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:** | ***2018.012P*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  ***Grapevine virus H*, a new species in the genus *Vitivirus*** | | | |
|  | | | |
| **Author(s):** | | | |
| Thierry Candresse  Armelle Marais | | | |
| **Corresponding author with e-mail address:** | | | |
| Thierry Candresse (thierry.candresse@inra.fr) | | | |
| **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:** | | | |
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|  | | | |
| Date first submitted to ICTV: | | | June 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: 2018.012P.N.v1.Vitivirus\_spc** |

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.   Illumina sequencing of cDNAs prepared from total RNAs extracted from phloem scrappings or double stranded RNAs purified from a grapevine (cv. unknown) collected in Portugal (Candresse et al., 2018) was performed. The authors have determined the complete genome sequence of an isolate (TT2016-3) of a novel virus named grapevine virus H (GVH) and discussed its phylogenetic relationships with other *Vitivirus* genus members.  The genome organization (**Figure 1**) places the GVH TT2016-3 isolate in the *Vitivirus* genus. The genome harbors five open reading frames (ORFs) as is typical for vitiviruses and, in particular, ORF2 encodes a ca. 20-kDa product which is characteristic of members of this genus. The putative product of ORF1 contains conserved motifs for a viral methyltransferase, a viral helicase and an RNA-dependent RNA polymerase. ORF3 encodes the movement protein (MP). ORF4 encodes the CP and ORF5 encodes a small protein with homologies to nucleic acid-binding proteins of *Betaflexiviridae* members.  Phylogenetic analyses based on the complete replicase (**Figure 2**) or the coat protein (**Figure 3**) amino acid sequences support the placement the TT2016-3 isolate in the *Vitivirus* genus.  In conclusion, the GVH TT2016-3 isolate has a typical *Vitivirus* genome organization and clear phylogenetic affinities with members of this genus but its divergence from all other sequenced *Vitivirus* genus members falls clearly outside of the species demarcation criteria. Its molecular properties, phylogeny and genetic distance from other viruses suggest that this virus is a member of a new *Vitivirus* species, for which the name *Grapevine virus H* is proposed.  The species demarcation criteria in the *Vitivirus* genus are: (Adams *et al*., 2012)   * Natural host range: Grapevine * 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 replicase (REP) and CP gene sequences and of the encoded proteins by GVH (isolate TT2016-3) with other sequenced *Vitivirus* members shows at best 54.4% nt sequence identity (50.9% aa sequence identity) for the REP gene and 65.0% nt identity (66.5% aa identity) for the CP gene, respectively. These values are clearly outside the species demarcation criteria.   **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 TT2016-3 isolate of grapevine virus H (GVH). The various open reading frames are indicated by rectangular boxes. REP, replicase; MP, movement protein; CP, capsid protein; NABP, nucleic acid-binding protein; A(n), polyA 3’ tail.



**Figure 2.** Unrooted neighbor-joining phylogenetic tree reconstructed using the complete amino acid sequences of the replicase of *Vitivirus* genus members. Strict amino acid sequence identity distances were used for construction of the tree, and the statistical significance of branches was evaluated by bootstrap analysis (1,000 replicates). Only values higher than 70% are indicated. The scale bar represents 10% amino acid sequence divergence. For some viruses, only partial sequences are available and were used. The TT2016-3 isolate of grapevine virus H is indicated in bold with a red star.



**Figure 3.** Unrooted neighbor-joining phylogenetic tree reconstructed using the complete amino acid sequences of the coat protein of *Vitivirus* genus members. Strict amino acid sequence identity distances were used for construction of the tree, and the statistical significance of branches was evaluated by bootstrap analysis (1,000 replicates). Only values higher than 70% are indicated. The scale bar represents 10% amino acid sequence divergence. The TT2016-3 isolate of grapevine virus H is indicated in bold with a red star.

| **References:** |
| --- |
| Candresse *et al*. (2018) Determination of the complete genomic sequence of grapevine virus H, a novel vitivirus infecting grapevine. Arch Virol, 163:277-280. https://doi.org/10.1007/s00705-017-3587-7  Adams *et al.* (2012) Family *Betaflexiviridae*. In: Virus Taxonomy-Ninth Report on the International Committee on Taxonomy of Viruses. King *et al*. eds. Elsevier Academic Press: Cambridge, MA, USA, pp. 920–941 |