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:	***2015.001a-dP***	(to be completed by ICTV officers)

Short title: Create one new genus with two new species in the family *Virgaviridae*
(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):

Sekine KT, Wylie SJ, Adkins S, Bragard C, Gilmer D, Man WS, Melcher U, Ratti C, Ryu KH, Adams MJ

Corresponding author with e-mail address:

Mike Adams (mike.adams.ictv@gmail.com)

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)	Virgaviridae and Benyviridae SG

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

Approved unanimously

Date first submitted to ICTV: April 2015
Date of this revision (if different to above): May 2015

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	***2015.001aP***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Goravirus (new)***
Subfamily:	
Family:	***Virgaviridae***
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)**
Gentian ovary ringspot virus	S	RNA1: AB976029 RNA2: AB976030
Drakaea virus A	Canning Mills	RNA1: KP760461 RNA2: KP760462

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

Gentian ovary ringspot virus (GORV)

Atsumi et al (2015) described the detection and identification of a novel virus from gentian in Japan and tentatively named it gentian ovary ringspot virus.

The virus was readily transmitted by pollen grains and caused ringspot symptoms on the ovaries of inoculated plants similar to those first observed in the field. The virus could also be transmitted mechanically to petunia and tobacco. A virus isolate was obtained by repeated single-lesion isolation from *Nicotiana benthamiana* and purified virions were shown to be infectious. The virions were rod-shaped and about 20nm in width, but it was difficult to determine their length because of disintegration during purification. RNA from virions was of two sizes, approximately 6000 nt and 4000 nt, similar in size to the dsRNAs that were isolated from diseased tissue.

After sequencing of cDNA from purified virions and prediction of ORFs it was clear that GORV was related to members of the family *Virgaviridae*. Members of this family have rod-shaped virions and (depending on the genus) 1, 2 or 3 genomic RNAs.

RNA1 of GORV has two predicted ORFs, the first of which is a replication protein containing

methyltransferase and helicase domains. The second is the RdRp; this is usually expressed as a readthrough product in the family *Virgaviridae* and we assume that this may be the case with GORV although there is no direct experimental evidence. The first ORF of RNA2 is a coat protein and subsequent ORFs encode the triple gene block proteins (involved in virus cell-to-cell movement) and a cysteine-rich protein (CRP) that was shown to act as a suppressor of gene silencing.

All these proteins have clear similarities to the corresponding proteins of viruses in the family *Virgaviridae*, particularly in genera *Pecluvirus* and *Hordeivirus*, although amino acid identities were modest (<42% in the replication protein) which would certainly confirm it as a distinct species and probably a separate genus (Adams et al., 2009). There were tRNA-like structures at the 3'-termini of both RNAs that are also characteristic of members of the *Virgaviridae*. However, the genome organization differs from that in the existing genera (Figure 1).

Drakaea virus A (DrVA)

Ong et al., (2015) subsequently reported a virus sequence determined from *Drakea livida* (wild orchids) in Australia. Partial sequences were obtained by Illumina sequencing and sequences were then confirmed and completed by RT-PCR and Sanger sequencing. This DrVA isolate has a bipartite genome of 4490 nt (RNA1) and 2905 nt (RNA2) and a genome organization identical to GORV. DrVA and GORV had 47% aa (55% nt) identity between their replicases, 36% aa (50% nt) between CPs, 29-46% aa (48-55% nt) between homologues of TGBps and 17% aa (43% nt) between CRPs.

Phylogenetic analyses confirm that the viruses are members of the family *Virgaviridae* and that they are most closely related to the genera *Pecluvirus* and *Hordeivirus*. They group with one another but cannot sensibly be included in an existing genus (Figure 2).

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2015.001bP***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Virgaviridae***
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2015.001cP***	(assigned by ICTV officers)

To name the new genus: *Goravirus*

Assigning the type species and other species to a new genus

Code	***2015.001dP***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Gentian ovary ringspot virus

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

2

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Genome organization and phylogenetic analyses show that that the viruses cannot be classified within any of the existing genera (see above).

Origin of the new genus name:

From the name of the type species ***G****entian* ***o****vary* ***r****ingspot virus*

Reasons to justify the choice of type species:

First member to be characterized.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

The two viruses are only distantly related (<50% aa identity between homologous genes) and clearly belong to different species. More rigorous demarcation criteria will be developed if further members of the genus are reported.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Adams MJ, Antoniw JF, Kreuze J (2009). *Virgaviridae*: a new family of rod-shaped plant viruses. Arch Virol 154:1967-1972

Atsumi G, Tomita R, Yamashita T, Sekine K-T (2015). A novel virus transmitted through pollination causes ring-spot disease on gentian (*Gentiana triflora*) ovaries. J Gen Virol 96:431-439

Ong JWL, Phillips RD, Dixon KW, Jones MGK, Wylie SJ (2015). Characterisation of the first two viruses described from wild populations of hammer orchids (*Drakaea* spp.) in Australia. Plant Pathol., in press, DOI: 10.1111/ppa.12396

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.

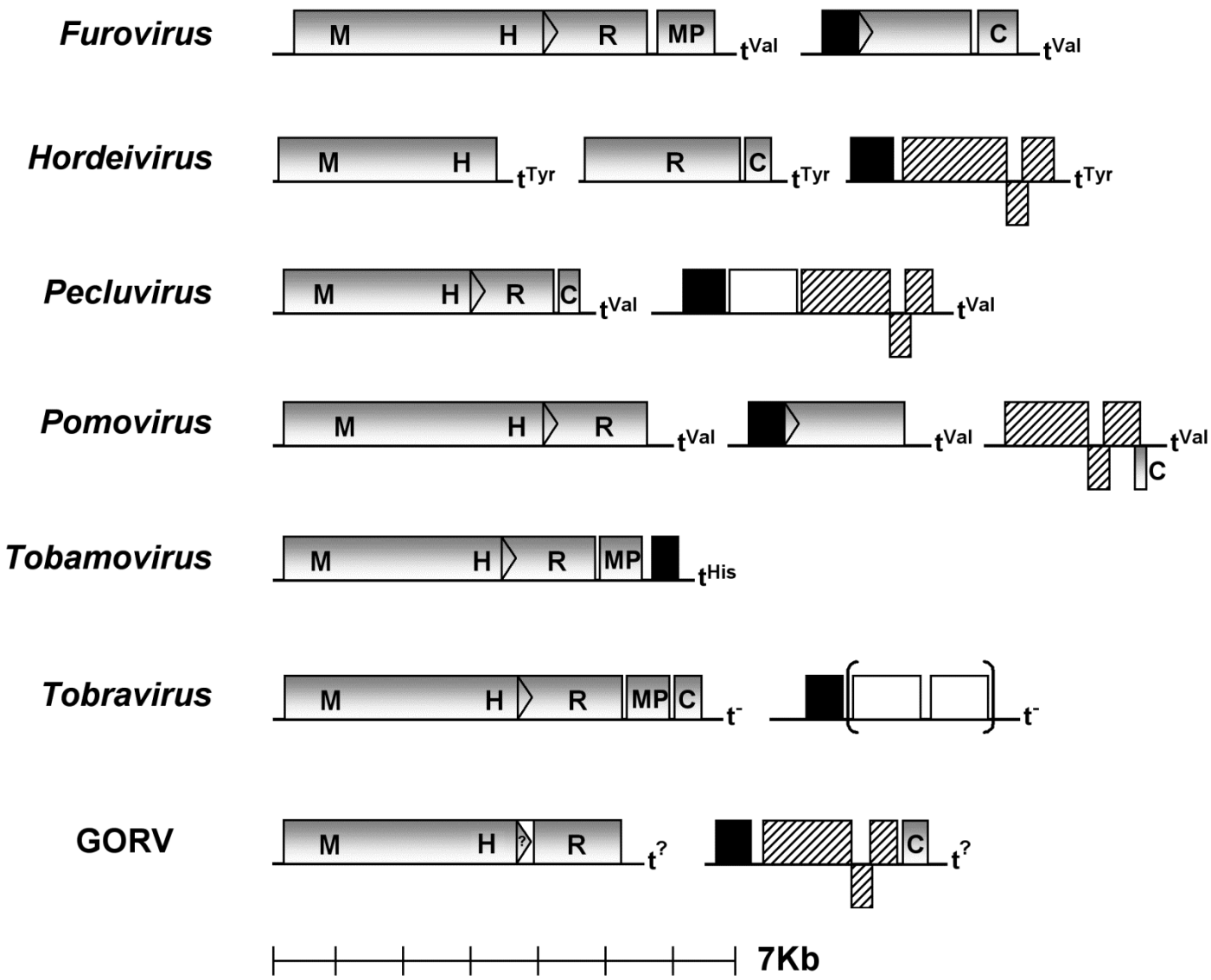

Figure 1. Diagram showing the genome organization of GORV and the 6 genera currently included in the family *Virgaviridae*. Domains marked in the replication proteins are Methyltransferase (M), Helicase (H) and RNA-dependent RNA polymerase (R). Triple gene block proteins (TGB) are cross-hatched and coat proteins in black. MP, movement protein of the '30K' superfamily; C, cysteine-rich protein (silencing suppressor). Positions of "leaky" stop codons are shown by triangles (►). $t^{Val/Tyr/His/-}$: t-RNA like structure accepting Valine, Tyrosine, Histidine or not aminoacylated respectively. Brackets indicate ORFs that are missing from some strains.

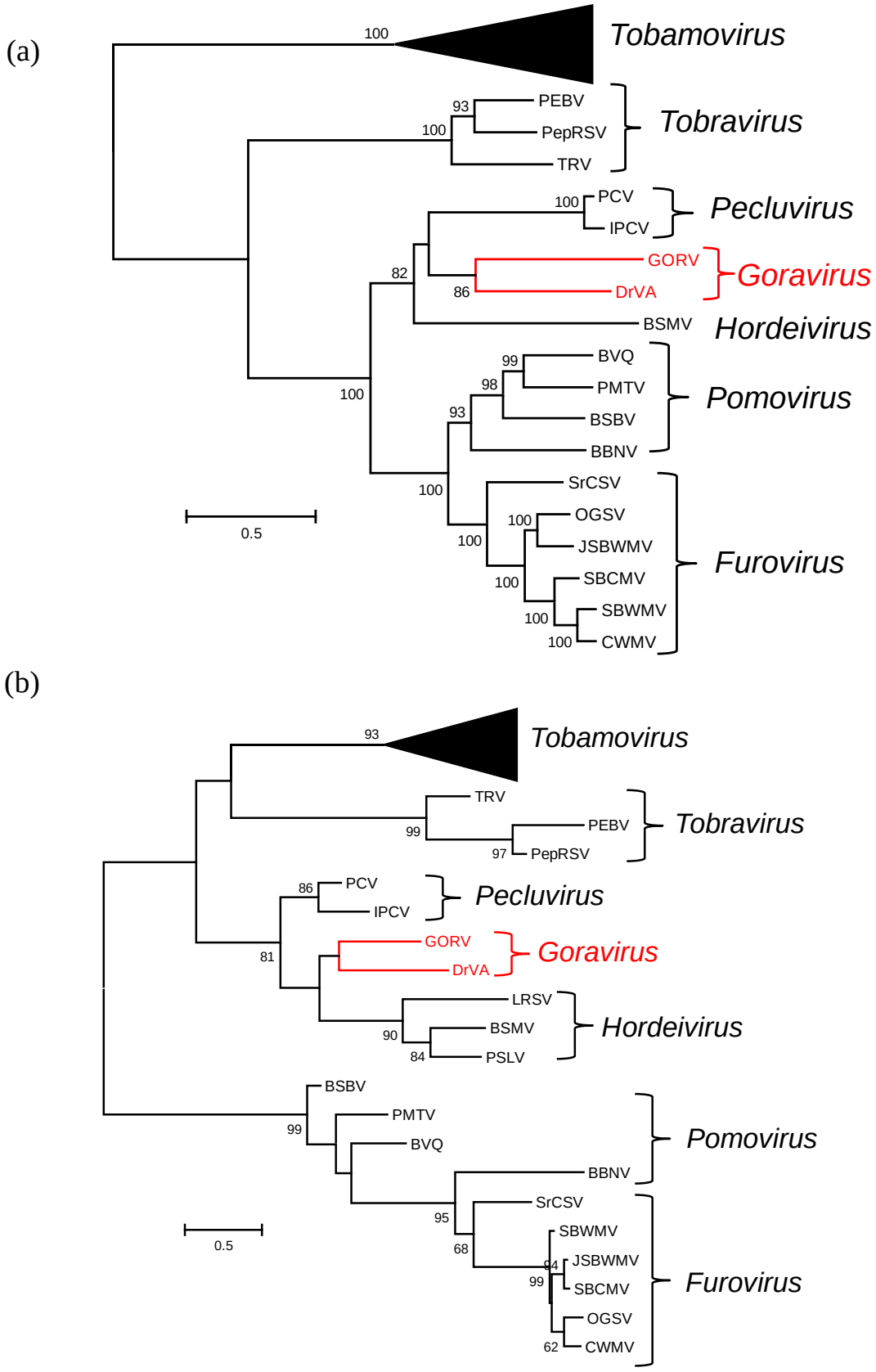

Figure 2. Maximum likelihood phylogenetic analysis of (a) the concatenated amino acid sequences of the replicase (methyltransferase/helicase) and RdRp and (b) the coat protein showing the position of GORV and DrVA (red) in the proposed genus Goravirus within the family *Virgaviridae*. The branch for the 30 members of the genus *Tobamovirus* has been collapsed. The percentage bootstrap support (from 1000 replicates) is shown where >60%. Tree produced in MEGA 6.06.