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:** | ***2012.008aP*** | (to be completed by ICTV officers) |

**Short title:** create a new species in the genus *Nanovirus*
(e.g. 6 new species in the genus *Zetavirus*)

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

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

J E Thomas; j.thomas2@uq.edu.au, HJ Vetten (heinrich-josef.vetten@jki.bund.de ), on behalf of the Nanoviridae Study Group

**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) | Nanoviridae 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**

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 | ***2012.008aP*** | (assigned by ICTV officers) |
|---|---|---|

**To create 1 new species within:**

| | |
|---|---|
| Genus: | ***Nanovirus*** |
| Subfamily: | |
| Family: | ***Nanoviridae*** |
| 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.

| **And name the new species:** | **GenBank sequence accession number(s) of reference isolate:** |
|---|---|
| *Faba bean yellow leaf virus* | European Nucleotide Archive accession numbers HE654123 to HE654130 |

**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

Criteria used as guidelines for species demarcation in the 9th report [1] are:

- Differences in natural host range
- Differences in the number and types of vector aphid species
- Different reactions to antibodies to individual species
- Differences in CP aa sequences of >15%, and/or
- Overall nt sequence identity of <75% is generally indicative of a distinct species.

The report states that:
"Since several nanovirids are now known to have overlapping host ranges and to be transmitted by a similar range of aphid species, biological criteria appear no longer useful for species discrimination within a genus. Although species-specific monoclonal antibodies (where available) can be used for species discrimination, preference should nowadays be given to the molecular criteria specified above."

A genetically distinct and hitherto undescribed nanovirus has recently been described from the Gedeo region of southern Ethiopia [2]. The molecular properties of this virus were obtained from a single isolate (Eth-231). The virus, for which the name Faba bean yellow leaf virus (FBYLV) is proposed, has a genome consisting of eight circular, single-stranded DNA components, ranging in size from 972-1002 nt, and with a total genome size of 7935 nt. All eight DNAs appear to be structurally similar to nanoviruses in having a common stem loop sequence and one major open reading frame (ORF) that potentially encodes one of the eight distinct nanovirus proteins.

The overall genome sequence shares 66.4 – 72.8% identity with other nanoviruses (Table 1) and the various components are most closely related phylogenetically to *Milk vetch dwarf virus* (MDV), *Faba*

*bean necrotic yellows virus* (FBNYV) and *Faba bean necrotic stunt virus* (FBNSV, Fig. 1). The stem-loop structure differs from that of other nanoviruses (FBNYV, FBNSV, MVD), in the length and sequence of the stem. In addition, the common sequence motifs flanking the stem loop, which are proposed to act as binding sites for the M-Rep protein, are also somewhat different in DNA-N and -S as compared with those of FBNYV, FBNSV, and MDV. The LXCXE motif, which invariably occurs in the Clink protein of all other members of the family is absent from the deduced amino acid sequence from the DNA-C.

FBYLV (four isolates tested) has an epitope profile distinct from FBNYV and FBNSV, when tested against a panel of seven monoclonal antibodies to nanoviruses.

Although FBYLV shares CP amino acid sequence identities of 87.2% and 88.4% with FBNSV and FBNYV, respectively, and thus does not fully meet the second molecular criterion for nanovirus species demarcation ([1], differences of >15% in CP aa sequences), all other data presented provide compelling evidence for considering FBYLV a distinct nanovirus species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

## References:


[1] Vetten, H.J., Dale, J.L., Grigoras, I, Gronenborn, B., Harding, R., Randles, J.W., Sano, Y., Thomas, J.E., Timchenko, T. and Yeh, H.-H. 2011. Family *Nanoviridae*, pp. 395-404. In: King, A.M.Q., Adams, M.J., Carstens, E.C, and Lefkowitz, E.J. (eds). Virus Taxonomy, Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier/Academic Press, London.

[2] Abraham, A. D., Varrelmann, M., and Vetten, H. J. (2012). Three distinct nanoviruses, one of which represents a new species, infect faba bean in Ethiopia. Plant Disease. 96:1045-1053.


## 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.

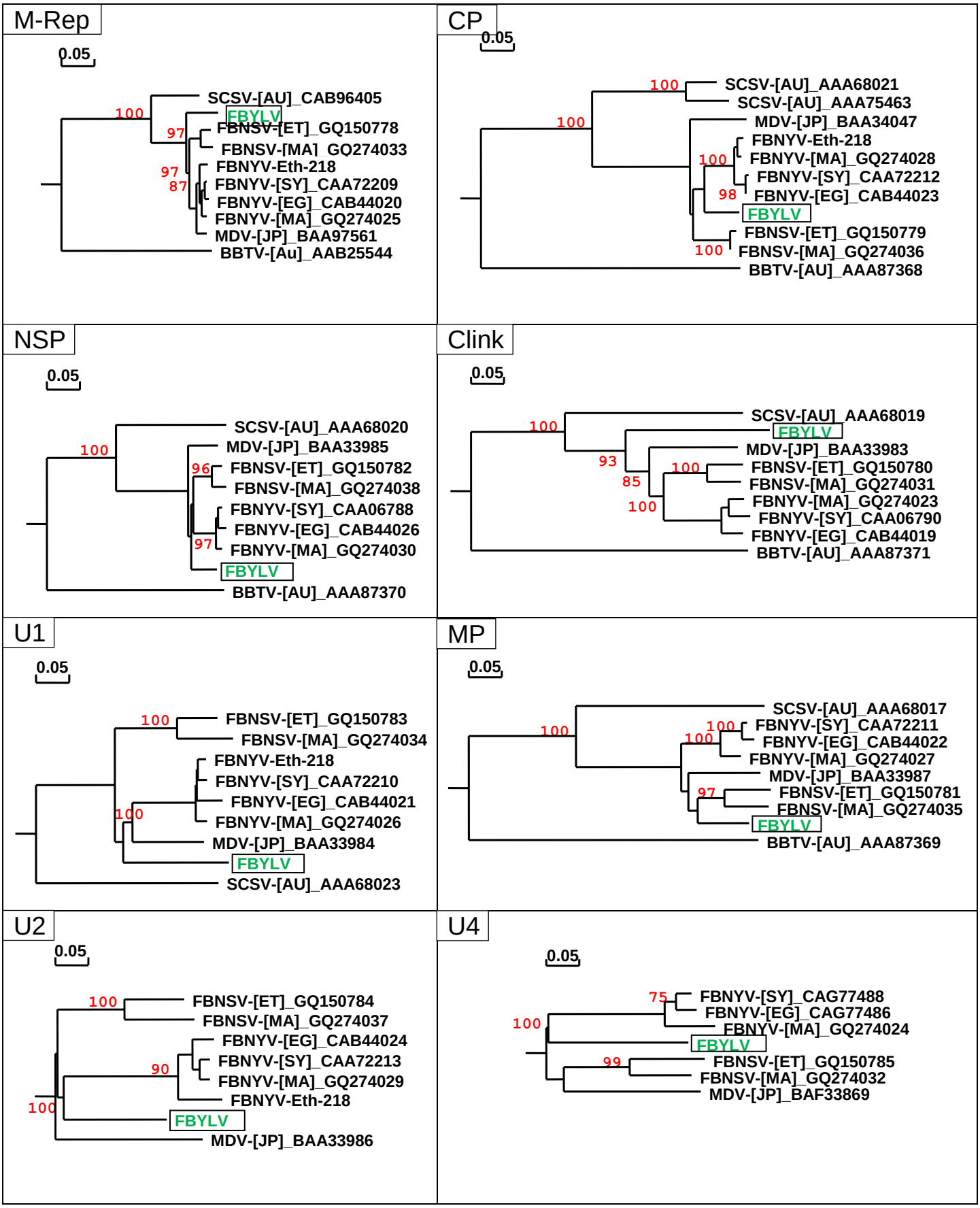
**Table 1.** Total nucleotide and amino acid (coding) sequence identities between homologous DNAs of Eth-FBYLV and other members of the family *Nanoviridae*

| | DNA components[a] | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | R | | S | | M | | C | | N | | U1 | | U2 | | U4 | | Mean | |
| Virus[b] | nt | aa | nt | aa | nt | aa | nt | aa | nt | aa | nt | aa | nt | aa | nt | aa | nt | aa |
| FBNSV-Eth | 87.5 | 90.9 | 75.3 | 87.2 | 68.4 | 81.3 | 70.0 | 60.4 | 75.8 | 91.5 | 70.0 | 65.6 | 60.1 | 65.3 | 62.4 | 54.7 | 70.4 | 74.6 |
| FBNYV-Eg | 88.2 | 90.9 | 78.0 | 88.4 | 64.8 | 80.4 | 70.3 | 58.0 | 75.8 | 89.5 | 69.0 | 65.6 | 58.6 | 61.2 | 57.4 | 55.2 | 70.4 | 73.6 |
| MDV-Jp | 86.6 | 92.0 | 78.4 | 82.6 | 65.3 | 79.5 | 73.8 | 59.2 | 76.5 | 90.8 | 71.3 | 68.7 | 69.7 | 60.3 | 60.8 | 50.9 | 72.8 | 73.0 |
| SCSV-Au | 77.7 | 82.2 | 63.8 | 56.7 | 62.5 | 45.0 | 59.5 | 40.5 | 63.9 | 68.0 | 58.8 | 37.0 | - | - | - | - | 64.4 | 54.9 |
| BBTV-Au | 56.9 | 53.1 | 48.4 | 17.4 | 49.7 | 17.6 | 52.7 | 17.0 | 55.5 | 44.1 | - | - | - | - | - | - | - | - |

a Nucleotides (nt) and amino acids (aa); – indicates that a comparison was not possible due to the fact that a homologous DNA component has not yet been identified for the other nanovirus.

b *Faba bean necrotic stunt virus* (FBNSV) from Holetta, Ethiopia (Eth); *Faba bean necrotic yellows virus* (FBNYV) from Egypt (Eg); *Milk vetch dwarf virus* (MDV) from Japan (Jp); and *Subterranean clover stunt virus* (SCSV) and *Banana bunchy top virus* (BBTV) from Australia (Au).

**Fig. 1.** Neighbor-joining dendrograms illustrating the amino acid sequence relationships in the master replication (M-Rep), capsid (CP), cell-cycle link (Clink), movement (MP), nuclear shuttle (NSP), U1, U2, and U4 proteins encoded by the eight DNAs of Eth-231 and, in the M-Rep, CP, U1, and U2 proteins encoded by the four DNAs of Eth-218 with the homologous proteins of *Banana bunchy top virus* (BBTV), *Faba bean necrotic yellows virus* (FBNYV), *Faba bean necrotic stunt virus* (FBNSV), *Milk vetch dwarf virus* (MDV), and *Subterranean clover stunt virus* (SCSV). Because sequence information is available for genetically distinct isolates of some nanovirus species, the sequences of FBNYV isolates from Egypt (EG), Syria (SY), and Morocco (MA) and FBNSV isolates from Ethiopia (ET) and Morocco (MA) were included in the comparison. Vertical branch lengths are arbitrary and horizontal distances are proportional to the number of base substitutions per site (see scale bar). Sequence alignments and dendrograms were produced using DNAMAN (version 6, Lynnon Biosoft, Quebec, Canada) which uses a CLUSTAL-type algorithm. Dendrograms were bootstrapped 1,000 times (scores are shown at nodes).


M-Rep
0.05
SCSV-[AU]_CAB96405
FBYLV
FBNSV-[ET]_GQ150778
FBNSV-[MA]_GQ274033
FBNYV-Eth-218
FBNYV-[SY]_CAA72209
FBNYV-[EG]_CAB44020
FBNYV-[MA]_GQ274025
MDV-[JP]_BAA97561
BBTV-[Au]_AAB25544
100
97
97
87
CP
0.05
SCSV-[AU]_AAA68021
SCSV-[AU]_AAA75463
MDV-[JP]_BAA34047
FBNYV-Eth-218
FBNYV-[MA]_GQ274028
FBNYV-[SY]_CAA72212
FBNYV-[EG]_CAB44023
FBYLV
FBNSV-[ET]_GQ150779
FBNSV-[MA]_GQ274036
BBTV-[AU]_AAA87368
100
100
100
98
100
NSP
0.05
SCSV-[AU]_AAA68020
MDV-[JP]_BAA33985
FBNSV-[ET]_GQ150782
FBNSV-[MA]_GQ274038
FBNYV-[SY]_CAA06788
FBNYV-[EG]_CAB44026
FBNYV-[MA]_GQ274030
FBYLV
BBTV-[AU]_AAA87370
100
96
97
Clink
0.05
SCSV-[AU]_AAA68019
FBYLV
MDV-[JP]_BAA33983
FBNSV-[ET]_GQ150780
FBNSV-[MA]_GQ274031
FBNYV-[MA]_GQ274023
FBNYV-[SY]_CAA06790
FBNYV-[EG]_CAB44019
BBTV-[AU]_AAA87371
100
93
85
100
100
U1
0.05
FBNSV-[ET]_GQ150783
FBNSV-[MA]_GQ274034
FBNYV-Eth-218
FBNYV-[SY]_CAA72210
FBNYV-[EG]_CAB44021
FBNYV-[MA]_GQ274026
MDV-[JP]_BAA33984
FBYLV
SCSV-[AU]_AAA68023
100
100
MP
0.05
SCSV-[AU]_AAA68017
FBNYV-[SY]_CAA72211
FBNYV-[EG]_CAB44022
FBNYV-[MA]_GQ274027
MDV-[JP]_BAA33987
FBNSV-[ET]_GQ150781
FBNSV-[MA]_GQ274035
FBYLV
BBTV-[AU]_AAA87369
100
100
100
97
U2
0.05
FBNSV-[ET]_GQ150784
FBNSV-[MA]_GQ274037
FBNYV-[EG]_CAB44024
FBNYV-[SY]_CAA72213
FBNYV-[MA]_GQ274029
FBNYV-Eth-218
FBYLV
MDV-[JP]_BAA33986
100
90
100
U4
0.05
FBNYV-[SY]_CAG77488
FBNYV-[EG]_CAG77486
FBNYV-[MA]_GQ274024
FBYLV
FBNSV-[ET]_GQ150785
FBNSV-[MA]_GQ274032
MDV-[JP]_BAF33869
75
100
99