This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.078-080B***	(to be completed by ICTV officers)

Short title: Reclassification of the Family Microviridae
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐	**2** ☐	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐			

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

Bentley Fane bfane@email.arizona.edu

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

NEW SUBFAMILY

(If more than one subfamily is to be created, please complete additional copies of this module)

Code	***2008.078B***	(assigned by ICTV officers)

To create a new Subfamily assigned as follows:

Family:	***Microviridae***
Order:	***unassigned***

Code	***2008.079B***	(assigned by ICTV officers)

To name the new Subfamily: *Gokushovirinae*

Code	***2008.080B***	(assigned by ICTV officers)

To assign the following genera to the new subfamily:
Bdellomicrovirus, Spiromicrovirus, Chlamydiamicrovirus.

Code		(assigned by ICTV officers)

To assign the following species to be unassigned in the new subfamily (i.e. within the subfamily but not assigned to any genus):

Argument to justify the creation of a new Subfamily:

Structural and evolutionary studies conducted with members of the Bdellomicroviruses, Chlamydiamicroviruses, and Spiromicroviruses demonstrate that members of these three genera share common properties that are different from the øX174 group (*Microvirus*). Members of these three genera are missing the pentameric spikes at the 5-fold axes of symmetry, which are encoded by *Microvirus* G genes (2, 5). In agreement with this, these phages have no G gene homolog (1, 4, 6, 7). Members of the proposed *Gokushovirinae* have a "mushroom-like" protrusion at the 3-fold axes of symmetry, absent from *Microviruses*, encoded by an extra domain in the major capsid gene(2). Capsid assembly occurs without the help of an external scaffolding protein (1, 4, 7), and accordingly these phages are missing the external scaffolding gene (gene D in øX174). Due to the absence of gene G and D homologs, the proposed *Gokushoviruses* have genomes that are about 20% smaller than those of the
Microviruses.

Phylogenetic analyses have been conducted with four proteins common to all members of the *Microviridae*. The results of this analysis were published in the VIII Report of the International Committee on Taxonomy of Viruses, and are reproduced in the annex (3). Regardless of the protein used in these studies, the trees split the

Argument to justify the creation of a new Subfamily:

family members into two deep branches, which support the formation of two subfamilies: *Gokushovirinae* and *Microvirina*e.

Origin of the new Subfamily name:

Japanese for very small, to account for their genomes being small than the Microviruses (Micro: Greek for small).

References:

1. Brentlinger K., Hafenstein, S., Novak, C. R., Fane, B. A., Birgon, R., McKenna, R., and Agbandje-McKenna, M. (2002). *Microviridae*, a family divided. Isolation, characterization and genome sequence of a øMH2K, a bacteriophage of the obligate intracellular parasitic bacterium *Bdellovibrio bacteriovorus*. *J. Bacteriol.* **184,** 1089-1094.

2. Chipman, P..R., Agbandje-McKenna, M., Renaudin, J., Baker, T. S., and McKenna, R. (1998). Structural analysis of the Spiroplasma virus, SpV4, implications for evolutionary variation to obtain host diversity among the Microviridae. *Structure* **6,** 135-45.

3. Fane, B. A. (2006) The Microviridae. In: *Virus Taxonomy: The Classification and Nomenclature of Viruses. The Eighth Report of the International Committee on Taxonomy of Viruses* . Eds: A. Ball, C. Fauquet, M. Mayo, J. Maniloff. Academic Press / Elsevier.

4. Liu, B. L., J. S. Everson, B. A. Fane, P. Giannikopoulou, E. Vretou, P. R. Lambden, and I. N. Clarke. 2000. The molecular characterization of a bacteriophage (Chp2) from *Chlamydia psittaci*. *J. Virol.* **74,** 3646 -9.

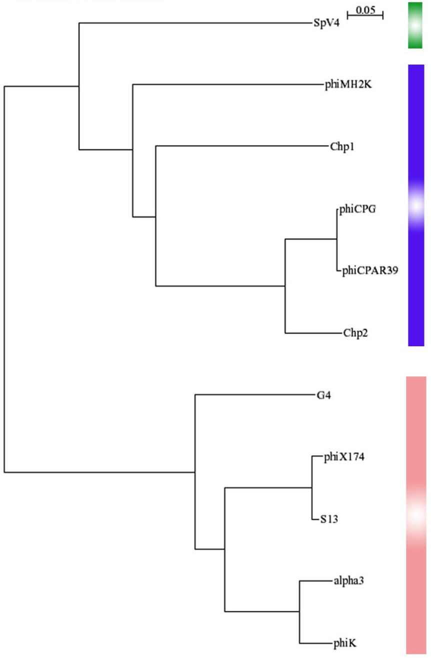
5. McKenna, R. Ilag, L. L., and Rossmann, M. G. (1994). Analysis of the single-stranded DNA bacteriophage øX174 at a resolution of 3.0 A. *J. Mol. Biol.* **237,** 517-543.

6. Renaudin, J., Paracel, M. C., and Bove, J. M. (1987). Spiroplasma virus 4: nucleotide sequence of the viral DNA, regulatory signals and the proposed genome organization. *J. Bacteriol.* **169,** 4950-4961.

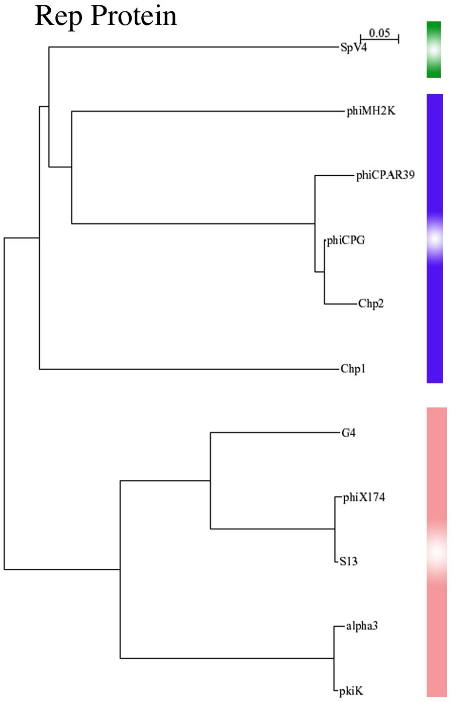
7. Storey, C. C., Lusher, M., and Richmond, S. J. (1989). Analysis of the complete nucleotide sequence of Chp1, a phage which infects *Chlamydia psittaci*. J. Gen. Virol. **70,** 3381-3390.

Annexes: Phylogenetic analyses of Microvirus coat proteins, reproduced from in the VIII Report of the International Committee on Taxonomy of Viruses.

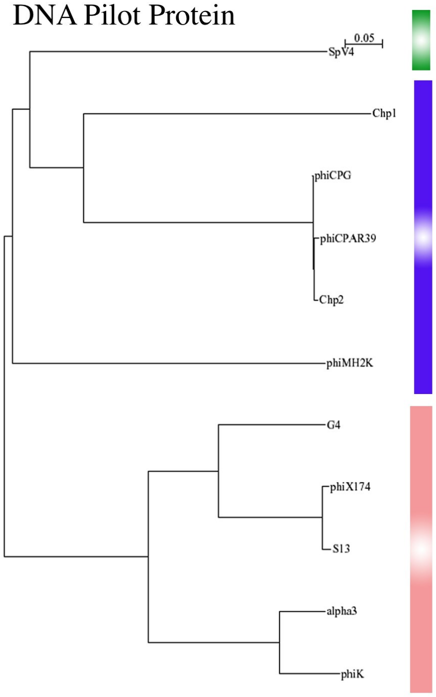
Coat Protein



Rep Protein



DNA Pilot Protein



Internal Scaffolding Protein