This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

**Part 1:** **TITLE, AUTHORS, etc**

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| **Code assigned:** | ***2018.010P*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  ***Blackberry virus A*, a new species in the genus *Vitivirus*** | | | |
|  | | | |
| **Author(s):** | | | |
| Mohamed Hassan  Ioannis E. Tzanetakis | | | |
| **Corresponding author with e-mail address:** | | | |
| Ioannis E. Tzanetakis 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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | *Beta*-, *Gamma*-, and *Deltaflexiviridae* Study Group (Chair: Ioannis Tzanetakis) | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | May 24th 2018 |
| Date of this revision (if different to above): | | |  |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
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**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module: 2018.010P.N.v1.Vitivirus\_spa.xlsx** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. |

A double-stranded RNA-enriched fraction was extracted from symptomatic leaves of blackberry (cultivar Osage) collected in Arkansas (Hassan et al., 2018). cDNA was prepared from double-stranded RNAs and used as template for high throughput sequencing. The full genome of the new virus, named blackberry virus A (BVA), was obtained using overlapping PCRs followed by Sanger sequencing (GenBank accession No. MG254193). The BVA genome contains five open reading frames (ORFs) (**Figure 1**), encoding the viral replicase, a 20-kDa protein of unknown function, the movement, coat and nucleic acid-binding proteins, and has the characteristic organization of the genus *Vitivirus*. Phylogenetic analyses based on the complete replicase (**Figure 2**) or coat protein sequences (**Figure 3**) support the placement of BVA in the *Vitivirus* genus.

Pairwise comparisons of these taxonomically-relevant genes (replicase and coat protein) with recognized members of the genus showed identity levels below the species demarcation thresholds. In conclusion, based upon available data, we propose recognition of a new species in the genus *Vitivirus* named *Blackberry virus A,* represented by the isolate BVA-Osage.

The species demarcation criteria in the *Vitivirus* genus (Adams *et al*., 2012) are:

* Natural host range: Blackberry
* Serological specificity: N/A
* Epidemiology: vector species, N/A
* Differences in dsRNA patterns: N/A
* Less than about 72% nucleotide (nt) identity or 80% amino acid (aa) identity between their coat protein (CP) or polymerase genes: Comparison of the RdRp and CP gene products with homologs from sequenced vitiviruses indicates <46% aa identity for the replicase and <70% aa identity for the CP. Based on these data and the species demarcation criteria for vitiviruses, BVA represent a new member of the genus.

**Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance



**Figure 1.** Genome organization of blackberry virus A. Abbreviations: Mtr: methyltransferase; Hel: helicase; AlkB: 2OG-Fe(II) oxygenase domain; RdRp: RNA dependent RNA polymerase (replicase); MP: movement protein; CP: coat protein: NABP nucleic acid-binding protein. ORF2 encodes a hypothetical protein of unknown function.



**Figure 2.** Cladogram of the replicase of sequenced vitiviruses. Multiple sequence alignments were generated by Clustal W, and the unrooted cladograms were constructed using neighbor joining. The bootstrap consensus trees were inferred from 1,000 bootstrap pseudoreplicates and presented as percentage values. Blackberry virus A is highlighted with a red circle.

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**Figure 3.** Cladogram of the coat protein of sequenced vitiviruses. Multiple sequence alignments were generated by Clustal W, and the unrooted cladograms were constructed using neighbor joining. The bootstrap consensus trees were inferred from 1,000 bootstrap pseudoreplicates and presented as percentage values. Blackberry virus A is highlighted with a red circle.

| **References:** |
| --- |
| * Hassan M., Shahid M.S. and Tzanetakis I.E. Molecular characterization and detection of a novel vitivirus infecting blackberry. Archives of Virology, in press |