



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	2015.003a-dP	(to be completed by ICTV officers)			
Short title: Create five species in the genus <i>Potyvirus</i> , reassign one species from genus <i>Potyvirus</i> to genus <i>Macluravirus</i> and abolish a related species in the genus <i>Macluravirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input checked="" type="checkbox"/>	8 <input checked="" type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	<i>Potyviridae</i>
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ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:

May 2015

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

EC comment: Please supply missing reference for Minutillo et al 2015 in the reference list.

SG response: Done

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	2015.003aP	(assigned by ICTV officers)
To create 5 new species within:		
Genus:	<i>Potyvirus</i>	Fill in all that apply. <ul style="list-style-type: none"> • If the higher taxon has yet to be created (in a later module, below) write “(new)” after its proposed name. • If no genus is specified, enter “unassigned” in the genus box.
Subfamily:		
Family:	<i>Potyviridae</i>	
Order:		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Catharanthus mosaic virus</i>	Welwitchia	KP742991
<i>Donkey orchid virus A</i>	SW3.1	JX156422
<i>Sunflower mild mosaic virus</i>	Entre Rios	JQ350738
<i>Tamarillo leaf malformation virus</i>	A	KM523548
<i>Vanilla distortion mosaic virus</i>	VDMV-Cor	KF906523

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
 - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria.**
 - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- [Further material in support of this proposal may be presented in the Appendix, Module 9](#)

The family *Potyviridae* consists of plant viruses with a single stranded, positive sense RNA genome and flexuous, filamentous particles. Genomes have a VPg covalently linked to the 5'-end and the 3'-terminus is polyadenylated. Genomes encode a large precursor polyprotein (except in the case of genus *Bymovirus*, which is bipartite and encodes two polyproteins) that is self-cleaved into a set of functional proteins that is strongly conserved throughout the family. The genus *Potyvirus* is easily the largest in the family and has economically important members in all parts of the world. They are transmitted by aphids in a non-persistent manner. The genome is monopartite and the polyprotein is cleaved into 10 products. Each of these proteins has at least some strongly conserved motifs and the cleavage sites also have distinctive patterns. An additional small ORF named PIPO has also been identified which is expressed with the N-terminal part of the P3 protein after frameshifting (Rodamilans *et al.*, 2015).

According to criteria published in the ICTV 9th Report (Adams *et al.*, 2011), species are distinguished by the following criteria:

- Genome sequence relatedness: different species have CP aa sequence identity less than ca. 80%; and nt sequence identity less than 76% either in the CP or over the whole genome. There are also differences in polyprotein cleavage sites.
- Host range and key host reactions; lack of cross protection.
- Different inclusion body morphology.

- Antigenic properties: serological relatedness may help in distinguishing species.

The five viruses described below all appear to represent new species in the genus. For each, there is at least one complete genome sequence in the public domain and this shows the expected ORFs, conserved motifs and cleavage sites. The molecular criteria to create new species have been satisfied. For four species there are peer-reviewed publications giving the provenance of the virus(es) and additional biological data. For Sunflower mild mosaic virus there is no peer-reviewed publication available, but a draft of a publication is available at asagir.org.ar, which describes the procedure used to generate the sequence, and some biological information. Phylogenetic analysis of the complete polyprotein coding sequences (Annex Figure 1) supports the placement of these viruses as distinct species within the genus *Potyvirus*.

Catharanthus mosaic virus

Catharanthus mosaic virus (CatMV) was first described from *Catharanthus roseus* (Madagascar periwinkle) in Brazil in 2011 (Maciel *et al.*, 2011). The first complete genome sequence of 9636 nt was derived from a symptomatic garden plant the gymnosperm *Welwitschia mirabilis* in Australia (Accession KP742991). CatMV-Welwitschia is the first potyvirus described from a gymnosperm. CatMV isolate Welwitschia was mechanically inoculated to *N. benthamiana*, *Chenopodium amaranticolor* and *C. quinoa* plants. The virus systemically infected *N. benthamiana* plants and locally infected both *Chenopodium* species tested. The genome sequence was obtained from an infected *N. benthamiana* plant using both high-throughput and Sanger sequencing approaches. The sequence was confirmed by three independent high-throughput sequencing runs. The sequence has all the molecular characteristics typical of a potyvirus. When analysed phylogenetically, CatMV did not fit into any existing groups within the genus *Potyvirus*. The complete CatMV polyprotein had 38-45% aa pairwise identity with those of other members of the genus *Potyvirus*.

Donkey orchid virus A

High-throughput sequencing was used to identify a new potyvirus from a single wild asymptomatic plant of *Diuris laxiflora* (Bee orchid, Donkey orchid). It was named Donkey orchid virus A (DOVA) isolate SW3.1 (Wylie *et al.*, 2013). The genome sequence of 9868 nt (GenBank accession JX156422) has all the molecular characteristics typical of a potyvirus. No attempt was made to mechanically transmit the virus or to determine other biological characteristics. Phylogenetically, the polyprotein did not share close identity with any recognized group within the genus *Potyvirus*; it shared less than 42% aa pairwise identity with all described potyvirus polyproteins.

Sunflower mild mosaic virus

Symptoms of chlorotic mild mosaic were described in sunflower (*Helianthus annuus*) in 1994 from commercial crops of sunflower in Parana, Entre Rios Province, Argentina. The virus was transmitted by the aphid *Myzus persicae*, but not by seed or dodder (Lenardon, 1994). Sunflower mild mosaic virus (SuMMoV) was named in 2010 from infected Argentinian sunflower crops. In 2013 the complete genome (9718 nt) of SuMMoV isolate Entre Rios from Argentina was released (GenBank accession JQ350738). Although a description of the virus is not formally published, an informal document describing details of the research is available at the asagir.org.ar website (Giolitti *et al.*). The genome sequence was obtained using a high-throughput sequencing approach. The complete genome sequence has all the molecular characteristics typical of a potyvirus. The viral polyprotein shared highest aa pairwise identity (50-54%) with members of the tobacco etch virus group within genus *Potyvirus*.

Tamarillo leaf malformation virus

In 1991, Colombian tamarillo (*Solanum betaceum*) plantations were affected by a severe disease described as ‘virosis’, which subsequently spread to all tamarillo growing regions in the country. The disease was associated with at least four viruses, including potato virus Y, cucumber mosaic virus, potato leafroll virus and an unidentified potyvirus (Garcia *et al.*, 2011). Degenerate potyvirus primers were used to amplify a fragment of the genome of the unidentified virus, which revealed it to be a previously undescribed potyvirus (Ayala *et al.*, 2010). The complete genome sequence (9676 nt) of Tamarillo leaf malformation virus (TaLMV) isolate A (GenBank accession KM523548) was published in 2015 (Gutiérrez *et al.*, 2015). The sequence was obtained using a high-throughput sequencing strategy. The sequence has all the molecular characteristics typical of a potyvirus. The complete genome sequence shared greatest aa identity (65%) with Columbian datura virus (CDV), originally identified from *Brugmansia* plants growing in a tamarillo production area of Putumayo province, Brazil. The coat protein sequences of TaLMV and CDV shared 76 % aa pairwise identity. TaLMV shared greatest identity with members of the tobacco etch virus group of genus *Potyvirus*.

Vanilla distortion mosaic virus

A routine quarantine inspection in the UK of Coriander (*Coriandrum sativum*) plants imported from India revealed symptoms of chlorosis, bronzing and necrosis on petioles and stems of one plant (Adams *et al.*, 2014). The sample was tested using a general potyvirus antibody in an ELISA test, for which it was positive. Total cDNA was sequenced using a high-throughput sequencing approach. A sequence of 9573 nt was identified as an isolate of Vanilla distortion mosaic virus (VDMV), a virus first named in 2006 from *Vanilla planifolia* and *Stevia sp* in India (unpublished), for which partial genome sequences were available (AY943944-6, AY948436-7, AM261869). Another partial genome sequence has recently become available from Zinnia in India (KJ013533). The Coriander isolate was named VDMV-Cor and its sequence was granted GenBank accession code KF906523. The Coriander isolate shared greater than 90% aa identity with the partial genome sequences of VDMV isolates previously described. The sequence has all the molecular characteristics typical of a potyvirus. The polyprotein sequence of VDMV shared greatest pairwise identity (46-48%) with members of the TuMV, SPFMV and TEV groups within genus *Potyvirus*.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- Either to abolish a taxon entirely (when only part (a) needs to be completed)
- Or to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	2015.003bP	(assigned by ICTV officers)
To remove the following taxon (or taxa) from their present position:		
<i>Artichoke latent virus</i>		
The present taxonomic position of these taxon/taxa:		
Genus:	<i>Potyvirus</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Potyviridae</i>	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

A latent virus in globe artichoke was first described in 1959 by Costa and colleagues. Artichoke latent virus (ArLV) was assigned by Rana *et al.*, (1982) to the genus *Potyvirus* based on biology, ultrastructure and serology. Accordingly, *Artichoke latent virus* was first listed as a member of the potyvirus group (later a species in the genus *Potyvirus*) in the ICTV 5th Report (1991). In 2015 the complete genome sequences of three isolates (ITBr05, FR37, FR50) of ArLV, one from Italy and two from France, and all from Globe Artichoke (*Cynara cardunculus* var. *scolymus*) were described (Minutillo *et al.*, 2015). The genome sequence of isolate ITBr05 from Italy was determined from Sanger sequencing of overlapping cDNA clones synthesized from viral RNA extracted from a *N. benthamiana* plant, and by 5' RACE. The complete genome sequence was 8278 nt long, and it was granted GenBank accession KF155694 (not publically available at time of writing). French isolates FR37 (8287 nt) and FR50 (8291) were sequenced using a high-throughput sequencing approach directly from artichoke host plants. The complete genome sequences of the French isolates FR37 and FR50 were granted GenBank accessions KP405232 and KP405233, respectively. These are publically available and isolate FR50 is reported to have 97.3% nt identity to ITBr05 (Minutillo *et al.*, 2015). Phylogenetic comparison of the deduced polyprotein sequence placed the French isolates of ArLV closest (51% aa identity) to Chinese yam necrotic mosaic virus (CYNMV), the only macluravirus for which a complete genome is currently available. The ArLV polyprotein sequences share less than 20% aa pairwise identity with those of members of the genus *Potyvirus*. Polyproteins of viruses in the same genus within the *Potyviridae* usually have >40% aa identity (Adams *et al.*, 2005)

Part (b) re-assign to a higher taxon

Code	2015.003cP	(assigned by ICTV officers)
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To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	<i>Macluravirus</i>
Subfamily:	
Family:	<i>Potyviridae</i>
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created write “(new)” after its proposed name and complete relevant module to create it. If no genus is specified, enter “unassigned” in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
 - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
 - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Macluraviruses resemble members of the genus *Potyvirus* in their transmission by aphids but virions are slightly shorter. They form a distinct group in phylogenetic analyses and have different polyprotein consensus cleavage sites (Adams *et al.*, 2011).

The newly described ArLV genomes share macluravirus-like characteristics with that of CYNMV, including (i) the absence of a P1 cistron and a shorter HC-Pro than members of genus *Potyvirus*, (ii) the PIPO is unusually short, in this case 56 amino acids, (iii) lack of consensus in polyprotein cleavage sites -6 to -3, a conserved lysine at -2, and a Q(E)/M(A,I) cleavage site consensus, and (iv) the conserved DAG motif of the *Potyvirus* coat protein is absent.

Phylogenetic comparison of the deduced polyprotein sequence placed the French isolates of ArLV closest (51% aa identity) to Chinese yam necrotic mosaic virus (CYNMV), the only macluravirus for which a complete genome is currently available (see Annex Fig. 1).

ArLV and the partial genome sequence of RaLV isolate Cy42 (CI-CP cistrons) share identities above the accepted potyvirus species delimitation of less than 76% nt or 80% aa identity for either the full genome or the coat protein. The ArLV and RaLV isolates also showed strong serological cross-reactions. This is confirmed by phylogenetic analysis of the 3'-terminus of the genome of macluraviruses (Annex Fig. 2) The name Artichoke latent virus has priority over Ranunculus latent virus, which should now be considered as strains of ArLV. It is thereby proposed that the taxon Ranunculus latent virus be abolished (refer to Module 8 in this proposal).

Thus, it is proposed that Artichoke latent virus be moved from its current placement in the genus *Potyvirus*, to the genus *Macluravirus*.

MODULE 8: REMOVE and MOVE

Use this module whenever an existing taxon needs to be removed:

- Either to abolish a taxon entirely (when only part (a) needs to be completed)

- Or to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	2015.003dP	(assigned by ICTV officers)
To remove the following taxon (or taxa) from their present position:		
<i>Ranunculus latent virus</i>		
The present taxonomic position of these taxon/taxa:		
Genus:	<i>Macluravirus</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Potyviridae</i>	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		YES

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

Ranunculus latent virus (RaLV) isolate Cy42 (CI-CP cistrons) shares nucleotide and amino acid identities with those of Artichoke latent virus (ArLV) above the accepted potyviridae species delimitation of less than 76% nt or 80% aa identity for either the full genome or the coat protein. The ArLV and RaLV isolates also showed strong serological cross-reactions.

This is confirmed by phylogenetic analysis of the 3'-terminus of the genome of macluraviruses (Annex Fig. 2) The name Artichoke latent virus was assigned by Rana *et al.*, (1982), and thus has priority over Ranunculus latent virus, assigned by Turina *et al.*, 2006, isolates of which should now be considered as strains of Artichoke latent virus (refer to Module 7 in this proposal).

Thus, it is proposed that the taxon *Ranunculus latent virus* be abolished from its current placement in the genus *Macluravirus*.

Part (b) re-assign to a higher taxon

Code		(assigned by ICTV officers)
To re-assign the taxon (or taxa) listed in Part (a) as follows:		
Genus:		Fill in all that apply. <ul style="list-style-type: none"> • If the higher taxon has yet to be created write "(new)" after its proposed name and complete relevant module to create it. If no genus is specified, enter " unassigned " in the genus box.
Subfamily:		
Family:		
Order:		

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
 - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
 - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

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MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Adams MJ, Antoniw JF, Fauquet CM (2005). Molecular criteria for genus and species discrimination within the family *Potyviridae*. *Archives of Virology* 150:459–479

Adams MJ, Zerbini FM, French R, Rabenstein F, Stenger DC, Valkonen JPT. (2011). Family *Potyviridae*. In: *Virus Taxonomy, Ninth Report of the International Committee on Taxonomy of Viruses* (A.M.Q. King, M.J. Adams, E.B. Carstens & E.J. Lefkowitz, eds), pp. 1069-1089. Elsevier Academic Press, London.

Adams IP, Rai S, Deka M, Harju V, Hodges T, Hayward G, Skelton A, Fox A, Boonham N. (2014). Genome sequence of vanilla distortion mosaic virus infecting *Coriandrum sativum*. *Archives of Virology* 159: 3463-3465.

Ayala M, González P, Gutiérrez P, Cotes J, Marín M (2010) Caracterización serológica y molecular de potyvirus asociados a la virosis del tomate de árbol en Antioquia (Colombia). *Acta Biológica Colombiana* 15:143–162

García YG, Montoya MM, Gutiérrez PA. (2011). Obtención de anticuerpos específicos para la detección del Tamarillo leaf malformation virus (TaLMV) en tomate de árbol. *Acta Biológica Colombiana* 16: 135-147.

Giolitti F, de Breuil S, Bejerman N, Lenardon S. Complete nucleotide sequence and genetic organization of Sunflower mild mosaic virus (SuMMoV). Sourced from asagir.org.ar, April 14 2015.

Gutiérrez, P. A., Alzate, J. F., Montoya, M. M. (2015). Genome sequence of a virus isolate from tamarillo (*Solanum betaceum*) in Colombia: evidence for a new potyvirus. *Archives of Virology* 160:557-560

Koh SH, Li, H, Admiraal R, Jones MGK, Wylie SJ (2015) Catharanthus mosaic virus: a potyvirus from a gymnosperm, *Welwitschia mirabilis*. *Virus Research* 203: 41-46

Lenardon, S.L. 1994. Síntomas de etiología viral en cultivos de girasol. In *Enfermedades del Girasol en la Argentina. Manual de reconocimiento*. V.R. Pereyra and A.R. Escande: 99-103

Maciel SC, Silva RF.d. Reis MS, Jidão AS, Rosa DD, Giampan JS, Kitajima EW, Rezende JAM, Camargo LE. 2011. Characterization of a new potyvirus causing mosaic and flower variegation in *Catharanthus roseus* in Brazil. *Scientia Agricola* 68: 687–690.

Minutillo SA, Marais A, Mascia T, Faure C, Svanella-Dumas L, Theil S, Payet A, Perennec S, Schoen L, Galletelli D, Candresse, T. (2015). Complete nucleotide sequence of Artichoke latent virus shows it to be a member of the genus *Macluravirus* in the family *Potyviridae*. *Phytopathology*. <http://dx.doi.org/10.1094/PHYTO-01-15-0010-R>

Rana GL, Russo M, Gallitelli D, Martelli GP (1982). Artichoke latent virus: characterisation, ultrastructure and geographical distribution. *Annals of Applied Biology* 101:279–289

additional material in support of this proposal

References:

Rodamilans, B., Valli, A., Mingot, A., San León, D., Baulcombe, D., López-Moya, J. J., García, J. A. (2015). RNA polymerase slippage as a mechanism for the production of frameshift gene products in plant viruses of the Potyviridae family. *Journal of Virology* JVI-00337.

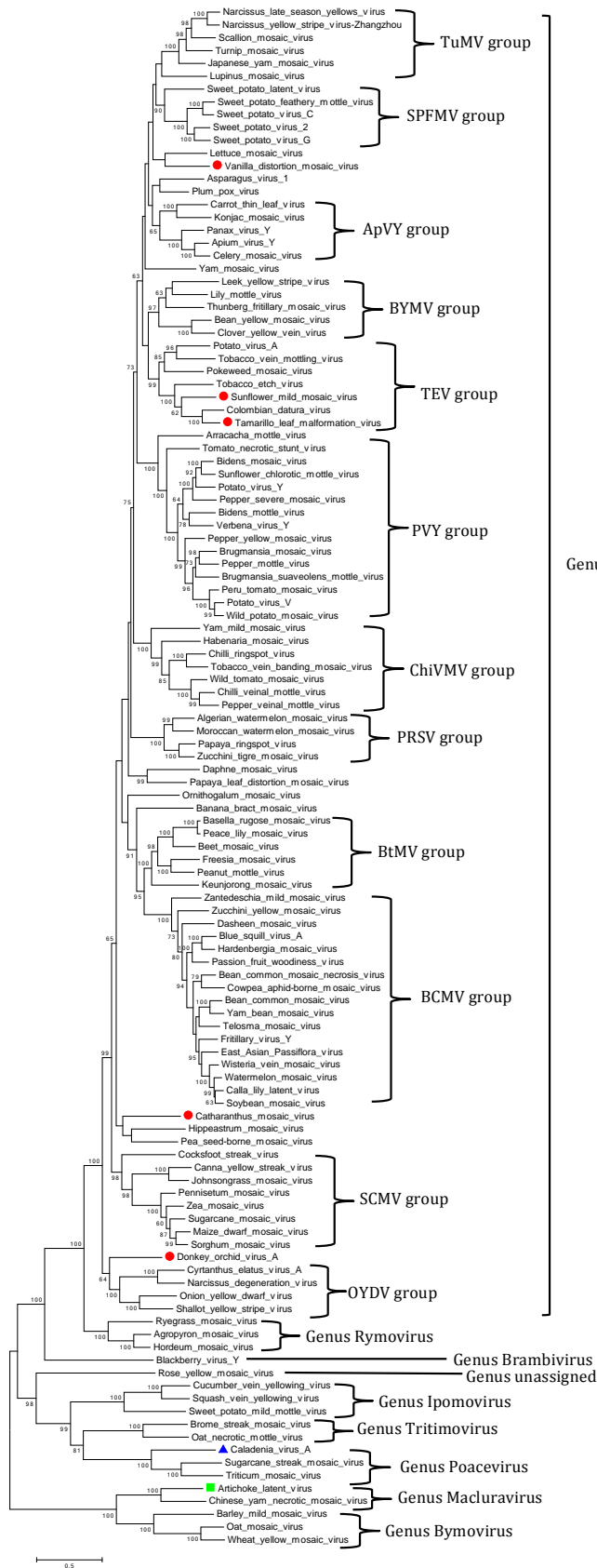
Turina, M., Ciuffo, M., Lenzi, R., Rostagno, L., Mela, L., Derin, E., Palmano, S. (2006). Characterization of four viral species belonging to the family *Potyviridae* isolated from *Ranunculus asiaticus*. *Phytopathology*, 96: 560-566.

Wylie, S. J., Li, H., Dixon, K. W., Richards, H., Jones, M. G. (2013). Exotic and indigenous viruses infect wild populations and captive collections of temperate terrestrial orchids (*Diuris* species) in Australia. *Virus research* 171: 22-32.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Figure 1. Estimated phylogeny of polyprotein amino acid sequences deduced from completely sequenced isolates of members of the family *Potyviridae*. Representative members of genera *Brambivirus*, *Bymovirus*, *Ipomovirus*, *Macluravirus*, *Poacevirus*, *Potyvirus*, *Rymovirus*, *Tritimovirus*, and one virus, Rose yellow mosaic virus, for which a genus is currently unassigned, were used. Members of genera are indicated, and within genus *Potyvirus*, recognized groupings are shown. Each virus with a red dot beside its name is proposed here as a new species within genus *Potyvirus*. Artichoke latent virus, which is proposed for reclassification from genus *Potyvirus* to *Macluravirus*, is indicated by a green square. Caladenia virus A, indicated by a blue triangle, is the subject of a separate proposal in the genus *Poacevirus*. The tree was deduced in Mega6.06 after alignment by ClustalW using the Maximum Likelihood method based on the JTT matrix-based model with 10,000 bootstrap replicates. Branch lengths are proportional to genetic distance in units of amino acid substitutions per site. Bootstrap support for branches >60% is shown at the junctions of branches.



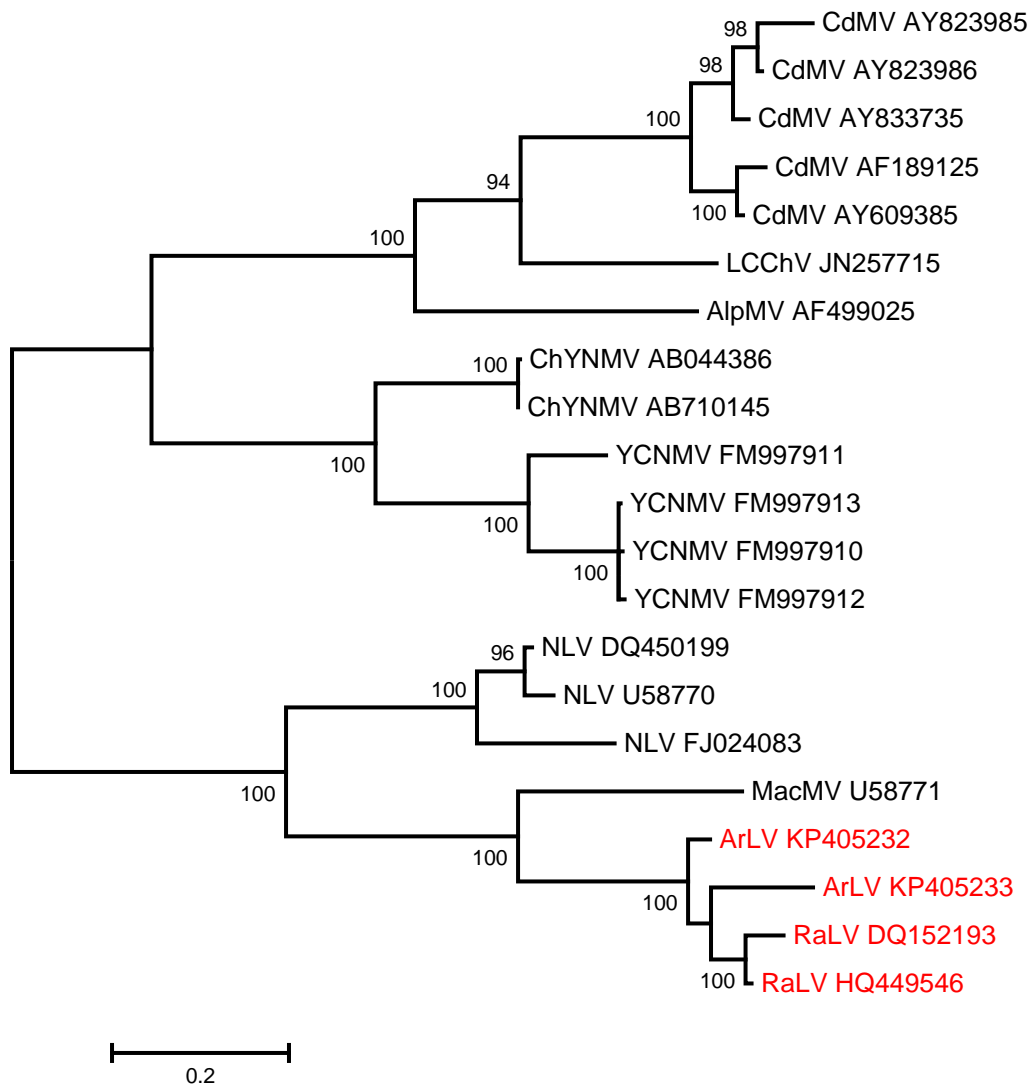


Figure 2. Unrooted maximum likelihood tree based on the C-terminal part of the polyprotein (part of the NIb and the complete coat protein) of macluravirus isolates showing in red the grouping of isolates of *Artichoke latent virus* (ArLV) and *Ranunculus latent virus* (RaLV). The percentage bootstrap support (from 1000 replicates) is shown where >60%. Tree produced in MEGA 6.06. Other abbreviations: AlpMV, *Alpinia mosaic virus*; CdMV, *Cardamom mosaic virus*; ChYNMV, *Chinese yam necrotic mosaic virus*, LCChV, large cardamom chirke virus, MacMV, *Maclura mosaic virus*; NLV, *Narcissus latent virus*, YCNMV, yam chlorotic necrotic mosaic virus.