Potyviridae, a proposed family of plant viruses

The potyvirus group was one of the six plant virus groups, defined largely on the basis of particle length [1]. At that time, the group contained 16 serologically related viruses with flexuous particles 730–760 nm in length. From the Fourth Report of the International Committee on Taxonomy of Viruses [11], a paraphrase of the potyvirus group description might be: viruses with flexuous filamentous particles 680–900 nm long and 11 nm wide having one coat polypeptide and one molecule of linear positive-sense ssRNA which characteristically induces pinwheel inclusions in the cytoplasm of infected plants. The Fourth Report listed 48 aphid-borne viruses as definitive members of the potyvirus group. Possible members of the group were subdivided into aphid-borne (56 viruses), fungal-borne (5 viruses), mite-borne (5 viruses), and whitefly-borne (1 virus) categories. In the manuscript for the Figth Report of the ICTV (collated for the VIIIth International Congress of Virology, August 1990, Berlin, for publication in the *Archives of Virology*) members of this working group listed 73 definitive members, and possible members were separated into aphid-borne (74 viruses), fungal-borne (5 viruses), mite-borne (7 viruses), and whitefly-borne (1 virus) categories.

In 1984 the editors of the CMI/AAB Descriptions of Plant Viruses tentatively subdivided the potyvirus group into four subgroups based on vectors. This sub-grouping was for convenience because the group had grown so large and because it seemed the most logical way to subdivide the group (A. F. Murant, pers. comm.). Although the ICTV listed the fungal-, mite-, and whitefly-borne categories as possible members, others felt that these viruses should be excluded from the potyvirus group until more information was available on the affinities of these viruses to the aphid-borne members [3, 4]. In the 1988 Set of Descriptions of Plant Viruses, the barley yellow mosaic virus group, which included the fungal-borne viruses, was listed as a separate group independent from the potyvirus group. This group was established due to the findings that the fungal-borne possible members of the potyvirus group have a bimodal particle distribution and a bipartite genome [5, 9].

When the nucleotide sequence of the capsid protein gene of barley yellow mosaic virus was obtained, differences and similarities with aphid-borne potyviruses were found [6–8]. The capsid protein gene is located on the 3′-proximal region of RNA 1 and codes for a 297 amino acid protein with an M_r of 32,334; the capsid protein is produced by proteolytic processing; the N- and C-terminal regions of the capsid protein are removed by mild proteolysis of intact particles; and the capsid protein had only small blocks of amino acids homologous to those of potyviruses in other vector groups. These results, together with the bipartite genome, their transmission by a fungus, and the absence of a serological relationship with aphid-borne potyviruses [14] led to the submission of a proposal for a BYMOVIRUS group to the Plant Virus Subcommittee just prior to the Berlin Congress and too late to be acted upon.

A Potyvirus Taxonomy Workshop was held in Braunschweig, Federal Republic of Germany on 3–4 September 1990 with 65 participants from 14 countries. After reviewing

current knowledge on potyviruses and discussing the significance in changes to the Rules of Nomenclature of Viruses approved at the Berlin Congress (rules which required latin binominal genus and species names were modified), workshop participants voted their approval of establishing a family of plant viruses called *Potyviridae* to include three genera and one possible genus. The three approved genera were the genus *Potyvirus* containing the aphid-borne viruses with potato virus-Y as the type species, the genus *Baymovirus* composed of the fungal-transmitted viruses with barley yellow mosaic virus as the type species, and the genus *Ryemovirus* with ryegrass mosaic virus as the type species. The possible genus (*Ipomovirus*) was to include the whitefly-borne virus, sweet potato mild mottle virus.

This family was proposed because all viruses in the three genera and one possible genus have flexuous, filamentous particles which contain a positive sense ssRNA genome and pinwheel inclusions accumulate in the cytoplasm of infected plants. The genome of potyviruses has a poly(A) tract at the 3′ end, a genome-linked protein covalently attached to the 5′ terminus of the genome, and functional proteins are generated by processing polyprotein precursors. These features and a distinctive replication gene module places them in the proposed supergroup of picorna-like plant viruses [2]. The baymoviruses have poly(A) tracts on the 3′ ends of both genome RNA species and have a replication gene module on RNA 1 similar to that of the potyviruses, but RNA 2 of the baymoviruses shows striking differences in organization when compared with the 5′-terminal region of the potyvirus genome [7, 8]. The ryemoviruses, based on wheat streak mosaic virus (C. L. Niblett, pers. comm.), have particles which are similar to the potyviruses but are shorter (700 nm) and contain a monopartite ssRNA genome of 8.5 kb and a larger coat protein (M_r = 42 k). This ryemovirus genome has a 3′-terminal poly(A) tract, a translational strategy based on polyprotein processing, the coat protein gene maps to the 3′ end (10% homology to four potyviruses) followed by a 185 AA protein with 54% homology to the potyvirus NIb putative polymerase, and further in the 5′ direction is a 332 AA protein with 34% homology to potyvirus cylindrical inclusion protein. Less is known about the genome organization of sweet potato mild mottle virus.

There is some serological relationship among a few viruses in different genera. For instance, barley mild mosaic baymovirus is serologically related to bean yellow mosaic potyvirus and it also reacted with a broad spectrum turnip mosaic potyvirus antiserum [13]; ryegrass mosaic and wheat streak mosaic ryemoviruses are related to turnip mosaic and Johnson grass mosaic potyviruses, respectively [10, 12]; and the whitefly transmitted sweet potato mild mottle virus is related to Johnson grass mosaic potyvirus [12]. However, the viruses within a genus are much more closely related by nucleotide or coat protein amino acid sequence comparisons and serology [15]. While vector type seems to be correlated with other characters in defining the genera, lack of transmission by a vector does not preclude assignment to a genus because other molecular or serological properties are reliable for this task.

These genus names were chosen to avoid confusion with common acronyms. Thus, BaYMV for barley yellow mosaic virus avoids confusion with BYMV for bean yellow mosaic virus, so this acronym was used to form baymovirus. This allowed the first three letters of the host name to be used for the other genera for uniformity, i.e., ryemovirus and ipomovirus, with potyvirus used for the other genus because it is an established term. Participants preferred to maintain similar family (*Potyviridae*) and genus (*Potyvirus*) names rather than to alter accepted usage.

This proposal to establish the *Potyviridae* with the potyvirus, baymovirus, and ryemovirus genera and the possible ipomovirus genus will be submitted by the Potyvirus Working Group to the Plant Virus Subcommittee of the ICTV. If approved by the Plant Virus Subcommittee it will be submitted to the ICTV at their next executive committee meeting. Another group of genus names has been proposed to the Plant Virus Subcommittee of the ICTV by Bob Milne: eupotyvirus (for clear distinction from the family name, *Potyviridae*), bymovirus (the originally proposed group name; [14]), and rymovirus (no possible genus name was proposed).

Comments on this proposal are welcome and should be directed to any member of the committee: G. Adam, O. W. Barnett, A. A. Brunt, W. G. Dougherty, J. H. Hill, J. Hammond, I. Uyeda, R. Jordan, K. Makkouk, D. Purcifull, S. T. Ohki, R. Goldbach, J. R. Edwardson, E. Shikata, J. Dijkstra, D. D. Shukla, F. Morales, and G. P. Martelli.

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