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:	***2015.004a-eD***	(to be completed by ICTV officers)

Short title: To create genus *Toursvirus* in family *Ascoviridae*, and to move species *Diadromus pulchellus ascovirus 4a* from genus *Ascovirus* to genus *Toursvirus*
(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):

Sassan Asgari, Dennis Bideshi, Yves Bigot, Xiao-Wen Cheng and Brian A. Federici

Corresponding author with e-mail address:

s.asgari@uq.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)	Ascoviridae Study Group

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

all members in agreement with the proposal

Date first submitted to ICTV:	13.05.2015
Date of this revision (if different to above):	05.08.2015

ICTV-EC comments and response of the proposer:

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.004aD***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Ascoviridae***
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	***2015.004bD***	(assigned by ICTV officers)

To name the new genus: *Toursvirus*

Assigning the type species and other species to a new genus

Code	***2015.004cD***	(assigned by ICTV officers)

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

Diadromus pulchellus ascovirus 4a	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:**

1

Reasons to justify the creation of a new genus:

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

Recent phylogenetic studies presented in PIEGU B, ASGARI S., BIDESHI D., FEDERICI B.A. & BIGOT Y. 2015. Evolutionary relationships of iridoviruses and divergence of ascoviruses from invertebrate iridoviruses in the superfamily Megavirales. Mol Phylo Evol 84:44-52, demonstrated that Diadromus puchellus ascovirus 4a (DpAV-4a) belongs to an evolutionary ascovirus lineage that is distinct from those gathering all other known ascoviruses. In term of genetic distance, DpAV-4a is equally distant from some invertebrate iridoviruses (IIV6 and IIV31) and the other members of genus *Ascovirus*. However, it is clearly monophyletic with the ascoviruses. DpAV-4a has a genome with a size (~116 kpb) that is significantly different to those of IIV6, IIV31 and the viruses of the genus *Ascovirus* (156-200 kpb). Moreover, its genome organization is completely different from those found in other ascoviruses.

Origin of the new genus name:

DpAV-4a is a virus that was discovered and described by Yves Bigot in 1997, when he was working in a research laboratory of entomology (IRBI) located in Tours. DpAV-4a was also found in fields of leeks around Tours where it was found infecting the leek-moth *Acrolepiopsis assectella*, and the parasitoid wasps *Diadromus pulchellus* and *Diadromus collaris*.

Reasons to justify the choice of type species:

DpAV-4a is the only species so far described in this genus.

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.

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	***2015.004dD***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

To move species *Diadromus pulchellus ascovirus 4a* from genus *Ascovirus* to genus *Toursvirus*

The present taxonomic position of these taxon/taxa:

Genus:	***Ascovirus***	Fill in all that apply.
Subfamily:		
Family:	***Ascoviridae***	
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

Recent phylogenetic studies presented in Piegu et al., 2015 demonstrated that Diadromus puchellus ascovirus 4a (DpAV-4a) belongs to an evolutionary ascovirus lineage that is distinct from those gathering all other known ascoviruses. DpAV-4a has a genome with a size (~116 kb) that is significantly different to those of the viruses of the *Ascovirus* genus (156-200 kb). Moreover, its genome organization is completely different from those found in other ascoviruses.

Part (b) re-assign to a higher taxon

Code	***2015.004eD***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Toursvirus* (new)**	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.
Subfamily:		
Family:	***Ascoviridae***	
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 10

Recent phylogenetic studies presented in Piegu et al., 2015 demonstrated that DpAV-4a belongs to an evolutionary ascovirus lineage that is distinct from those gathering all other known ascoviruses. In term of genetic distance, DpAV-4a is equally distant from some invertebrate iridoviruses (IIV6 and IIV31) and the other members of genus *Ascovirus*. However, it is clearly monophyletic with the ascoviruses. DpAV-4a has a genome with a size (~116 kpb) that is significantly different to those of IIV6, IIV31 and the viruses of the *Ascovirus* genus (156-200 kpb). Moreover, its genome organization is completely different from those found in other ascoviruses. All together, it seems to be appropriate to reassign it to a novel genus proposed in module 3 of the present proposal.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Bigot Y, Rabouille A, Sizaret PY, Hamelin MH & Periquet G. 1997. Particle and genomic characteristics of a new member of the *Ascoviridae*: Diadromus pulchellus ascovirus. J Gen Virol. 78:1139-1147.
2. Bigot Y, Rabouille A, Doury G, Sizaret PY, Delbost F, Hamelin MH & Periquet G. 1997. Biological and molecular features of the relationships between Diadromus pulchellus ascovirus, a parasitoid hymenopteran wasp (*Diadromus pulchellus*) and its lepidopteran host, *Acrolepiopsis assectella*. J Gen Virol. 78:1149-1163.
3. Stasiak K, Renault S, Federici BA & Bigot Y. 2005. Characteristics of pathogenic and mutualistic relationships of ascoviruses in field populations of parasitoid wasps. J Insect Physiol. 51:103-115.
4. Bigot Y, Asgari S, Bideshi D.K., Chang XW, Federci BA & Renault S. 2011. Family *Ascoviridae*. King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (eds) Virus Taxonomy: Classification and Nomenclature of Viruses. Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier, San Diego pp. 147-152.
5. Bigot Y, Renault S, Nicolas J, Moundras C, Demattei MV, Samain S, Bideshi DK & Federici BA. 2009. Symbiotic virus at the evolutionary intersection of three types of large DNA viruses; iridoviruses, ascoviruses, and ichnoviruses. PLoS One, 4:e6397.
6. Piégu B, Asgari S., Bideshi D., Federici B.A. & Bigot Y. 2015. Evolutionary relationships of iridoviruses and divergence of ascoviruses from invertebrate iridoviruses in the superfamily Megavirales. Mol Phylo Evol. 84:44-52.

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.

The four main differences of DpAV-4a with respect to the properties of the members of the *Ascovirus* genus are at the levels of its genome size, virion shape, phylogenetic position and biology.

1 - Like other ascoviruses, the DpAV-4a genome consists of a circular dsDNA molecule. Its size is however lower than that of the members of the *Ascovirus* genus; 119 kb versus about 156-200 kb. In some hosts, the DpAV-4a genome is carried as free circular DNA like in nuclei of its wasp host, *Diadromus pulchellus*, and is transmitted vertically to the wasp progeny. However, vertical transmission in wasp vectors is not known to occur with the other ascoviruses.

2 - Virions of the members of the *Ascovirus* genus are either bacilliform, ovoidal or allantoid in shape, depending on the species, have complex symmetry, and are large, measuring about 130 nm in diameter by 200-400 nm in length. Each DpAV-4a particle is about 220 nm long and 150 nm wide. The main difference comes from its shape that looks to that of a flattened rice-grain shape.

3 - The phylogeny of the nine core genes shared by the *Ascoviridae*, *Iridoviridae* and *Marseilleviridae* is robust and supports that DpAV-4a belongs to the *Ascoviridae* but within a lineage distinct to that of the *Ascovirus* genus (Fig. 1).

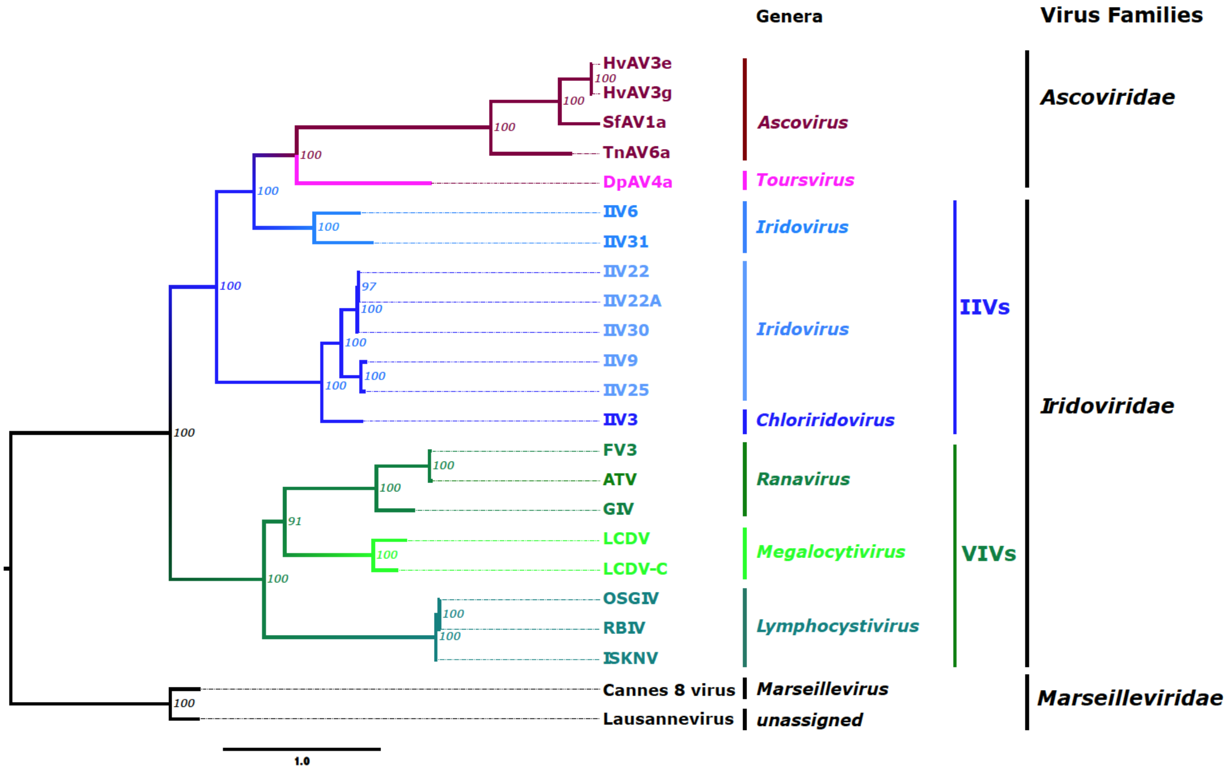

Fig. l. Phylogenetic tree obtained with nine core proteins shared by the *Ascoviridae*, *Iridoviridae* and *Marseilleviridae*. The tree was calculated using Mafft or Muscle alignments curated with Gblock (parameters were: -t=p -e=-gb1 -b2=N -b3=40 -b4=2 -b5=a -v=120), except for the RNAse III orthologues, for which the complete sequence alignment was used. Alignments were concatenated and trees based on maximum likelihood were calculated with PhyML. Parameters used were WAG (substitution matrix), 0 (proportion of invariable sites), 7 in a, and 5 in f (number of relative substitution rate categories), and F (substitution model). The protein substitution model, the proportion of invariable sites, the number of relative substitution, number of rate categories and substitution model for ML trees were selected and evaluated by ProtTEST 3. The best model was chosen on the basis of the Akaike Information Criterion. Numbers in italics at nodes indicate bootstrap values (%) retrieved from 1000 replicates. Branch lengths were proportional to genetic distances. The taxonomic levels from the genera to the families are indicated in the right margin.

4 - Depending on its wasp host, DpAV-4a can behave as a mutualist virus, like in the wasp *Diadromus pulchellus*, or as a pathogen, like in the leek-moth *Acrolepiopsis assectella* and the wasp *Ictoplectis tunetana*. However, mutualistic association of the other ascoviruses with parasitoids has not been recorded. In fact, they all kill the lepidopteran host as well as the developing parasitoid egg.

Relationship of iridoviruses and ascoviruses and where DpAV-4a fits

Based on phylogenetic studies (e.g. Fig. 1, and Piégu et al., 2015), ascoviruses and invertebrate iridoviruses share a common ancestor. However, considering their genomics and biology (capsid shape, genome configuration, genome size, cytopathology, vectorisation mode), separation of the two families appears reasonable. Otherwise, one could similarly consider merging marseilleviruses and pithoviruses with iridoviruses (the question might be: are they iridoviruses of amoebae and algae, respectively?). Nevertheless, this aspect requires ongoing discussions between the two SGs and perhaps requires more phylogenetic studies.

As indicated above, DpAV-4a is equally distant from some invertebrate iridoviruses (IIV6 and IIV31) and the other members of the genus *Ascovirus*. However, it is clearly monophyletic with the ascoviruses. In addition, DpAV-4a shares more biological and genomic features with ascoviruses than invertebrate iridoviruses.