ICTV Virus Taxonomy Profile: Potyviridae

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Abstract

The Potyviridae is the largest family of RNA plant viruses, members of which have single-stranded, positive-sense RNA genomes and flexuous filamentous particles 680–900 nm long and 11–20 nm wide. There are eight genera, distinguished by the host range, genomic features and phylogeny of the member viruses. Genomes range from 8.2 to 11.3 kb, with an average size of 9.7 kb. Most genomes are monopartite but those of members of the genus Bymovirus are bipartite. Some members cause serious disease epidemics in cultivated plants. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the taxonomy of the Potyviridae, which is available at www.ictv.global/report/potyviridae.

VIRION

The flexuous, filamentous particles are 680–900 nm long and 11–20 nm wide, with helical symmetry and a pitch of about 3.4 nm (Table 1). Particles of some viruses are longer in the presence of divalent cations than in the presence of EDTA. Virion sedimentation coefficient $S_{20, w}$ is 137–160S; density in CsCl is 1.31 g cm$^{-3}$; extinction coefficient $E_{260}$ is 2.4–2.7. Virions contain a core capsid protein (CP) of 30–47 kDa; the tip of the capsid may contain the virus-encoded proteins genome-linked protein (VPg) and helper-component proteinase (HC-Pro) [1]. Virions contain about 5% RNA by weight [2]. Virions are moderately immunogenic; there are serological relationships among many members. Some monoclonal antibodies react with most aphid-transmitted potyviruses [3, 4].

GENOME

The single-stranded, positive-sense genome ranges from 8.2 kb (members of the species Artichoke latent virus, genus Macluravirus) to 11.3 kb (members of the species Wheat yellow mosaic virus, genus Bymovirus), with an average of around 9.7 kb (Table 2). The genomes have a VPg covalently linked to the 5’ end, and the 3’ terminus is polyadenylated. Most genomes are monopartite but those of members of the genus Bymovirus are bipartite. The genome of members of the species Potato virus Y, the type species of the genus Potyivirus, is organized as described in Fig. 1. The single large ORF of
monopartite genomes encodes a single polyprotein that is cleaved into functional proteins at semi-conserved sites by three self-encoded proteases. Bipartite *Bymovirus* genomes encode two polyproteins that are cleaved by two proteases [5]. A second small ORF, PIPO, is generated by a polymerase slip-page mechanism and is expressed as the trans-frame protein P3N-PIPO [6–8]. Coding region order and protein sequences are generally conserved throughout the family, although one of or both the P1 and the HC-Pro N-terminal coding regions may be lacking and a genus-specific or species-specific region may be present instead (Table 2). The coat protein of most isolates of the type species, *Potato virus Y*, contains 267 amino acids.

### REPLICATION

Viruses are transmitted horizontally by arthropods or plasmophorids; some are transmitted vertically in seed. Some members cause serious disease epidemics in cultivated plants. Members of a few species infect over 30 plant families, but most infect one or a few host species or families [9] (Table 2).

### TAXONOMY

The family is divided into eight genera, the members of which are distinguished by host range, genomic features and phylogeny (Table 2). The species demarcation criteria, based upon the large ORF or its protein product, are generally accepted as $<76\%$ nucleotide identity and $<82\%$ amino acid identity. If the complete ORF sequence is not available, similar criteria can be used for the coat protein coding region and its product. The corresponding thresholds for species demarcation using nucleotide identity values for other coding regions range from $58\%$ (P1 coding region) to $74–78\%$ (other regions), although these ranges are exceeded in some cases [10].

### Table 2. Characteristics of members of the eight genera and two unassigned species in the family *Potyviridae*

| Genus      | Type species                                      | Genome organization | Genom size range (kb) | Host range | Vectors | Notable features                                                                 |
|------------|---------------------------------------------------|---------------------|-----------------------|------------|---------|----------------------------------------------------------------------------------|
| Brachyvirus (1 species) | Blackberry virus Y | Monopartite | 10.8 | Rubus species | Unknown | *Alk1* domain encoded in a very large P1 coding region. HC-Pro lacks motifs for genome amplification and systemic movement. Members lack P1 and HC-Pro coding regions. RNA2 encodes an HC-Pro-like protein unique to bymoviruses. |
| Bymovirus (6 species) | Barley yellow mosaic virus | Bipartite | RNA1: 7.2–7.6 RNA2: 2.2–3.6 | Gramineae | Unknown | Whitefly (Bemisia tabaci) Aphids Some members lack the P1 and/or HC-Pro coding regions and encode a P1b protein instead, performing a role in host RNAi suppression. No P1 coding region and the HC-Pro region is shorter than in potyviruses. Unusually long 5′ NTR with 12 translation initiation codons and three ORFs. |
| Ipomovirus (6 species) | Sweet potato mild mottle virus | Monopartite | 9.0–10.8 | Wide | Unknown | Wheat curl mite (TriMV) Aphids |
| Macluravirus (8 species) | Maclura mosaic virus | Monopartite | 8.2 | Wide | Unknown | |
| Poacevirus (3 species) | Triticum mosaic virus | Monopartite | 9.7–10.2 | Gramineae and Orchidaceae | Wide | Wheat curl mite (TriMV) Aphids |
| Potyvirus (160 species) | Potato virus Y | Monopartite | 9.4–11.0 | Wide | Unknown | |
| Rymovirus (3 species) | Ryegrass mosaic virus | Monopartite | 9.4–9.5 | Gramineae | Unknown | Eriophyd mites |
| Tritimovirus (6 species) | Wheat streak mosaic virus | Monopartite | 9.2–9.6 | Gramineae | Unknown | Eriophyd mites |
| Unassigned | Rose yellow mosaic virus | Monopartite | 9.5 | Rosa sp. | Unknown | P1 protein rather than HC-Pro serves as a suppressor of gene silencing. |
| Unassigned | Spartina mottle virus | Unknown | Unknown | Gramineae | Unknown | |

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Fig. 1. Genome organization of a typical member of the genus *Potyvirus*. Viruses of other genera may differ as described in Table 2. VPg, viral protein genome-linked; P1-Pro, protein 1 protease; HC-Pro, helper component protease; P3, protein 3; PIPO, pretty interesting *Potyviridae* ORF; 6K, six kilodalton peptide; CI, cytoplasmic inclusion; Nla-Pro, nuclear inclusion A protease; Nlb, nuclear inclusion B RNA-dependent RNA polymerase; CP, coat protein. Cleavage sites of P1-Pro (O), HC-Pro (●) and Nla-Pro (●) are indicated.
RESOURCES
Full ICTV Online (10th) Report: www.ictv.global/report/potyviridae.

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Conflicts of interest
The authors declare that there are no conflicts of interest.

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