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:	***2015.002aP***	(to be completed by ICTV officers)

Short title: Create one species in the genus *Poacevirus*, family *Potyviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☒

Author(s):

Wylie, Stephen (Chair)	s.wylie@murdoch.edu.au
Adams, Michael J.	mike.adams.ictv@gmail.com
Kreuze, Jan F.	j.kreuze@cgiar.org
Lopez-Moya, Juan Jose	juanjose.lopez@cragenomica.es
Ohshima, Kazusato	ohshimak@cc.saga-u.ac.jp
Rabenstein, Frank	frank.rabenstein@jki.bund.de
Stenger, Drake C.	dstenger@fresno.ars.usda.gov
Wang, Aiming	aiming.wang@agr.gc.ca
Zerbini, F. Murilo	zerbini@ufv.br

Corresponding author with e-mail address:

Stephen Wylie s.wylie@murdoch.edu.au

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)	Potyviridae

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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	***2015.002aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Poacevirus***
Subfamily:	
Family:	~~*Potyvirus*~~*Potyviridae*
Order:	

Fill in all that apply.
- 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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Caladenia virus A	KP1	JX156425

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 two existing species in the genus *Poacevirus* are *Triticum mosaic virus* (TriMV) and *Sugarcane streak mosaic virus* (SCSMV). TriMV is transmitted by an eriophyid mite (mite transmission unconfirmed for SCSMV) but neither is closely related to other mite-transmitted potyvirids in the genera *Tritimovirus* and *Rymovirus*.

Caladenia virus A

Symptomatic terrestrial orchid plants were tested for the presence of viruses in an endangered orchid collection located in a greenhouse in Australia. The collection is used to propagate vulnerable orchid species to boost wild populations. Total polyadenylated cDNA from each plant was pooled, then sequenced using a high-throughput sequencing approach. Virus-specific primers were designed from a putative virus-derived genome sequence of 9847 nt. The specific primers were used to screen 5-15 plants each of 12 orchid species in the collection. Of these, four plants of *Caladenia arenicola*, and one each of *C. latifolia* and *Drakaea elastica* were identified as positive for the virus. These six plants exhibited mild (*Caladenia* spp) to severe (*D. elastica*) streaking symptoms typical of virus infection. RT-PCR products were sequenced using the Sanger method and the sequences gained were identical to one another and to the genome sequence (Wylie *et al*., 2012). Thus, the available genome sequence of Caladenia virus A (CalVA) isolate KP1 (JX156425) is a consensus derived from six virus isolates, as defined by the population of CalVA genomes present in one infected plant. Eight polymorphic sites were identified within the genome, three of which were non-synonymous. It is unclear whether these polymorphisms represent variation between the six pooled isolates, or variation within isolates. Attempts to mechanically transmit the virus to plants of *N. benthamiana*, *Chenopodium amaranticolor*, and *C. quinoa* were unsuccessful (unpublished).

Phylogenetically, the genome sequence of CalVA-KP1 had greatest amino acid (aa) identities (38-39% aa) with the two members of the genus *Poacevirus* but less than 20% aa identities with other members of the *Potyviridae*. Neither of the conserved aphid-transmission motifs KITC or PTK within the potyvirus HC-Pro were present, nor was the DAG motif present in the coat protein, indicating that CalVA is not aphid transmitted. The mode of transmission for CalVA is unknown. The zinc finger-like mite transmission motif of TriMV was present in the CalVA genome, suggestive that it may be mite transmitted. CalVA represents the first member of the genus *Poacevirus* that was not derived from a poaceous host.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

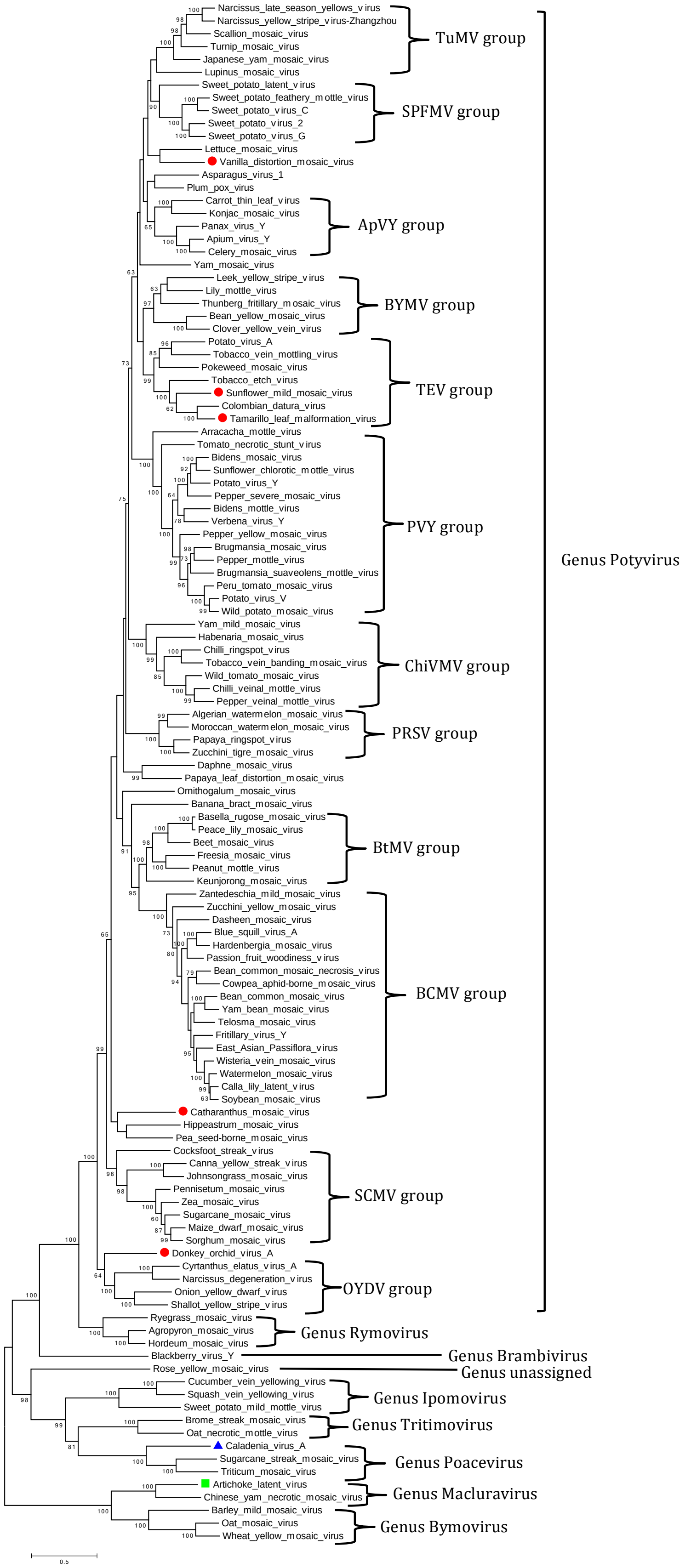
References:

Wylie, S. J., Tan, A. J., Li, H., Dixon, K. W., & Jones, M. G. K. (2012). Caladenia virus A, an unusual new member of the family *Potyviridae* from terrestrial orchids in Western Australia. *Archives Virol*ogy*157*: 2447-2452.

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*. Caladenia virus A, here proposed as a member of the genus *Poacevirus*, is indicated by a blue triangle. 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 being proposed 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 (see separate proposal). The tree was deduced in Mega v6.06 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.


Narcissus_late_season_yellows_virus
Narcissus_yellow_stripe_virus-Zhangzhou
Scallion_mosaic_virus
Turnip_mosaic_virus
Japanese_yam_mosaic_virus
Lupinus_mosaic_virus
TuMV group
Sweet_potato_latent_virus
Sweet_potato_feathery_mottle_virus
Sweet_potato_virus_C
Sweet_potato_virus_2
Sweet_potato_virus_G
SPFMV group
Lettuce_mosaic_virus
● Vanilla_distortion_mosaic_virus
Asparagus_virus_1
Plum_pox_virus
Carrot_thin_leaf_virus
Konjac_mosaic_virus
Panax_virus_Y
Apium_virus_Y
Celery_mosaic_virus
ApVY group
Yam_mosaic_virus
Leek_yellow_stripe_virus
Lily_mottle_virus
Thunberg_fritillary_mosaic_virus
Bean_yellow_mosaic_virus
Clover_yellow_vein_virus
BYMV group
Potato_virus_A
Tobacco_vein_mottling_virus
Pokeweed_mosaic_virus
Tobacco_etch_virus
● Sunflower_mild_mosaic_virus
Colombian_datura_virus
● Tamarillo_leaf_malformation_virus
TEV group
Arracacha_mottle_virus
Tomato_necrotic_stunt_virus
Bidens_mosaic_virus
Sunflower_chlorotic_mottle_virus
Potato_virus_Y
Pepper_severe_mosaic_virus
Bidens_mottle_virus
Verbena_virus_Y
Pepper_yellow_mosaic_virus
Brugmansia_mosaic_virus
Pepper_mottle_virus
Brugmansia_suaveolens_mottle_virus
Peru_tomato_mosaic_virus
Potato_virus_V
Wild_potato_mosaic_virus
PVY group
Genus Potyvirus
Yam_mild_mosaic_virus
Habenaria_mosaic_virus
Chilli_ringspot_virus
Tobacco_vein_banding_mosaic_virus
Wild_tomato_mosaic_virus
Chilli_veinal_mottle_virus
Pepper_veinal_mottle_virus
ChiVMV group
Algerian_watermelon_mosaic_virus
Moroccan_watermelon_mosaic_virus
Papaya_ringspot_virus
Zucchini_tigre_mosaic_virus
PRSV group
Daphne_mosaic_virus
Papaya_leaf_distortion_mosaic_virus
Ornithogalum_mosaic_virus
Banana_bract_mosaic_virus
Basella_rugose_mosaic_virus
Peace_lily_mosaic_virus
Beet_mosaic_virus
Freesia_mosaic_virus
Peanut_mottle_virus
Keunjorong_mosaic_virus
BtMV group
Zantedeschia_mild_mosaic_virus
Zucchini_yellow_mosaic_virus
Dasheen_mosaic_virus
Blue_squill_virus_A
Hardenbergia_mosaic_virus
Passion_fruit_woodiness_virus
Bean_common_mosaic_necrosis_virus
Cowpea_aphid-borne_mosaic_virus
Bean_common_mosaic_virus
Yam_bean_mosaic_virus
Telosma_mosaic_virus
Fritillary_virus_Y
East_Asian_Passiflora_virus
Wisteria_vein_mosaic_virus
Watermelon_mosaic_virus
Calla_lily_latent_virus
Soybean_mosaic_virus
BCMV group
● Catharanthus_mosaic_virus
Hippeastrum_mosaic_virus
Pea_seed-borne_mosaic_virus
Cocksfoot_streak_virus
Canna_yellow_streak_virus
Johnsongrass_mosaic_virus
Pennisetum_mosaic_virus
Zea_mosaic_virus
Sugarcane_mosaic_virus
Maize_dwarf_mosaic_virus
Sorghum_mosaic_virus
SCMV group
● Donkey_orchid_virus_A
Cyrtanthus_elatus_virus_A
Narcissus_degeneration_virus
Onion_yellow_dwarf_virus
Shallot_yellow_stripe_virus
OYDV group
Ryegrass_mosaic_virus
Agropyron_mosaic_virus
Hordeum_mosaic_virus
Genus Rymovirus
Blackberry_virus_Y
Genus Brambivirus
Rose_yellow_mosaic_virus
Genus unassigned
Cucumber_vein_yellowing_virus
Squash_vein_yellowing_virus
Sweet_potato_mild_mottle_virus
Genus Ipomovirus
Brome_streak_mosaic_virus
Oat_necrotic_mottle_virus
Genus Tritimovirus
▲ Caladenia_virus_A
Sugarcane_streak_mosaic_virus
Triticum_mosaic_virus
Genus Poacevirus
■ Artichoke_latent_virus
Chinese_yam_necrotic_mosaic_virus
Genus Macluravirus
Barley_mild_mosaic_virus
Oat_mosaic_virus
Wheat_yellow_mosaic_virus
Genus Bymovirus
0.5