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:** | ***2018.014P*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  *Grapevine virus J*, a new species in the genus *Vitivirus* | | | |
|  | | | |
| **Author(s):** | | | |
| Alfredo Diaz-Lara, Deborah Golino, Maher Al Rwahnih | | | |
| **Corresponding author with e-mail address:** | | | |
| Maher Al Rwahnih, malrwahnih@ucdavis.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 14th 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:** 2018.014P.N.v1.Vitivirus\_spe.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:**

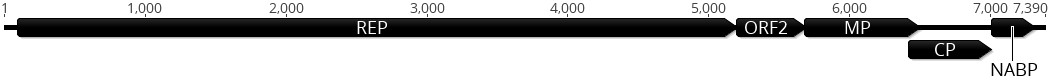
| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ 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 novel RNA virus was detected in grapevine (*Vitis vinifera*) cultivar ‘Kizil Sapak’ by high-throughput sequencing (HTS), and named grapevine virus J (GVJ) isolate KS (Diaz-Lara et al., 2018). The complete genome sequence of GVJ isolate KS is 7,379 nt long (GenBank: MG637048; Fig. 1) and is integrated by five putative open reading frames (ORFs) and 5’ and 3’ untranslated regions of 95 and 69 nt respectively. ORF1 encodes a polypeptide of 1,702 amino acids (aa) and comprises the following domains: viral methyltransferase; alkylation B (AlkB); viral RNA helicase; RNA-dependent RNA polymerase. A 20 kDa protein of unknown function is encoded by ORF2 (164 aa), which is typical of members of the genus *Vitivirus*. ORF3 corresponds to a movement protein (273 aa). A predicted coat protein (CP) was identified from ORF4 (197 aa). Finally, the 103 aa integrating the ORF5 are associated with a putative RNA binding protein present in vitiviruses. A full-length comparison with the NCBI database identified 75% identity (12% query coverage) with grapevine virus D (GVD).

Based on the genomic arrangement, sequence homology and phylogenetics (Fig. 2), the novel virus should be placed within the genus *Vitivirus*, subfamily *Trivirinae*, family *Betaflexiviridae*. Considering the current species demarcation criteria inside the genus *Vitivirus* (King et al., 2011), GVJ isolate KS represents a new species for which the name *Grapevine virus J* is proposed. The replicase gene of GVJ isolate KS shares less than 72% nt identity or 80% aa identity with those from other vitiviruses.

The criteria demarcating species in the genus *Vitivirus* are:

* The natural host range: Grapevine
* Serological specificity using discriminatory polyclonal and monoclonal antibodies: N/A
* Epidemiology: individual species or groups of species are transmitted by different types and species of vectors, N/A
* Differences in dsRNA pattern: N/A
* Less than about 72% nt identity (or 80% aa identity) between their CP or polymerase genes: The polymerase gene of GVJ shares less than 72% nt identity or 80% aa identity with other species in the genus *Vitivirus*. Based on this sequence, the closest relative of GVJ is the species *Grapevine virus D* (GVD), with 69% nt and 66% aa identities.
* **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 the KS isolate of grapevine virus J (GVJ). Five predicted open reading frames (ORFs) are: REP, replicase; ORF2, unknown function; MP, movement protein; CP, coat protein; NABP, nucleic acid binding protein.



**Figure 2.** Phylogenetic inference of grapevine virus J (GVJ) isolate KS in relation to members of the genus *Vitivirus*. Actinidia virus A (AcVA, JN427014); actinidia virus B (AcVB, NC\_016404); agave tequilana leaf virus (ATLV, NC\_034833); arracacha virus V (AVV, NC\_034264); grapevine Pinot gris virus (GPGV, NC\_015782); grapevine virus A (GVA, NC\_003604); grapevine virus B (GVB, NC\_003602); grapevine virus D (GVD, KX828708, Y15892); grapevine virus E (GVE, NC\_011106); grapevine virus F (GVF, NC\_018458); grapevine virus G (GVG, MF405923); grapevine virus H (GVH, MF521889); grapevine virus I (GVI, MF927925); grapevine virus K (GVK, NC\_035202); heracleum latent virus (HLV, X79270) and mint virus 2 (MV-2, AY913795). Neighbor-Joining tree based on the amino acid sequences of the replicase (a) and coat protein (b) using the Poisson model of substitution and 1,000 replicates. Horizontal branch length is proportional to genetic distance; the scale bars represent changes per site. Bootstrap values less than 50% are not shown. Position of GVJ is indicated with a red box.

| **References:** |
| --- |
| * King AM, Lefkowitz E, Adams MJ, Carstens EB (2011) Virus taxonomy: ninth report of the international committee on taxonomy of viruses. Elsevier, Amsterdam. * Diaz-Lara A, Golino D, Al Rwahnih M. Genomic characterization of grapevine virus J, a novel virus identified in grapevine. Archives of virology. 2018 Mar 7:1-3. |