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:** | ***2015.023aP*** | (to be completed by ICTV officers) |

**Short title:** create *Blueberry mosaic associated virus* as a distinct species in the genus *Ophiovirus*
(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):**

I.E. Tzanetakis

**Corresponding author with e-mail address:**

E-mail: itzaneta@uark.edu

**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) | *Ophioviridae* study group |

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

The Ophioviridae study group members have seen and discussed the proposal and fully agree with the proposal to create blueberry mosaic associated virus as new taxonomic species in the genus Ophiovirus.

| | |
|---|---|
| Date first submitted to ICTV: | 4/1/2015 |
| Date of this revision (if different to above): | |

**ICTV-EC comments and response of the proposer:**

EC comment: Please correct figure to change Rhabdovirus to Rhabdoviridae (the genus Rhabdovirus does not exist).

Response: This was done

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 | ***2015.023aP*** | (assigned by ICTV officers) |

**To create 1 new species within:**

| | |
|---|---|
| Genus: | ***Ophiovirus*** |
| Subfamily: | |
| Family: | ***Ophioviridae*** |
| 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)** |
|---|---|---|
| *Blueberry mosaic associated virus* | Arkansas-5 | KJ704366-KJ704368 |

**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

Species demarcation criteria for the genus *Ophiovirus*:

(i) Amino acid sequence of coat protein differing by more than 15%

(ii) Differences in natural host range

(iii) Differences in CP size

(iv) Different number, organization and/or size of genome segments.

(v) No or distant serological relationship between CPs

Blueberry mosaic disease first reported in the 1950s in Michigan (Varney, 1957). Symptoms include mild to brilliant mottle and mosaic patterns on foliage. Mosaic has also been documented in several regions of North America including Arkansas, British Columbia, Indiana, Kentucky, New Jersey, New York, Oregon and Washington as well as several other parts of the globe including South America, Europe, New Zealand and South Africa (Martin et al., 2012; Thekke-Veetil et al., 2015). More than 60 isolates from North America and Slovenia have been studied (movement and nucleoprotein regions). Data suggest that virus populations are under stringent purification selection but there are indications of reassortments between RNAs 2 and 3 (Thekke-Veetil et al., 2015)

**Blueberry mosaic associated virus (BlMaV) belong to the *Ophioviridae* family**

(vi) Number of genome segments of the ophiovirus group can be 3 or 4. For BlMaV the number of genome segments is 3, the RNA4 has not been found. Nucleic acid: three molecules of negative sense ssRNA. RNA 1- 7963nt, RNA 2 – 1934 nt, RNA 3-1570nt (KJ704366.1, KJ704367.1, KJ704368.1 respectively)

(vii) . RNA1: p1: RNA-dependent RNA-polymerase: 272 kDa, p2: function unknown: 23 kDa; RNA 2: Putative Movement Protein: 58 kDa; RNA 3: Putative nucleocapsid protein: 50 KDa (all proteins are deduced using the genomic information; Thekke-Veetil et al., 2014).
(viii) Genome structure resembling that of members of the genus *Ophiovirus*.
(ix) Phylogenetic analysis using the RNA dependent RNA polymerase protein sequences BlMaV groups with members of the genus *Ophiovirus,* in trees constructed with RdRp sequences. The closest species is the type member of the genus, *Citrus psorosis virus*, (CPsV) with which BlMaV clusters in a distinct clade (see Annex; Thekke-Veetil et al., 2014)
(x) Mechanical transmission: Undetermined

The proposed species differs from all existing species in the following properties:
(xi) The size of the RNA segments and proteins differs from the other members of the genus. This meets species demarcation criterion No. 4.
(xii) At the amino acid level, BlMaV and CPsV did not show amino acid identities higher than 42% (RdRp; Thekke-Veetil et al., 2014) whereas the nucleoprotein identities are 35%. This meets species demarcation criterion No. 1.
(xiii) The narrow host range of BlMaV differs from the host ranges of other ophioviruses (demarcation criterion No. 2)

The above data support the notion that BlMaV is a distinct species in the genus *Ophiovirus*.

## MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

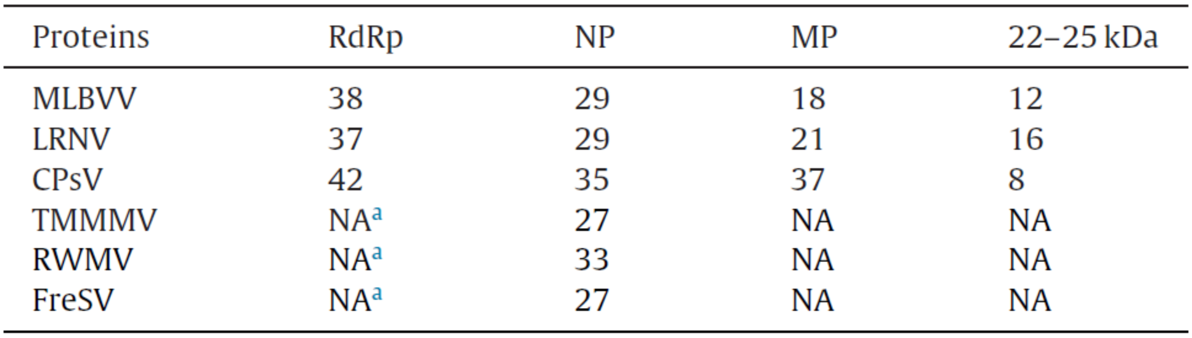
Martin, R.R., Polashock, J.J., Tzanetakis, I.E., 2012. New and emerging viruses of blueberry and cranberry. Viruses 4, 2831–2852.
Varney, E.H., 1957. Mosaic and shoestring virus diseases of cultivated blueberry in New Jersey. Phytopathology 47, 307–309.
Thekke-Veetil, T., Ho, T., Keller, K.E., Martin, R.R., Tzanetakis, I.E., 2014. A new ophiovirus is associated with blueberry mosaic disease. Virus Res. 189,92–96.
Thekke-Veetil, T., Polashock, J.J., Marn, M.V., Plesko, I.M., Schilder, A.C., Keller, K.E., Martin, R.R. and Tzanetakis, I.E. 2015. Population structure of blueberry mosaic associated virus: Evidence of reassortment in geographically distinct isolates. Virus Res. 201, 79-84

**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. Percentage (%) of amino acid identities of orthologous proteins of blueberry mosaic

associated virus and other members of the genus *Ophiovirus*. Abbreviations: CPsV – Citrus psorosis virus, FreSV – Freesia sneak virus, LRNV – Lettuce ring necrosis virus, MLBVV – Mirafiori lettuce big-vein virus, RWMV – Ranunculus white mottle virus, TMMMV – Tulip mild mottle mosaic virus (from Thekke-Veetil et al., 2014).



| Proteins | RdRp | NP | MP | 22–25 kDa |
|---|---|---|---|---|
| MLBVV | 38 | 29 | 18 | 12 |
| LRNV | 37 | 29 | 21 | 16 |
| CPsV | 42 | 35 | 37 | 8 |
| TMMMV | NA[a] | 27 | NA | NA |
| RWMV | NA[a] | 33 | NA | NA |
| FreSV | NA[a] | 27 | NA | NA |

RdRp – RNA-dependent RNA polymerase; NP – nucleocapsid protein; MP – movement protein; NA – Not available.

[a] Only partial sequence of the RdRp is available.

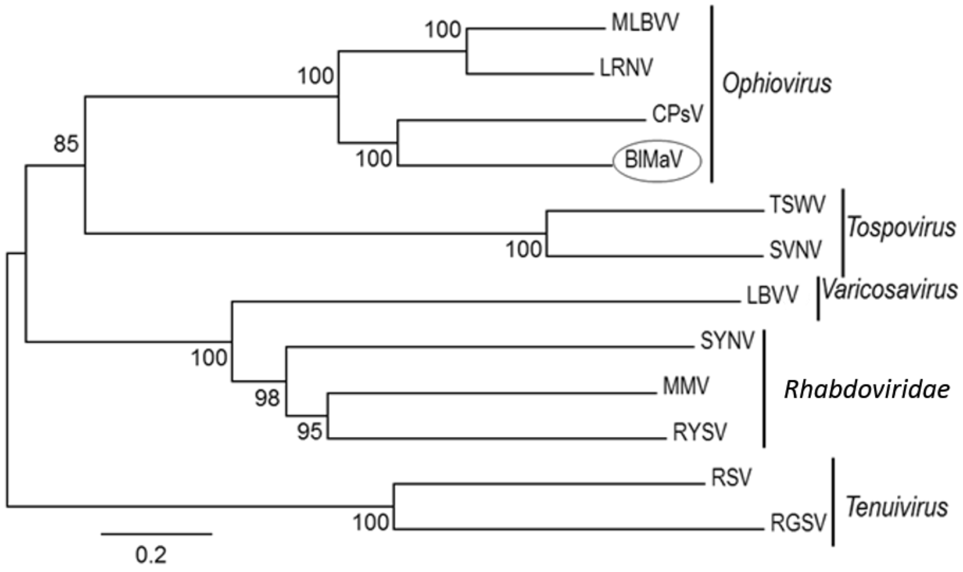


Fig. 1. Phylogenetic analysis using the RNA dependent RNA polymerase protein sequences of blueberry mosaic associated virus (BlMaV) and other negative-strand RNA viruses. Branch lengths are proportional to genetic distances between sequences. The tree was generated by the neighbor-joining method and bootstrap values (indicated for each branch node) were estimated using 1000 replicates. Branch lengths are proportional to genetic distances between sequences and the scale bar represents substitutions per amino acid site. LRNV – lettuce ring necrosis virus (Acc. No. YP 053236), MLBVV – Mirafiori lettuce big-vein virus (Acc. No. NP 848527), CPsV – Citrus psorosis virus (Acc.No. YP 089661), TSWV – Tomato spotted wilt virus (Acc. No. AEB33901.1), SVNV – Soybean vein necrosis virus (Acc. No. ADX01591), RGSV – Rice grassy stunt virus (Acc. No.NP 058528), RSV – Rice stripe virus (Acc. No. AFM93820), LBVaV – Lettuce big-vein associated virus (Acc. No. AFA36170), SYNV

– Sonchus yellow net virus (Acc. No. P31332), MMV –Maize mosaic virus (Acc. No. Q6E0W6), RYSV – Rice yellow stunt virus (Acc. No. O10378) (adapted from Thekke-Veetil et al., 2014).