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

Code assigned:	***2011.008a-dV***	(to be completed by ICTV officers)
Short title: Two new species and one new genus (*Tibrovirus*) in the family *Rhabdoviridae*		
Modules attached	**1** ☒ **2** ☒ **3** ☒ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☒	

Author(s) with e-mail address(es) of the proposer:

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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)	Rhabdoviridae Study Group

ICTV-EC or Study Group comments and response of the proposer:

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

MODULE 2: **NEW SPECIES**

Code	***2011.008aV***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Tibrovirus* (new)**
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Tibrogargan virus	GQ294472
Coastal plains virus	GQ294473

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

Tibrogargan virus (TIBV) and Coastal Plains virus (CPV) are members of the *Rhabdoviridae* by morhopology, general genome organization, and phylogenetic analysis of the sequence of each of the structural proteins (N, P, M, G and L). The available information is sufficient to establish two new species but several unique characteristics do not allow assignment of these viruses into any of the existing genera.

TIBV was initially isolated in 1976 from a pool of biting midges (*Culicoides brevitarsis*) in Queensland, Australia, and later from the blood of a healthy bovine (4). CPV was isolated in 1981 from the blood of a healthy steer in the Northern Territory (3). Neutralizing antibodies to each virus have been detected in a high proportion of tested cattle and water buffalo from northern Australia.

TIBV and CPV cross-react strongly in immunofluorescence and complement-fixation tests but they are distinct by neutralization test with a low level of cross-neutralization (3). TIBV also cross-reacts strongly in complementation tests and neutralization tests with Bivens Arm virus (BAV) that was isolated from *Culicoides insignis* in Florida, USA, and also infects cattle and water buffalo (5, 8). The antigenic relationship between TIBV and BAV suggests they may represent different species but genome sequence analysis (not yet available for BAV) would be necessary to clarify the taxonomic status of BAV.

The complete genomes sequences of TIBV (13,298 nt) and CPV (13,203 nt) have been reported (6). The genome organizations are very similar, containing 8 ORFs in the order 3'-N-P-M-U1-U2-G-U3-L-5' (Fig. 1), where N, P, M, G and L are the common rhabdovirus nucleoprotein, phosphoprotein, matrix protein, glycoprotein and polymerase protein genes. Small alternative ORFs also occur in each virus but in different genes. In TIBV, a small ORF (U4) overlaps the G gene; in CPV a small ORF overlaps the P gene (P'). The organization of these genomes is distinct from all other rhabdoviruses.

Amino acid identity of proteins encoded in the major ORFs are: N, 67%; P, 41%; M, 40%; U1, 29%; U2, 35%; G, 56%; U3, 19%; L, 55%. The proteins encoded in the novel ORFs (U1-U4) share no significant sequence identity with any other known proteins.

MODULE 3: **NEW GENUS**

Code	***2011.008bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

naming a new genus

Code	***2011.008cV***	(assigned by ICTV officers)

To name the new genus: *Tibrovirus*

Code	***2011.008dV***	(assigned by ICTV officers)

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

Tibrogargan virus

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:

Phylogenetic analysis using a segment of the L protein (1) or the complete sequences of the N and G and L proteins (Figs. 2-4) indicates that the genus *Tibrovirus* represent a distinct lineage amongst viruses which are associated with hematophagous insects, mammals and birds. The most closely related lineages are viruses in the genus *Ephemerovirus* and the Hart Park serogroup comprising Flanders virus and the two unassigned species *Ngaingan virus* and *Wongabel virus*. However, the tibrovirus lineage is deeply rooted in the tree and the genome organization is very distinct. Tibroviruses do not contain a second glycoprotein gene (G_{NS}) as occurs in the ephemeroviruses and Ngaingain virus; nor do they contain additional ORFs between P and M genes as occurs in the Hart Park serogroup viruses. Tibroviruses cross-react strongly in complement-fixation tests but react very weakly or not at all with other rhabdoviruses (2, 7).

The genus *Tibrovirus* therefore comprises arthropod-borne rhabdoviruses that are closely related antigenically, primarily infect cattle and water buffalo, and are transmitted by *Culicoides* species midges. The species form a distinct genetic lineage of viruses with a unique genome organization that features small ORFs preceding and following the G gene.

Origin of the new genus name:

The genus is named as a derivative of the name of the type species *Tibrogargan virus*

Reasons to justify the choice of type species:

Tibrogargan virus was the first of the two viruses to be isolated. There is a similar amount of genetic, morphological and epidemiological data available on each of the species.

Species demarcation criteria in the new genus:

The species demarcation criteria are based on low-level or no cross-reaction in virus-neutralisation tests supported by phylogenetic analysis and genetic diversity estimations using L and N gene sequences to establish that the species represents a distinct lineage. Typically, there will be <5% amino acid sequence diversity within species and >20% diversity between species.

References:

1. **Bourhy, H., J. A. Cowley, F. Larrous, E. C. Holmes, and P. J. Walker.** 2005. Phylogenetic relationships among rhabdoviruses inferred using the L polymerase gene. Journal of General Virology **86:**2849-2858.
2. **Calisher, C. H., N. Karabatsos, H. Zeller, J.-P. Digoutte, R. B. Tesh, R. E. Shope, A. P. A. Travassos da Rosa, and T. D. St. George.** 1989. Antigenic relationships among rhabdoviruses from vertebrates and hematophagous arthropods. Intervirology **30:**241-257.
3. **Cybinski, D. H., and G. P. Gard.** 1986. Isolation of a new rhabdovirus in Australia related to Tibrogargan virus. Australian Journal of Biological Sciences **39:**225-232.
4. **Cybinski, D. H., T. D. St. George, H. A. Standfast, and A. McGregor.** 1980. Isolation of Tibrogargan virus, a new Australian rhabdovirus, from *Culicoides brevitarsis*. Veterinary Microbiology **5:**301-308.
5. **Gibbs, E. P. J., C. H. Calisher, R. B. Tesh, J. S. Lazuick, R. Bowen, and E. C. Greiner.** 1989. Bivens Arm virus: A new rhabdovirus isolated from Culicoides insignis in Florida and related to Tibrogargan virus of Australia. Veterinary Microbiology **19:**141-150.
6. **Gubala, A., S. Davis, R. Weir, L. Melville, C. Cowled, and D. Boyle.** 2011. Tibrogargan and Coastal Plains rhabdoviruses: genomic characterisation, evolution of novel genes and seroprevalence in Australian livestock. Journal of General Virology doi:10.1099/vir.0.026120-0.
7. **Tesh, R. B., A. P. A. Travassos da Rosa, and J. S. Travassos da Rosa.** 1983. Antigenic relationship among rhabdoviruses infecting terrestrial vertebrates. Journal of General Virology **64:**169-176.
8. **Tuekam, T., E. C. Greiner, and E. P. J. Gibbs.** 1991. Seroepidemiology of Bivens Arm virus infections of cattle in Florida, St Croix and Puerto Rico. Veterinary Microbiology **28:**121-127.

Annex:

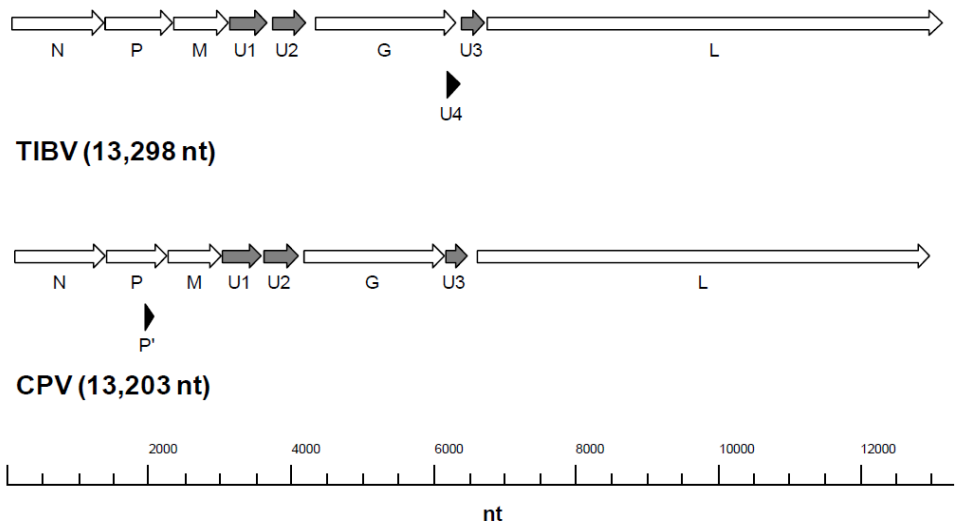

Figure 1. TIBV and CPV genome organization (from Gubala *et al.*,2011)

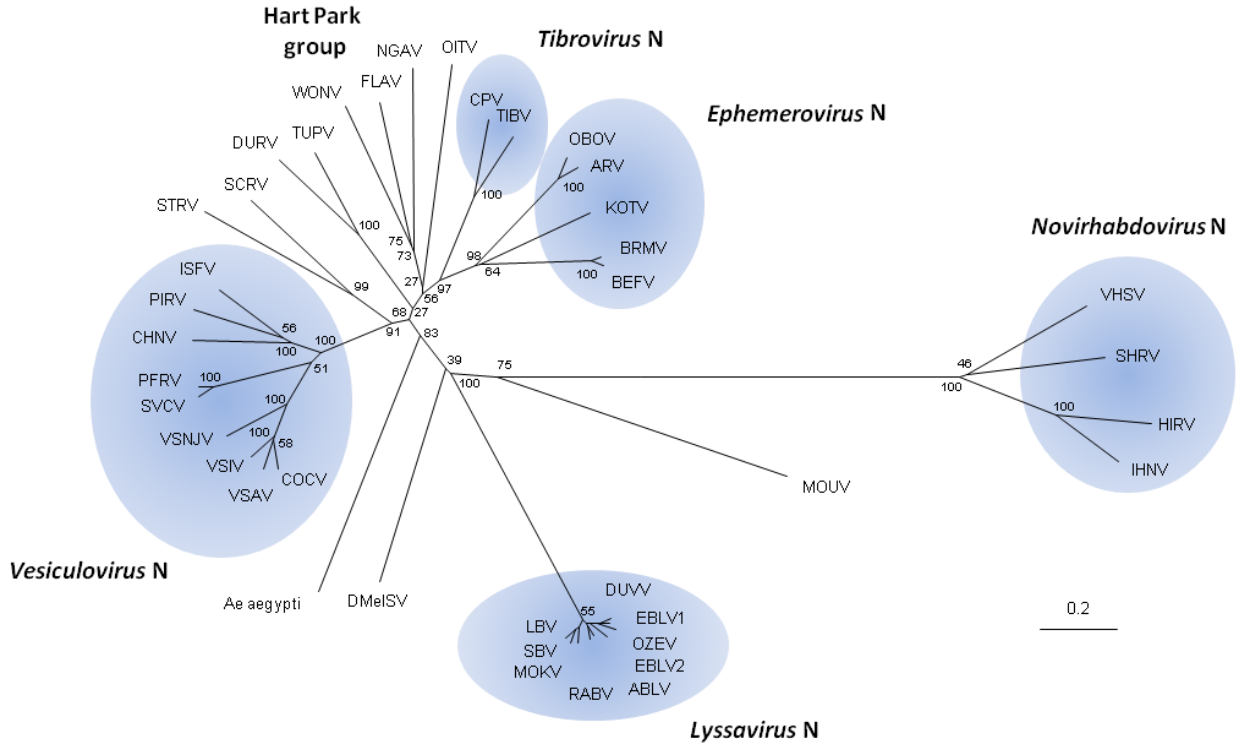

Figure 2. Phylogenetic relationship of animal rhabdovirus N protein complete amino acid sequences. The tree was generated in Mega 4.0 by the neighbour-joining method from a ClustalW multiple sequence alignment using default parameters. Branch lengths are proportional to the genetic distance between the sequences. Bootstrap values are expressed as a percentage of 1000 replicates.

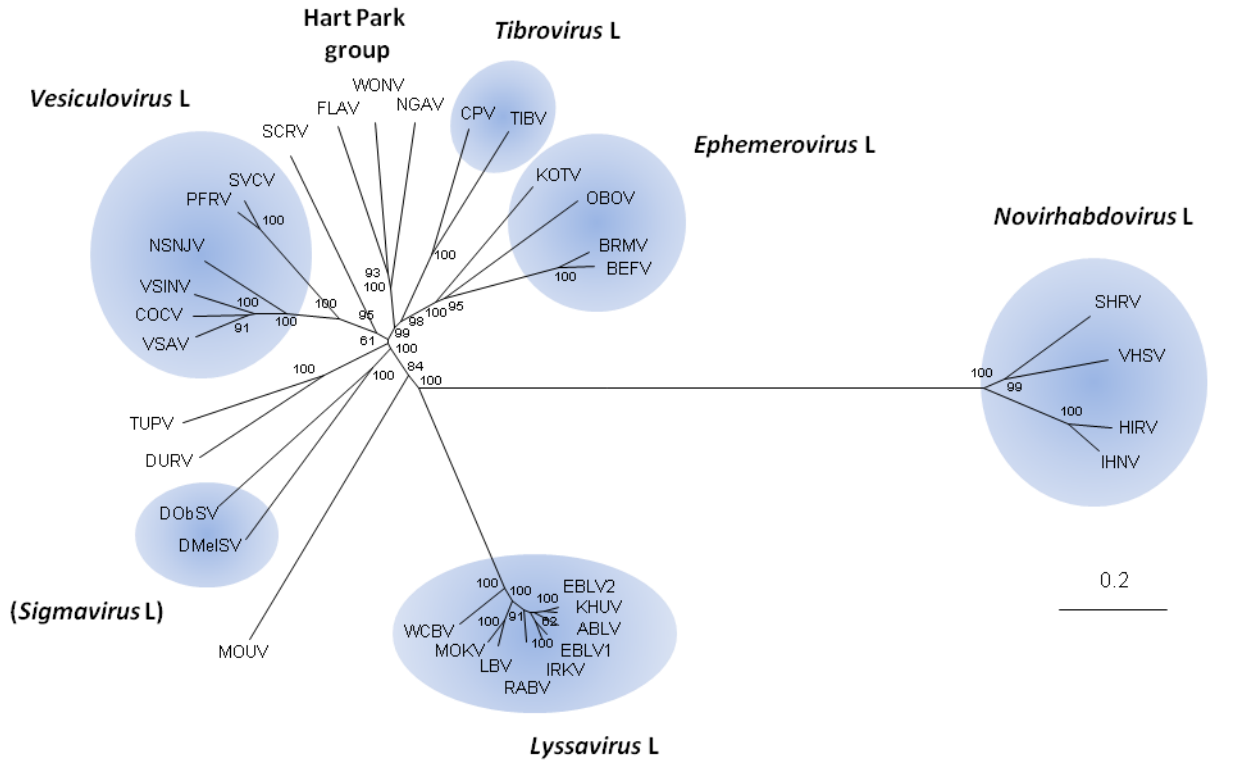

Figure 3. Phylogenetic relationship of animal rhabdovirus L protein complete amino acid sequences. The tree was generated in Mega 4.0 by the neighbour-joining method from a ClustalW multiple sequence alignment using default parameters. Branch lengths are proportional to the genetic distance between the sequences. Bootstrap values are expressed as a percentage of 1000 replicates.

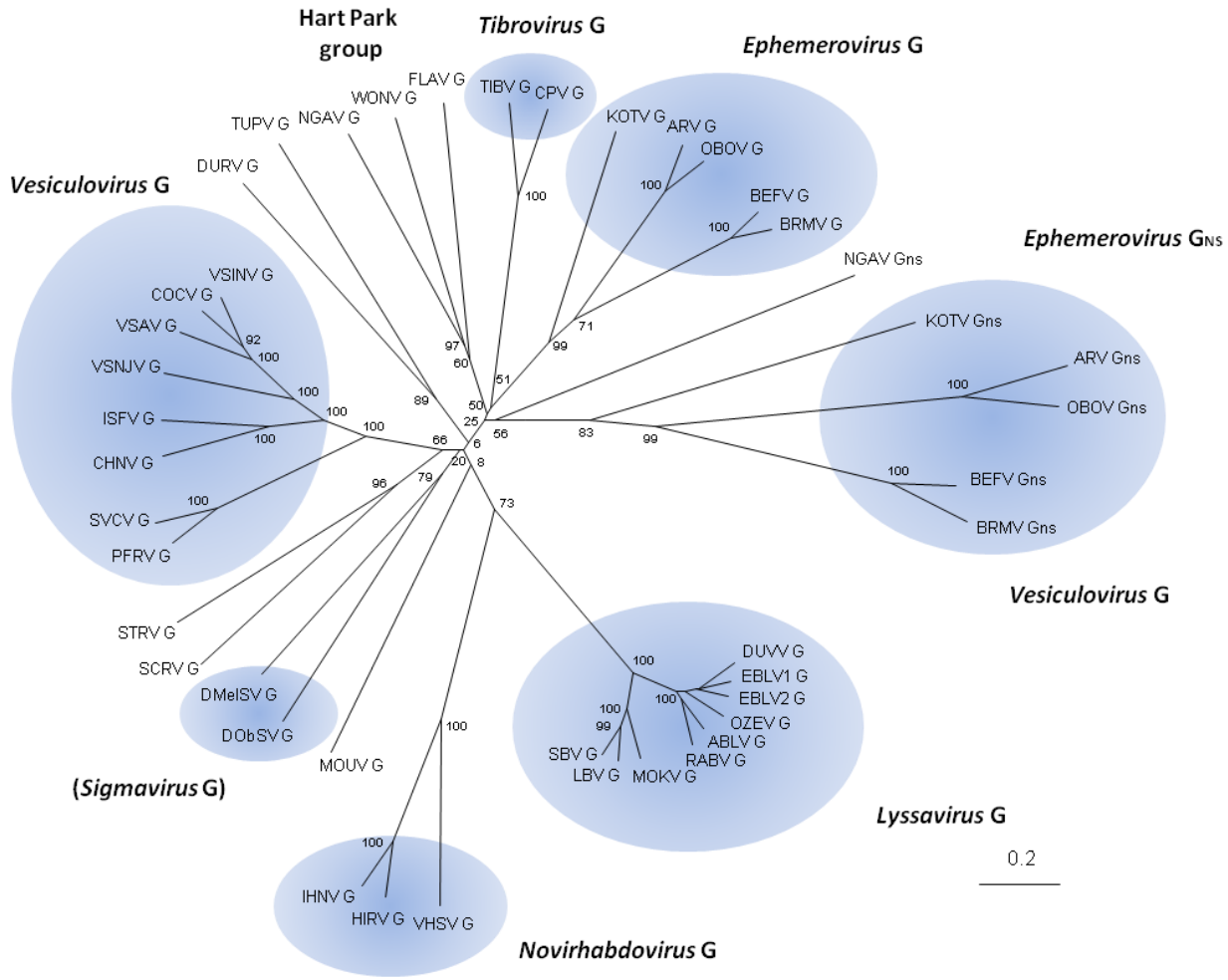

Figure 4. Phylogenetic replationship of animal rhabdovirus G and G_{NS} protein complete amino acid sequences. The tree was generated in Mega 4.0 by the neighbour-joining method from a ClustalW multiple sequence alignment using default parameters. Branch lengths are proportional to the genetic distance between the sequences. Bootstrap values are expressed as a percentage of 1000 replicates.