

Template for Taxonomic Proposal to the ICTV Executive Committee To create a new Family

Code[†] To create a new family* in an existing Order[°]

Code[†] To name the new family*

Code[†] To designate the following genera as part of the new family*:

Potexvirus
Mandarivirus
Allexivirus
Carlavirus
Foveavirus
Capillovirus
Vitivirus
Trichovirus

[†] Assigned by ICTV officers

[°] Leave blank is not appropriate

* repeat these lines and the corresponding arguments for each genus created in the family

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New Taxonomic Order

Order	
Family	<i>Flexiviridae</i>
Genus	<i>Potexvirus</i> <i>Mandarivirus</i> <i>Allexivirus</i> <i>Carlavirus</i> <i>Foveavirus</i> <i>Capillovirus</i> <i>Vitivirus</i> <i>Trichovirus</i>

List of Unassigned Species in the Family

Banana mild mosaic virus	[AF314662]	(BanMMV)
Citrus leaf blotch virus	[AJ318061]	(CLBV)
Sugarcane striate mosaic-associated virus	[AF315308]	(SCSMaV)

Argumentation to create a new family:

Viruses of the genera listed all infect plants and share:

1. Flexuous filamentous virions 12-13nm in diameter
2. Monopartite, positive sense, ssRNA genomes with a 3'-polyA tail
3. Translation of some ORFs from subgenomic mRNAs
4. Up to 6 open reading frames ordered from 5' to 3':
 - (a) An alpha-like replication protein (150-250 kDa) containing conserved methyl transferase, helicase and RNA-dependent RNA polymerase motifs
 - (b) One or more movement proteins, either a single protein of the '30K' superfamily (*Capillovirus*, *Trichovirus*, *Vitivirus*, CLBV) or a 'triple gene block' (remaining genera and viruses).
 - (c) The capsid (coat) protein (22-44 kDa)
 - (d) A sixth ORF in some genera may partially overlap the 3'-end of the coat protein gene and is thought to have nucleotide-binding properties.
5. An obvious phylogenetic relationship between the ORFs that they have in common (see Annex).

Creation of a family will also provide a home for related viruses that cannot be assigned to existing genera, as for example Citrus leaf blotch virus and at least two viruses that had previously been regarded as tentative members of the genus *Foveavirus* (Banana mild mosaic virus and Sugarcane striate mosaic-associated virus).

A set of two-way comparisons has been done to establish the percentage nucleotide and amino acid identity between the corresponding genes of all available sequences within the proposed family. The data will be described in detail in a paper for Virology Division News but they indicate that it is possible to assign a reasonably standard set of criteria for distinguishing strains from species. Distinct species have less than *ca.* 72% identical nucleotides or 80% identical amino acids between their entire coat protein or polymerase genes. Species from different genera usually have less than *ca.* 45% nucleotide or 40% amino acid identity in these genes.

A taxonomic system built around genome organization and coat protein phylogenetic analysis would group together only the genera *Potexvirus*, *Mandarivirus*, *Allexivirus*, *Carlavirus* and *Foveavirus*. However, phylogenetic analysis of the RdRp suggests that it would be unwise to exclude the other genera because the carla- and fovea-viruses associate more closely with these than with the potex- and allexi-viruses (see Annex, Fig. 1).

Origin of the proposed family name

Flexiviridae is derived from the English *Flexuous* referring to the structure of the particles of all members of all genera of the family.

References

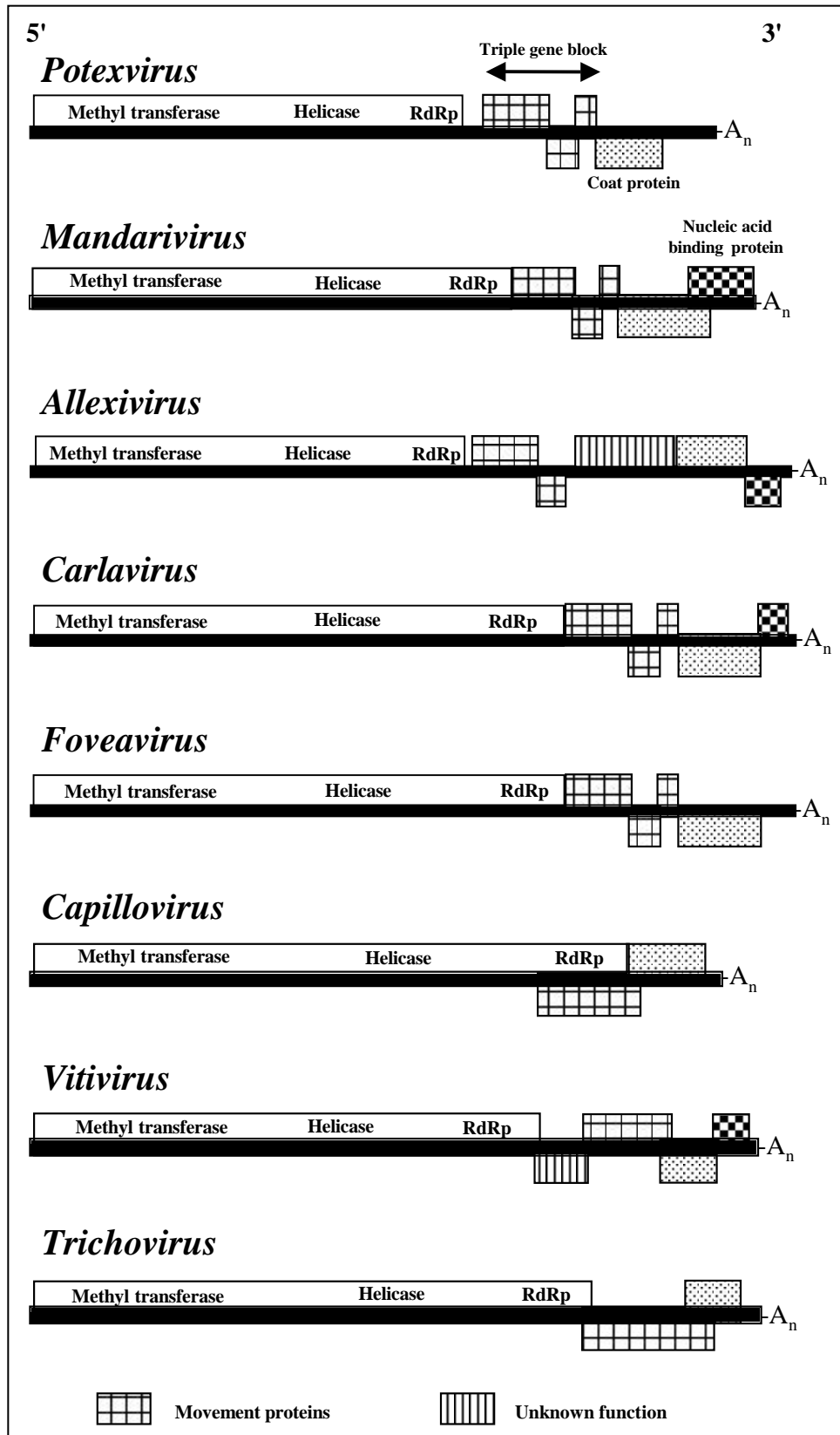
Hataya, T., Uchino, K., Arimoto, R., Suda, N., Sano, T., Shikata, E., and Uyeda, I. (2000). Molecular characterization of Hop latent virus and phylogenetic relationships among viruses closely related to carlaviruses. *Arch Virol.*, **145**, 2503-2524.

Melcher, U. (2000). The '30K' superfamily of viral movement proteins. *J Gen Virol.*, **81**, 257-266.

Morozov, S.Y. & Solovyev, A.G. (2003). Triple gene block: modular design of a multifunctional machine for plant virus movement. *J Gen Virol.*, **84**, 1351-1366.

Wong, S.-M., Lee, K.-C, Yu, H.-H. & Leong, W.-F. (1998). Phylogenetic analysis of triple gene block viruses based on the TGB 1 homolog gene indicate a convergent evolution. *Virus Genes* **16**, 295-302.

Annexes:



List of sequences used in phylogenetic analysis

Acc No	RefSeq	Virus	Genus	Acronym	Region
x98991	-	Garlic mite-borne filamentous virus	<i>Allexivirus</i>	GarMbFV	Coat protein
ab010300	NC_003375	Garlic virus A	<i>Allexivirus</i>	GarV-A	Polymerase and coat protein
ab010301	-	Garlic virus B	<i>Allexivirus</i>	GarV-B	Coat protein
ab010302	NC_003376	Garlic virus C	<i>Allexivirus</i>	GarV-C	Polymerase and coat protein
ab010303	-	Garlic virus D	<i>Allexivirus</i>	GarV-D	Coat protein
aj292230	NC_004012	Garlic virus E	<i>Allexivirus</i>	GarV-E	Polymerase and coat protein
u89243	NC_001800	Garlic virus X	<i>Allexivirus</i>	GarV-X	Polymerase and coat protein
m97264	NC_003795	Shallot virus X	<i>Allexivirus</i>	ShVX	Polymerase and coat protein
d14995	NC_001749	Apple stem grooving virus	<i>Capillovirus</i>	ASGV	Polymerase and coat protein
x82547	NC_003689	Cherry virus A	<i>Capillovirus</i>	CVA	Polymerase and coat protein
ab051848	NC_002795	Aconitum latent virus	<i>Carlavirus</i>	AcLV	Polymerase and coat protein
l25658	NC_003499	Blueberry scorch virus	<i>Carlavirus</i>	BIScV	Polymerase and coat protein
aj010697	-	Carnation latent virus	<i>Carlavirus</i>	CLV	Coat protein
s60150	-	Chrysanthemum virus B	<i>Carlavirus</i>	CVB	Coat protein
af024629	-	Cowpea mild mottle virus	<i>Carlavirus</i>	CPMMV	Coat protein
x81138	-	Garlic common latent virus	<i>Carlavirus</i>	GarCLV	Coat protein
aj292226	NC_003557	Garlic latent virus	<i>Carlavirus</i>	GarLV	Polymerase and coat protein
d10454	-	Helenium virus S	<i>Carlavirus</i>	HVS	Coat protein
ab032469	NC_002552	Hop latent virus	<i>Carlavirus</i>	HpLV	Polymerase and coat protein
ab051109	-	Hop mosaic virus	<i>Carlavirus</i>	HpMV	Coat protein
aj293570	-	Kalanchoe latent virus	<i>Carlavirus</i>	KLV	Coat protein
af015286	-	Lily symptomless virus	<i>Carlavirus</i>	LSV	Coat protein
af354652	-	Pea streak virus	<i>Carlavirus</i>	PeSV	Coat protein
d13364	-	Poplar mosaic virus	<i>Carlavirus</i>	PopMV	Coat protein
d14449	NC_001361	Potato virus M	<i>Carlavirus</i>	PVM	Polymerase and coat protein
d00461	-	Potato virus S	<i>Carlavirus</i>	PVS	Coat protein
aj311375	-	Narcissus common latent virus	<i>Carlavirus</i>	NCLV	Coat protein
d21829	NC_003462	Apple stem pitting virus	<i>Foveavirus</i>	ASPV	Polymerase and coat protein
af057035	-	Apricot latent virus	<i>Foveavirus</i>	ApLV	Coat protein
af017780	NC_001946	Cherry green ring mottle virus	<i>Foveavirus?</i>	CGRMV	Polymerase and coat protein
af237816	NC_002468	Cherry necrotic rusty mottle virus	<i>Foveavirus?</i>	CNRMV	Polymerase and coat protein
af318062	-	Peach sooty ringspot virus	<i>Foveavirus</i>	PeSRSV	Coat protein
af057136	NC_001948	Rupestris stem pitting-associated virus	<i>Foveavirus</i>	RSPaV	Polymerase and coat protein
af406744	NC_003093	Indian citrus ringspot virus	<i>Mandarivirus</i>	ICRSV	Polymerase and coat protein
af080448	-	Alternanthera mosaic virus	<i>Potexvirus</i>	AltMV	Coat protein
d26017	NC_001642	Bamboo mosaic virus	<i>Potexvirus</i>	BaMV	Polymerase and coat protein
af308158	NC_002815	Cactus virus X	<i>Potexvirus</i>	CVX	Polymerase and coat protein
u23414	NC_001658	Cassava common mosaic virus	<i>Potexvirus</i>	CsCMV	Polymerase and coat protein
d29630	NC_001753	Clover yellow mosaic virus	<i>Potexvirus</i>	CIYMV	Polymerase and coat protein
u62963	NC_001812	Cymbidium mosaic virus	<i>Potexvirus</i>	CymMV	Polymerase and coat protein
m62730	NC_001483	Foxtail mosaic virus	<i>Potexvirus</i>	FoMV	Polymerase and coat protein
x15342	-	Lily virus X	<i>Potexvirus</i>	LVX	Coat protein
d13747	NC_001441	Narcissus mosaic virus	<i>Potexvirus</i>	NMV	Polymerase and coat protein
d13957	NC_001748	Papaya mosaic virus	<i>Potexvirus</i>	PapMV	Polymerase and coat protein
af484251	NC_004067	Pepino mosaic virus	<i>Potexvirus</i>	PepMV	Polymerase and coat protein
z21647	NC_003849	Plantago asiatica mosaic virus	<i>Potexvirus</i>	PIAMV	Polymerase and coat protein
s73580	NC_003632	Potato aucuba mosaic virus	<i>Potexvirus</i>	PAMV	Polymerase and coat protein
x05198	NC_001455	Potato virus X	<i>Potexvirus</i>	PVX	Polymerase and coat protein
aj316085	NC_003400	Scallion virus X	<i>Potexvirus</i>	ScVX	Polymerase and coat protein

d12517	NC_003794	Strawberry mild yellow edge virus	<i>Potexvirus</i>	SMYEV	Polymerase and coat protein
ab066288	NC_004322	Tulip virus X	<i>Potexvirus</i>	TVX	Polymerase and coat protein
x06728	NC_003820	White clover mosaic virus	<i>Potexvirus</i>	WCIMV	Polymerase and coat protein
af314662	NC_002729	Banana mild mosaic virus	Unassigned	BanMMV	Polymerase and coat protein
aj318061	NC_003877	Citrus leaf blotch virus	Unassigned	CLBV	Polymerase and coat protein
af315308	NC_003870	Sugarcane striate mosaic associated virus	Unassigned	SCSMaV	Polymerase and coat protein
x75433	NC_003604	Grapevine virus A	<i>Vitivirus</i>	GVA	Polymerase and coat protein
x75448	NC_003602	Grapevine virus B	<i>Vitivirus</i>	GVB	Polymerase and coat protein
y07764	-	Grapevine virus D	<i>Vitivirus</i>	GVD	Coat protein
x79270	-	Heracleum latent virus	<i>Vitivirus</i>	HLV	Coat protein
m58152	NC_001409	Apple chlorotic leaf spot virus	<i>Trichovirus</i>	ACLSV	Polymerase and coat protein
af170028	NC_002500	Cherry mottle leaf virus	<i>Trichovirus</i>	ChMLV	Polymerase and coat protein
d88448	-	Grapevine berry inner necrosis virus	<i>Trichovirus</i>	GINV	Coat protein
d10172	-	Potato virus T	<i>Trichovirus</i>	PVT	Coat protein

Fig. 1. Phylogenetic (NEIGHBOR) analysis of the members of the proposed family Potexviridae using aa sequences of the RdRp region of the polymerase. Sequences were aligned using GCG PILEUP and genetic distances estimated by PROTDIST (Dayhoff PAM method). Trees were displayed in TreeView. Bootstrap values based on 100 replicates are shown where >60%.

