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Virology Division News

Phragmivirus, a new genus within the family *Potyviridae*

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Abstract

The plant-infecting virus family *Potyviridae* was previously formed by 12 genera, consisting of 249 virus species, with the majority of these classified in the largest genus, *Potyvirus*. Potyvirids are viruses with a ssRNA genome packaged in long filamentous particles. While members of genus *Bymovirus* have bipartite genomes, members of the remaining genera have monopartite genomes. All viruses in the family have a genome-linked protein (VPg) present at the 5' terminus of the genome, and all but celery latent virus (genus *Celavirus*) contain a polyadenylated tail at the 3' end. The members of the 12 genera are differentiated by genomic identity, various functional motifs, and biological factors such as the type of the transmission vector and host range. Demarcation criteria for a new genus include <46% nucleotide identity with potyvirids of other genera. Here we report the new genus *Phragmivirus* within the family *Potyviridae*, which has been accepted by the International Committee on Taxonomy of Viruses, becoming the 13th genus in the family. Genus *Phragmivirus* is represented by two virus species (*Phragmivirus phragmii* and *Phragmivirus spartinae*). Complete genome sequences are available for both members, namely common reed chlorotic stripe virus (CRCSV), and Spartina mottle virus (SpMV), respectively. The new genus name is derived from the botanical name of the host of CRCSV, *Phragmites australis*. The genome sequences of CRCSV and SpMV isolates resemble those of genus *Potyvirus*, but lack typical conserved aphid-transmission motifs.

Keywords: Virus taxonomy; ssRNA plant virus; *Patatavirales*; potyvirids; CRCSV; SpMV

Introduction

The family *Potyviridae* is the largest family of plant-infecting single-stranded RNA (ssRNA) viruses recognised by the International Committee on Virus Taxonomy (ICTV) [1]. The family name *Potyviridae* is derived from the genus *Potyvirus*, which in turn originates from one of the most studied potyvirus, the potato virus Y. The family consisted of 12 genera containing 249 species [2]. Three genera, *Beviovirus*, *Brambyvirus* and *Celavirus*, are monotypic, while the largest genus, *Potyvirus*, is comprised of 206 species (Table 1). In 2025, the family has been expanded to 259 species by the creation of eight species in the genus *Potyvirus* and two species in a newly established

genus. The new genus is named *Phragmivirus* and represents the 13th genus in the family *Potyviridae* [3].

Most potvirids are naturally confined to one or a small number of known host species, while members of some species such as the potyvirus turnip mosaic virus have very broad host ranges and cause significant damage to both agricultural and wild plants [4].

Virions in 12 of the 13 ratified genera within the family *Potyviridae* comprise flexuous and filamentous particles 650-959 nm in length and 11-20 nm wide, encapsidating monopartite ssRNA genomes, while members of genus *Bymovirus* possess bipartite genomes, packaged in two particles 500-600 nm and 250-300 nm in length. The positive sense ssRNA genomes typically consist of about 10,000 nucleotides (10 kb), with a range from 8.2 kb in macluraviruses and bevmovirus, both lacking the 5' P1 cistron, to the largest of 11.5 kb in celery latent virus, the only described member of genus *Celavirus*.

Table 1 The family *Potyviridae* showing current genera and numbers of species assigned to each genus.

Family	Genus ^a	Number of species
<i>Potyviridae</i>	<i>Potyvirus</i>	214
<i>Potyviridae</i>	<i>Macluravirus</i>	11
<i>Potyviridae</i>	<i>Ipomovirus</i>	7
<i>Potyviridae</i>	<i>Bymovirus</i>	6
<i>Potyviridae</i>	<i>Tritimovirus</i>	6
<i>Potyviridae</i>	<i>Poacevirus</i>	3
<i>Potyviridae</i>	<i>Rymovirus</i>	3
<i>Potyviridae</i>	<i>Roymovirus</i>	2
<i>Potyviridae</i>	<i>Arepavirus</i>	2
<i>Potyviridae</i>	<i>Phragmivirus</i>	2
<i>Potyviridae</i>	<i>Bevmovirus</i>	1
<i>Potyviridae</i>	<i>Brambyvirus</i>	1
<i>Potyviridae</i>	<i>Celavirus</i>	1

^aList of members of *Potyviridae* updated after ICTV ratification in 2025 [3]. Related, unclassified viruses are not included.

Table 2. Distinctive characteristics of viruses representative of species in the 13 genera of family *Potyviridae*, including the new genus *Phragmivirus*

Genus	<i>Arepavirus</i>	<i>Bevemovirus</i>	<i>Brambyvirus</i>	<i>Bymovirus</i>	<i>Celavirus</i>	<i>Ipomovirus</i>	<i>Macluravirus</i>	<i>Poacevirus</i>	<i>Phragmivirus</i>	<i>Potyvirus</i>	<i>Roymovirus</i>	<i>Rymovirus</i>	<i>Tritimovirus</i>
Example	Areca palm necrotic spindle-spot virus	Bellflower veinal mottle virus	Blackberry virus Y	Barley yellow mosaic virus	Celery latent virus	Sweet potato mild mottle virus	Chinese yam necrotic mosaic virus	Triticum mosaic virus	Common reed chlorotic stripe virus	Potato virus Y	Rose yellow mosaic virus	Ryegrass mosaic virus	Wheat streak mosaic virus
Genome size (approximate mean)	9400	8300	10800	7600 (RNA1), 3600 (RNA2)	11500	10800	8200	10200	9400	9700	9700	9500	9500
Distinctive genomic features	Lacks P1. Two HC-Pro-like genes (HC-Pro1 and HC-Pro2). 11 genes.	Lacks P1. HC-Pro lacks aphid transmission motifs. 10 genes.	Resembles genomes of members of <i>Potyvirus</i> but has a very large P1 gene containing an AlkB domain at the 5' terminal region. 11 genes.	Bipartite genome. Lacks HC-Pro. Contains a unique gene, P2, located 3' of P1 on segment 2. Unusually large 6K2 genes. 9 genes segment 1, 2 genes segment 2.	Very unusual. Genome non-polyadenylated. Very short 5'UTR and an unusually long 3'UTR. Lacks several typical potyvirus protease cleavage sites. Lacks 6K1 and 6K2 genes. Contains a P1-like gene, a gene of unknown function, no HC-Pro, a P3-like gene. 9 genes	Some members lack HC-Pro, and P1 assumes the gene silencing suppression function. CVYV, SqVYV and CocMoV contain a second P1-like gene, P1b, located 3' of P1. CBSV and UCBSV contain a unique Maf/HAM1-like gene located between the NIb and CP. Usually 11 genes.	Lacks the P1 gene. 10 genes.	Resembles genomes of members of <i>Potyvirus</i> but lacks aphid transmission motifs. 11 genes.	Resembles genomes of members of <i>Potyvirus</i> but lacks aphid transmission motifs. 11 genes. Smaller P1 proteins with 223-239 aa.	Polyadenylated genome encoding at least two ORFs, the large one post-translationally processed into 10 proteins, the small one processed into 3 proteins (P1, HCPro and P3N-PIPO). A subgroup of sweetpotato potyviruses contain also a third ORF (with PISPO, embedded in P1, generating P1N-PISPO) Order of the 11 genes conserved. Motifs for aphid transmission present in most members.	Resembles genomes of members of <i>Potyvirus</i> but lacks aphid transmission motifs. 11 genes	Resembles genomes of members of <i>Potyvirus</i> but lacks aphid transmission motifs. 11 genes. Smaller P1 proteins with 242-255 aa.	Resembles genomes of members of <i>Potyvirus</i> but lacks aphid transmission motifs. The P1 protein rather than the HC-Pro serves as a suppressor of gene silencing. 11 genes.
Transmission	unknown	unknown	unknown	<i>Polymyxa graminis</i> , a fungoid protist	Probably not by aphids	Whitefly	Aphids	Mites	Unknown	Aphids	Possibly by eriophyid mites	Eriophyid mites	Eriophyid mites
RNA polymerase slippage	Presence of PIPO in P3 region, with numerous A6 motifs (4-6) per genome	Presence of PIPO in P3 region	Presence of PIPO in P3 region	Presence of PIPO in the first cistron of RNA1	Presence of PIPO in P3 region	Presence of PIPO in P3 region. More than one A6 motif in most viruses (2-3 per genome)	Presence of PIPO in P3 region	Presence of PIPO in P3 region	Presence of PIPO in P3 region	Presence of PIPO in P3 region, and PISPO in P1 for several sweet potato infecting viruses. Mostly A6 motifs, except U6 in WMVBV	Presence of PIPO in P3 region	Presence of PIPO in P3 region	Presence of PIPO in P3 region

Discrimination of species and genera within the family *Potyviridae* is based mainly on whole-genome nucleotide (nt) and amino acid (aa) sequence identity thresholds, but also on genomic organization, including the presence or absence of certain genes and protein motifs, phylogenetic relationships, and biological factors which may include host range and vector specificity (Table 2). For example, members of genus *Potyvirus* possess one genome segment of approximately 10 kb, and are transmitted by aphids, whereas genomes of members of genus *Bymovirus* are divided into two segments of approximately 7.5 kb and 3 kb, lack the *HC-Pro* gene present in all members of *Potyvirus*, contain a *P2* gene unknown in members of *Potyvirus*, and are transmitted by protists (e.g., [5]) (Table 2).

The thresholds for species demarcation between sequences of complete viral genomes (nt) and the large open reading frame (ORF) (aa) are approximately <75–76% and <81–82% identities, respectively. Values marginally greater or lesser than these are usually regarded as different isolates of the same species, but specific genomic features and biological factors such as host and vector specificity have been used to argue inclusion or exclusion of isolates to distinct species [6, 7].

Genus discrimination within *Potyviridae* is usually determined upon comparison of complete genome sequences and the large ORF sequences. Viruses of different genera typically share <46% nt identity and <33% aa identity [7]. Exceptions occur, such as between members of the genus *Rymovirus* and members of the genus *Potyvirus*, which share identities ranging from 45–51% nt and 38–41% aa [7].

Genus *Phragmivirus*

Genus *Phragmivirus* is represented by two recently ratified virus species, *Phragmivirus phragmii* and *Phragmivirus spartinae*. The genus name *Phragmivirus* is derived from the host species *Phragmites australis* from which common reed chlorotic stripe virus was isolated. Gotz et al. [8], Hosseini et al. [9], Rose et al. [10], and Thomas et al. [11] proposed the novel genus name ‘Sparmovirus’ following *Spartina mottle virus*. However, common reed chlorotic stripe virus has priority, with the whole genome sequence completed and published by Yuan et al. in 2017 [12]. Therefore, the genus name acknowledges the first complete genome described.

Viruses belonging to the two *Phragmivirus* species, for which complete genomes are available, are common reed chlorotic stripe virus (CRCSV) isolate Tianshui (accession KY612317) and three isolates of *Spartina mottle virus* (SpMV), namely isolates DSMZ PV-0970 (MN788417), Q1371 (MW314142) and Q1372 (MW314143).

Hosts

The original host of CRCSV isolate Tianshui was common reed *Phragmites australis*, a wild plant from China [12]. CRCSV has not been identified in other hosts. Two host species were identified for *Spartina mottle virus* isolates. The original hosts were an unknown species of *Spartina* (isolate DSMZ PV-0970) from Germany, and plants of Bermuda grass *Cynodon dactylon* × *C. transvaalensis* (isolates Q1371 and Q1372) from Australia, but originating in the USA [11].

Genomes and polyproteins

The complete genome sequence of the CRCSV isolate Tianshui is named reed chlorotic stripe virus in the accession KY612317, but the virus was named common reed chlorotic stripe virus in the descriptive paper [12]. The genome of isolate Tianshui is 9426 nt in length, containing a poly (A) tail of 20 nucleotides at the 3' terminus, indicating a genome of 9406 nt without the poly-A tail. SpMV-DSMZ PV-0970 (MN788417) is 9376 nt, SpMV-Q1371 (MW314142) and SpMV-Q1372 (MW314143) are both 9346 nt, all not including the poly (A) tail. The three SpMV complete genome sequences

share 79-87% sequence identities and are included in the same species. Two partial sequences of SpMV (AF491351, AF491352) and three partial sequences of Bermuda grass mosaic virus (GU552269, HM008711, HM008712) share 74.0-99.7% nucleotide sequence identities with complete sequences, and as such, Bermuda grass mosaic virus is considered synonymous with *Spartina* mosaic virus.

The complete polyprotein sequence size of the CRCSV isolate is 3014 aa, SpMV-DSMZ PV-0970 is 3024 aa, and isolates SpMV-Q1371 and SpMV-Q1372 are both 3029 aa. Complete annotations of the expected gene products are provided ([Supplementary Table 1](#)).

The complete genome sequences of the CRCSV isolate and SpMV isolates share 53% nt identity and 46% aa identities. The complete genomes of these two viruses share 33-47% nucleotide identities with members of other genera of the family *Potyviridae*: *Rymovirus* (46-47%), *Potyvirus* (45-46%), *Arepavirus* (43%), *Tritimovirus* (42%), *Brambyvirus* and *Bevemovirus* (39%), *Roymovirus* and *Ipomovirus* (38%), *Macluravirus* (36%), *Celavirus* (35%) and *Bymovirus* (33%).

CRCSV and SpMV share 14-33% aa identities with members of other genera of the family *Potyviridae*: *Rymovirus* (33%), *Potyvirus* (31-32%), *Arepavirus* (18%), *Tritimovirus* (22%), *Brambyvirus* (23%), *Bevemovirus* (20%), *Roymovirus* (21%), *Ipomovirus* (19%), *Macluravirus* (18%), *Celavirus* (14%) and *Bymovirus* (17%) (Figure 1). Thus, CRCSV and SpMV are phylogenetically closer to one another than to viruses classified in other genera within family *Potyviridae*. Sequence identities closely follow the classification guidelines of [7], supporting their assignment to one genus.

Proteins and motifs

The P1 protein of the two newly identified phragmiviruses is significantly shorter (CRCSV: 240 aa; SpMV: 217–219 aa) than that of the most homologous potyviruses, periwinkle mild yellow mosaic virus (PwMYMV; 430 aa) and turnip mosaic virus (TuMV; 363 aa), but similar in length to the P1 protein of rymoviruses (242–255 aa). The size of other phragmiviral proteins fall within the range of those of members of genera *Potyvirus* and *Rymovirus* ([Table 3](#)). Additionally, phragmiviruses exhibit relatively lower calculated pI values, with SpMV at 7.71 and CRCSV at 6.12, compared to potyviruses and rymoviruses (typically near 9–10), but closer to tritimoviruses [13].

Despite their close relationship, phragmiviruses are phylogenetically distinct from members of these two genera ([Fig. 1](#)). Similar to potyviruses and rymoviruses, phragmiviral proteins are likely post-translationally cleaved from the long ORF into 10 mature proteins at conserved cleavage sites ([Table 3](#)).

The potyvirid-conserved HC-Pro motifs KITC and PTK linked to aphid transmission are not present in both viruses. The CP of SpMV does not contain the conserved aphid transmission motif DAG (DSD in SpMV), while the CRCSV CP contains the DAE variation of DAG, which is also found in the aphid-transmitted potyvirus chilli veinal mottle virus [14].

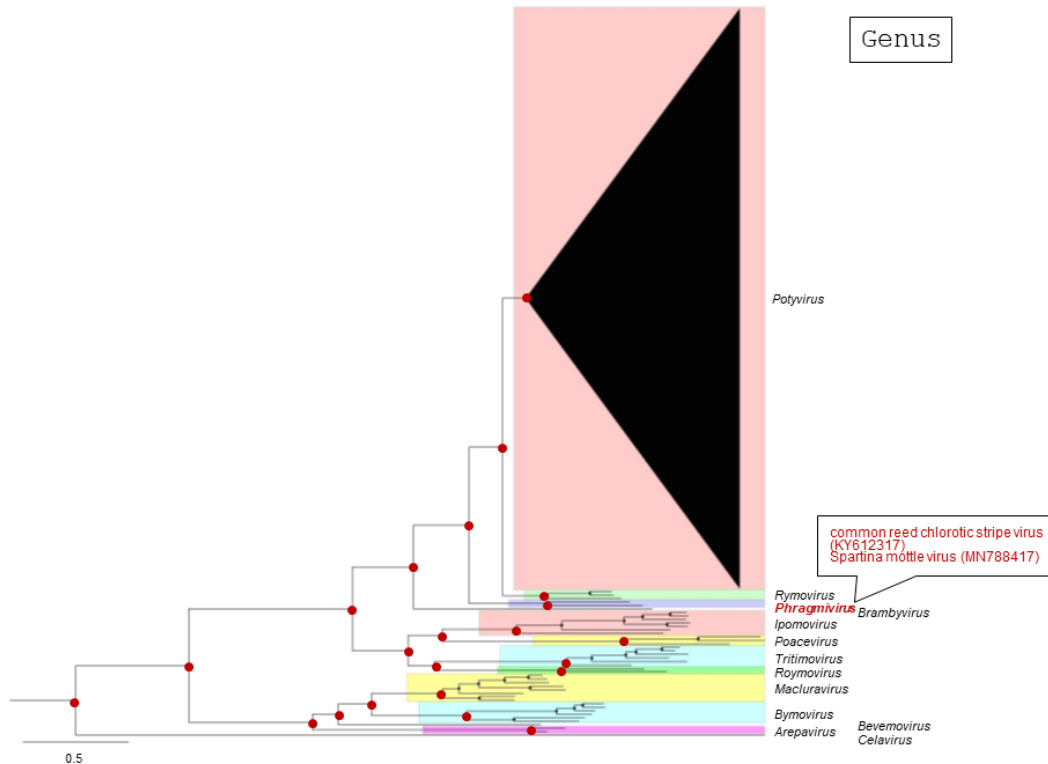


Figure 1. Phylogenetic tree was inferred using the complete polyprotein amino acid sequences of all potyvirids (Supplementary Table 2). The maximum likelihood (ML) tree was produced in PhyML v.3.1 [21] using the LG model [22] with gamma-distributed among-site rate variation; and a proportion of invariable sites was selected as the best substitution model by ModelTest-NG [23]. The phragmiviruses common reed chlorotic stripe virus (KY612317) and Spartina mottle virus (MN788417) are highlighted in red. Red dots indicate bootstrap values >90%, based on 100 pseudoreplicates. The scale bar represents 0.5 substitutions per site. The ML tree, midpoint rooted, was visualized using FigTree v1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>).

Phragmivirus - common reed chlorotic stripe virus, CRCSV (9,426 nt)

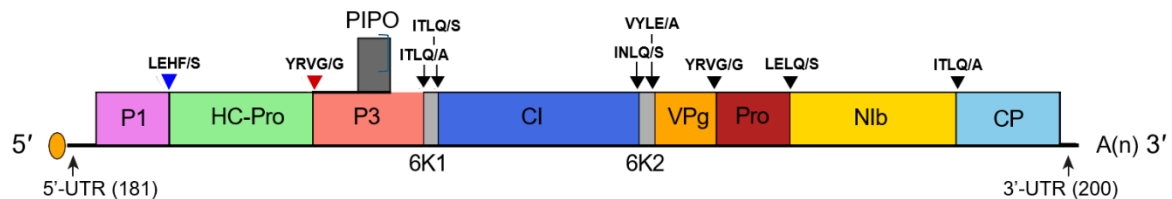


Figure 2. Genome organisation of the phragmivirus common reed chlorotic stripe virus. The ssRNA genome is represented by a line and the polyprotein ORF by an open box with the mature proteolytic products named. P1 (protein 1 protease), a protein with serine proteolytic activity responsible for cleavage at typically Tyr/Phe-Ser; HC-Pro (helper component protease), a protein with aphid transmission helper-component activity and cysteine proteolytic activity responsible for cleavage at typically Gly-Gly; P3 (protein 3); PIPO (pretty interesting *Potyviridae* ORF; expressed as the trans-frame P3N-PIPO protein); 6K1 (6 kDa peptide 1); CI (cylindrical inclusion); 6K2 (6 kDa peptide 2); VPg (virus protein genome-linked), the genome-linked virus protein covalently attached to the 5'-terminal nucleotide; represented here by an oval; Nla-Pro (the second of two functional regions of the Nla, nuclear inclusion a protease, susceptible to being proteolytically separated from the VPg region), a cysteine-like proteolytic activity responsible for cleavage at Gln/Glu-(Ser/Gly/Ala); Nlb (nuclear inclusion b), RNA-directed RNA polymerase; CP (coat protein). Cleavage sites of P1 (blue arrow), HC-Pro (red arrow), and Nla-Pro (black arrow) are indicated.

Natural transmission of both phragmiviruses is unknown. The absence in both viruses of the three conserved aphid-transmission motifs usually found in the HC-Pro (KITC- and PTK-like motifs) and in the CP (DAG motif) suggests that these viruses might not be transmitted by aphids, although experimental data will be required to confirm this. Bermuda grass mosaic virus isolates, considered as SpMV isolates, were reported to be poorly transmitted by aphids [9], hence the transmission properties need further investigation.

An additional ORF in the genome corresponds to PIPO [15, 16] (Fig 2). It can be found embedded within the P3 region, in the usual context for other potyvirids, and is accessible through the expected RNA transcriptional slippage mechanism occurring in a conserved unique G2A6 in CRCSV and SpMV accession MN788417 (isolate PV-0970), and G1A6 in SpMV MW314142 and MW314143. After slippage at these predicted sites, two putative extra gene products can be generated in each virus, namely P3N-PIPO or P3N-ALT. The first one results from the addition of an extra A in a fraction of the synthesized RNA progeny molecules (frame -1/+2), and the second in the case of a deletion of one nucleotide (frame +1), leading to a putatively truncated form because a stop will be reached at the second out-of-frame codon. In CRCSV, PIPO adds 101 extra aa to P3N to generate P3N-PIPO (253

aa, 28.9 kDa). For SpMV, PIPO adds 122 aa (121 in the case of two isolates different from PV-0970), generating P3N-PIPO (273 aa, 31.6 kDa).

Recombination in phragmiviruses

The representative sequence of all complete genomes of potyvirids were retrieved and used for recombination analysis using RDP4 method [17]. No potential recombination event was detected in the two phragmivirus sequences.

Concluding remarks

The genome organisation of the two known phragmiviruses closely resembles those of potyviruses in that all eleven genes are present in the same order, but they differ from them mainly in phylogeny. There are only two ratified phragmiviruses to date, and both appear to have limited host ranges. Their lack of typical aphid transmission motifs suggests they may have evolved modes of transmission that do not involve aphids. In that ways phragmiviruses resemble members of genera *Brambyvirus* (1 known species), *Poacevirus* (3), *Roymovirus* (2), *Rymovirus* (3) and *Tritimovirus* (4). In each of these genera the small number of species (to date) appear to have narrow host ranges and to have lost their aphid transmission motifs but retained the typical potyvirus genome architecture. We speculate that loss of aphid transmission motifs has left these viruses ‘marooned’ in a small number of hosts. The fact that the species of genus *Potyvirus* are by far the most numerous and apparently successful group in the family appears to be an indicator of the efficiency by which aphids transmit these viruses. The loss of aphid transmissibility, as sometimes occurs spontaneously in potyviruses (e.g. [18, 19, 20], and several others), is a likely trigger for speciation of potyvirids. The means by which these non-aphid-transmissible potyvirus-like groups are transmitted is, therefore, of great interest in understanding the basis of evolution in the *Potyviridae*.

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Data availability

All data are publicly available in the sequence databases.

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Author Contributions:

All authors contributed to the study conception, design, material preparation, data collection and analysis. Stephen Wylie wrote the first draft of the manuscript and all authors commented on subsequent versions of it. All authors read and approved the final manuscript.

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The authors declare there are no conflicts of interest.

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The research did not involve human participants or animals.

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Table 3. Predicted heptapeptide cleavage sites of the polyproteins of the phragmiviruses and selected potyviruses and rymoviruses

Virus	P1/HC-Pro ^a	HC-Pro/P3	P3/6K1	6K1/CI	CI/6K2	6K2/VPg	VPg/NlA-Pro	NlA/NlB	NlB/CP
Phragmiviruses									
CRCSV	²⁴⁰ LQLEHF/S	⁶⁹⁸ KNYRVG/G	¹⁰⁴⁴ GRITLQ/A	¹⁰⁹⁷ ETITLQ/S	¹⁷³⁶ GVINLQ/S	¹⁷⁸⁹ DRVYLE/A	²⁰⁰⁶ NGIQLE/C	²²⁴⁶ KALELQ/S	²⁷⁵⁹ DVITLQ/A
SpMV_1	²¹⁷ MRLIHF/S	⁶⁵⁷ KNYVVG/G	¹⁰⁰³ KDITLQ/A	¹⁰⁵⁶ ETIMLQ/S	¹⁶⁹⁶ GVITLQ/S	¹⁷⁴⁸ DGFLE/S	¹⁹⁵⁸ DSLNLG/G	²¹⁹⁷ ATLNLQ/S	²⁷⁰⁸ DTLHLQ/A
SpMV_2	²¹⁹ MRLIHY/S	⁶⁵⁸ KYLVG/G	¹⁰⁰⁵ KDITLQ/A	¹⁰⁵⁸ ETIMLQ/S	¹⁶⁹⁸ GVITLQ/S	¹⁷⁵⁰ DGFLE/S	¹⁹⁶⁰ DSLNLG/G	²¹⁹⁹ ATLNLQ/S	²⁷¹⁰ DTFQLQ/A
SpMV_3	²¹⁸ MRLIHY/S	⁶⁵⁹ KHYLVG/G	¹⁰⁰⁴ KDITLQ/A	¹⁰⁵⁷ ETIMLQ/S	¹⁶⁹⁷ GVITLQ/S	¹⁷⁴⁹ DGFLE/S	¹⁹⁵⁹ DSLNLG/G	²¹⁹⁸ ATLNLQ/S	²⁷⁰⁹ DTFQLQ/A
Potyviruses									
TuMV	³⁶³ HKIVHF/S	⁸²¹ KHYRVG/G	¹¹⁷⁶ KAVVHQ/A	¹²²⁸ PTVYHQ/T	¹⁸⁷² EAVHHQ/N	¹⁹²⁵ EPVTHE/A	²¹¹⁸ VPVDHE/S	²³⁶⁰ TAVYAQ/T	²⁸⁷⁷ ACVYHQ/A
PwMYMV	⁴³⁰ HEIIHY/S	⁸⁸⁹ KFYRVG/G	¹²²⁹ EPVAFQ/A	¹²⁷⁹ ERVDYQ/S	¹⁹¹³ ECVNFQ/S	¹⁹⁶⁵ DEVYQ/S	²¹⁵¹ NEVEFE/G	²³⁹¹ ELVCEQ/G	²⁹⁰⁶ EYVDFQ/S
Rymoviruses									
HoMV	²⁴⁴ NAIEHF/S	⁶⁹⁷ KEYNVG/G	¹⁰⁵¹ EEVKHQ/A	¹⁰⁹⁴ GSVYHQ/S	¹⁷⁴¹ ALVEHQ/S	¹⁷⁹⁴ EQVSFE/G	¹⁹⁸⁷ SQVGHE/S	²²²⁹ TDVEHQ/H	²⁷⁴⁹ TLVFHE/A
AgMV	²⁴⁴ KRIQHF/S	⁶⁹⁷ AEYNVG/G	¹⁰⁵⁰ EEVEHQ/A	¹¹⁰³ DAVYHQ/S	¹⁷⁴⁰ TLVEHQ/S	¹⁷⁹³ EQVTFE/G	¹⁹⁸⁶ SCVAHE/S	²²²⁸ TDVEHQ/H	²⁷⁴⁵ TLVYHE/A
RGMV	²⁵⁷ HTIKHY/S	⁷¹² LDYNVG/G	¹⁰⁶⁴ DTVTHQ/A	¹¹¹⁷ TVVTHQ/S	¹⁷⁵⁴ TLVHHQ/S	¹⁸⁰⁷ TRVHLE/G	²⁰⁰⁰ YSVQHE/S	²²⁴¹ EAVSHQ/S	²⁷⁵⁹ TKVVHE/A

^a Residues common to cleavage sites of both phragmiviruses are shaded in yellow. Corresponding common amino acids in potyviruses and rymoviruses are shaded in gray. Numbers indicate the position of the first amino acid residue of each protein partial sequence. Protein 1 (P1), Helper component protease (HC-Pro), Protein 3 (P3), Six Kilodalton protein 1 (6K1), Cytoplasmic Inclusion (CI), Six Kilodalton protein 2 (6K2), Viral Protein Genome-linked (VPg), Nuclear Inclusion a protease (NlA-Pro), Nuclear Inclusion b (NlB), and Capsid (Coat) Protein (CP). The potential cleavage site is indicated by /. Sequences: common reed chlorotic stripe virus (CRCSV, KY612317, genus *Phragmivirus*); Spartina mottle virus (SpMV_1-MN788417, SpMV_2-MW314142, and SpMV_3-MW314143, genus *Phragmivirus*); periwinkle mild yellow mosaic virus (PwMYMV, PP382205, genus *Potyvirus*); turnip mosaic virus (TuMV, AF169561, genus *Potyvirus*); Hordeum mosaic virus (HoMV, AY623627, genus *Rymovirus*); Agropyron mosaic virus (AgMV, AAS77619, genus *Rymovirus*); ryegrass mosaic virus (RGMV-AV, Y09854, genus *Rymovirus*).