPIVWSYMIINNEPPANWQAKGF PENAKFASFDTFDFVTN	293
cowpea	SVLAALRKDDNTLRRVCRLYAPITWNFMLTHKAPPSDWVAMGFKWDDRYAAAFDCFEYVEN	224
carya	AVFAVLK TQGGTLRRVCRLYAAVTWNYMLIHDAPPSDW PAMGFKRNERFAAFDCLDYVEN	243
narcissus	AVIAVLKKDASTLRRVCRLYAPVTWNYMLTHNAPPSDWAAMGFQHEDRFAAFDCFDYVEN	236
JaVC_A-31	SILAILKRDAGTLRRVCRLYAPVTWNHMLAHNSPPSDWAAMGFQYTERFAAFDCFDYVEN	234
JaVC_Bari	SILAILKRDAGTLRRVCRLYAPITWNHMLAHNSPPSDWAAMGFQYTERFAAFDCFDYVEN	234
carnation	AVFAVIR-EITTLRAF CRAFTITWNQMLFAKSPPENWQAKGYTHETRYAAFDVDFVQN	240
shallot	MVAVIK-EYSTLRQVCRCYAPVVWNYMLLNEQPPANWD AKGFTENTKYAAFDTF DAVTN	233
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melon	HSAMKPLEGLVRLPTDIEKLAHDVHKTNLSLNKARRNEKLLSTSSKISGGQQACEVKGEFK	353
cowpea	PAAIQPAEGLIRKPTSSEKIAHNTYKRLALDRSNRNEIYSNLNTEVTGGTLGPEISRNFN	284
carya	TAAIPPEGLIRKPTSNEYIAHNTYKRIALDRSNRNEPFGNLQTEITGGRGFEEIERNHL	303
narcissus	SAAVQPLEGLIRRP TP REKIAHDTHKDIALRAANRNQVFGNFSSGVTGGRNGPELTRNYG	296
JaVC_A-31	SAAVQPFEG LIGRPTPAEKIAHNTHKRLALDRANRNEKYASFEAEVTGGHVGPEIERGIW	294
JaVC_Bari	AAAVQPFEG LIRRP TP AEKIAHNTHKRLALDRANRNEKFANLEAEVTGGHVGPEIERSIW	294
carnation	PAAIQPLEGLLRIP TAEEKIAHATNKRRLALDRNRNARFSSTDSLVTGGMYGKDIKTNFN	300
shallot	KAAIQPLEGLIRAP TDAERIAFATHKKLALAKNSQNSRYANTS AEVTGGFFGCVPKNNFR	293
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melon	GNGSCS	359
cowpea	HAKK--	288
carya	RPNK--	307
narcissus	NSGLR-	301
JaVC_A-31	KR----	296
JaVC_Bari	KR----	296
carnation	GSNNSD	306
shallot	ENRC--	297

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**Percent Identity Matrix - created by Clustal 2.1**

	MYaV	CPPMV	carya	NCLV	A-31	JaVC-Ba	CLV	SLV
1: melon	100.00	32.16	30.13	34.12	30.93	31.96	35.12	38.14
2: cowpea	32.16	100.00	52.48	50.52	51.79	52.50	42.60	36.73
3: carya	30.13	52.48	100.00	54.76	48.30	47.96	38.57	36.43
4: narcissus	34.12	50.52	54.76	100.00	56.16	56.85	39.08	39.15
5: JaVC A-31	30.93	51.79	48.30	56.16	100.00	90.88	39.50	36.92
6: JaVC Bari	31.96	52.50	47.96	56.85	90.88	100.00	38.79	36.20
7: carnation	35.12	42.60	38.57	39.08	39.50	38.79	100.00	44.44
8: shallot	38.14	36.73	36.43	39.15	36.92	36.20	44.44	100.00

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