This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

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.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.018P*** | | | | (to be completed by ICTV officers) |
| **Short title:** One new species in the family *Closteroviridae* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| |  |  | | --- | --- | | Marc Fuchs (Chair) | mf13@cornell.edu | | Alexey A. Agranovsky | aaa@genebee.msu.su | | Moshe Bar-Joseph | mbjoseph@gmail.com | | Thierry Candresse | tc@bordeaux.inra.fr | | Valerian Dolja | doljav@science.oregonstate.edu | | Ioannis Livieratos | yannis.livieratos@gmail.com | | Giovanni P. Martelli | martelli@agr.uniba.it | | Hano Maree | hjmaree@sun.ac.za | | Michael J. Melzer | [melzer@hawaii.edu](mailto:melzer@hawaii.edu) | | Wulf Menzel | Wulf.Menzel@dsmz.de | | Angelantonio Minafra | [a.minafra@ba.ivv.cnr.it](mailto:a.minafra@ba.ivv.cnr.it) | | Sead Sabanadzovic | [SSabanadzovic@entomology.msstate.edu](mailto:SSabanadzovic@entomology.msstate.edu) | | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| |  |  | | --- | --- | | Marc Fuchs | [mf13@cornell.edu](mailto:mf13@cornell.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) | | | ***Closteroviridae*** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 2017 | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.018P.N.v1.Ampelovirus\_sp** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 3:** **NON-STANDARD**

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

|  |
| --- |
| non-standard proposal |
| **Title of proposal:** |
| **Text of proposal:** |
|  |

**Part 4:** **APPENDIX**: supporting material

Current species demarcation criteria in the family *Closteroviridae* (Martelli et al., 2012b) and justification of the proposal

Viruses of the family *Closteroviridae* have filamentous particles (650-2,200 nm in length) and monopartite or bipartite single-stranded RNA genomes with size varying from 12,000 to nearly 19,000 nucleotides (nt) in length (Figure 1). They are divided into four genera: *Closterovirus* (monopartite genome), *Ampelovirus* (monopartite genome), *Velarivirus* (monopartite genome) and *Crinivirus* (bipartite or tripartite genome) (Figure 2). Ampeloviruses are transmitted by pseudococcid mealybugs and soft scale insects, closteroviruses are transmitted by aphids, and criniviruses are transmitted by whiteflies. No vectors are known for velariviruses. Species demarcation criteria used for all genera in the family *Closteroviridae* are particle size, size of the coat protein, genome structure and organization (number and relative location of the ORFs), vector species and specificity, cytopathological features, host range, as well as amino acid sequence of relevant gene products, i.e. RNA-dependent RNA polymerase (RdRp), coat protein (CP), heat shock protein 70 homolog (HSP70h), differing by more than25%.

A novel putative virus was detected in grapevines displaying leafroll symptoms. This virus was tentatively named grapevine leafroll-associated virus 13 (GLRaV-13; Ito and Nakaune, 2016). The complete genome of GLRaV-13 isolate a177 is 17,608 nt long and contains eleven putative open reading frames (Figure 1A), resembling the genome organization of viruses in the genus *Ampelovirus* (family *Closteroviridae*). Phylogenetic trees based on the three taxonomically important RdRp, HSP70h, and CP amino acid (aa) sequences were consistent with GLRaV-13 belonging to a sister lineage of GLRaV-1 (Figure 2). Pairwise comparisons and BLAST analyses showed that the RdRp of GLRaV-13 shares maximum identities of 52% to that of GLRaV-1, while the HSP70h and CP have 44% and 36% identical aa content with orthologues encoded by the same virus (Table 1). GLRaV-13 is serologically distinct from GLRaV-1 and GLRaV-3 in DAS-ELISA. Taken together, GLRaV-13 is a virus distinct from any currently recognized member of the family *Closteroviridae*. Therefore, we propose to recognize *Grapevine leafroll-associated virus 13* (GLRaV-13) as a new species in the genus *Ampelovirus* of the family *Closteroviridae*.

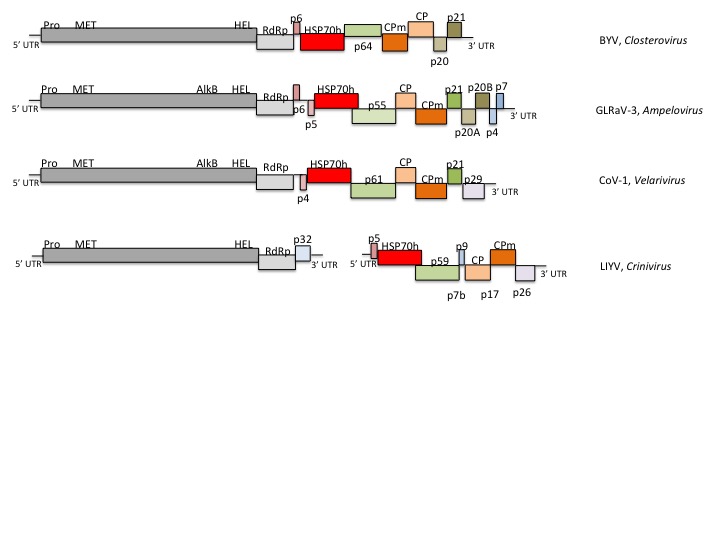
Table 1. Genetic relatedness of GLRaV-13, the new virus species, with GLRaV-1, its closest relative.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Acronym** | **Name** | **Most closely related virus** | **% CP aa sequence identity** | **% RdRP aa sequence identity** | **% HSP70h aa sequence identity** |
| GLRaV-13 | grapevine leafroll-associated virus 13 | grapevine leafroll-associated virus 1 (GLRaV-1) | 33-36 | 51-52 | 42-44 |

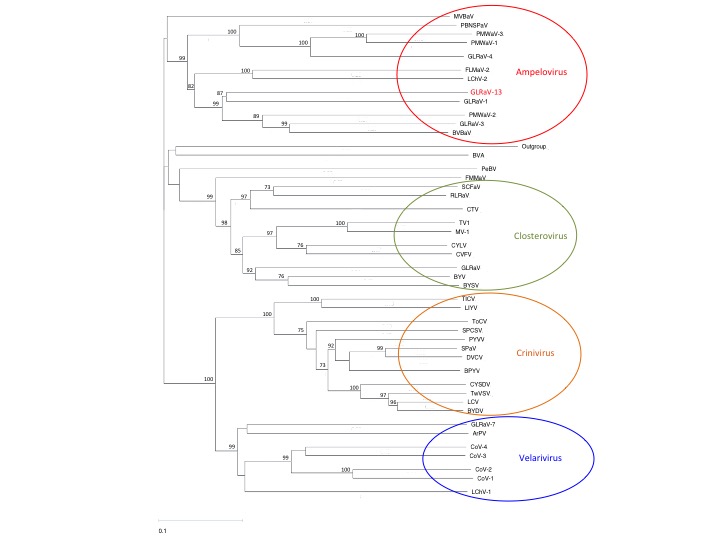
**A**



**B**



**Figure 1.** Schematic representation of the genome organization of grapevine leafroll-associated virus 13 (GLRaV-13) (panel A) compared with representative members of four genera (beet yellows virus from the genus *Closterovirus*, grapevine leafroll-associated virus 3 from the genus *Ampelovirus*, Cordyline virus 1 from the genus *Velarivirus*, and lettuce infectious yellows virus from the genus *Crinivirus*) within the family *Closteroviridae* (panel B). Blocks represent predicted open reading frames (ORFs). The replicase proteins are shown in grey with the papain-like protease (Pro), methyltransferase (Met), alkB domain (AlkB), helicase (HEL), and RNA-dependent RNA polymerase (RdRp) domains. Small transmembrane proteins (p4, p5 and/or p6) are shown in pink, the heat shock protein 70 homolog (HSP70h) in red, the coat protein (CP) in salmon, and the minor coat protein (CPm) in orange.



**Figure 2.** Maximum likelihood phylogenetic tree showing the relationships between grapevine leafroll-associated virus 13 and recognized members of the family *Closteroviridae* based on an alignment of the complete amino acid sequence of the heat shock protein 70 homolog using MUSCLE (Edgar 2004). The tree was generated with PhyML (Guindon et al., 2010) with 1,000 bootstrap replicates. Distances are proportional to branch lengths and the bar represents the genetic distance. The heat shock protein 70 from *Arabidopsis thaliana* (AEE75218) was used as outgroup. Branches with bootstrap values below 70% were collapsed. The position of GLRaV-13 in the genus *Ampelovirus* is shown in red. The GenBank accession number used for each virus is as follows: grapevine leafroll-associated virus 13 (GLRaV-13, LC052212), areca palm velarivirus 1 (ArPV1, KR349464), bean yellow disorder virus (BYDV, EU191904), beet pseudoyellows virus (BPYV, AY330918), beet yellow stunt virus (BYSV, U51931), beet yellows virus (BYV, AF056575), blackberry vein banding-associated virus (BVBaV, KC904540), blueberry virus A (BVA, AB733585), carnation necrotic fleck virus (CVFV, GU234166), carrot yellow leaf virus (CYLV, FJ869862), citrus tristeza virus (CTV, U16304), Cordyline virus 1 (CoV-1, HM588723), Cordyline virus 2 (CoV-2, JQ599282), Cordyline virus 3 (CoV-3, JQ599283), Cordyline virus 4 (CoV-4, JQ599284), cucurbit yellow stunting disorder virus (CYSDV,AY242077), diodia vein chlorosis virus (DVCV, CQ376201), fig leaf mottle-associated virus 2 (FLMaV-2, FJ473383), fig mild mottle-associated virus (FMMaV, FJ611959), grapevine leafroll-associated virus 1 (GLRaV-1, JQ023131), grapevine leafroll-associated virus 2 (GLRaV-2, JX513891), grapevine leafroll-associated virus 3 (GLRaV-3, EU259806), grapevine leafroll-associated virus 4 (GLRaV-4, FJ467503), grapevine leafroll-associated virus 7 (GLRaV-7, HE588185), lettuce chlorosis virus (LCV, FJ380118), lettuce infectious yellows virus (LIYV, U15440), little cherry virus 1 (LChV-1, EU715989), little cherry virus 2 (LChV-2, AF531505), mint vein banding-associated virus (MVBaV, KJ572575), mint virus 1 (MV-1, AY792620), persimmon virus B (PeBV, AB923924), pineapple mealybug wilt-associated 1 (PMWaV-1, AF414119), pineapple mealybug wilt-associated 2 (PMWaV-2, AF283103), pineapple mealybug wilt-associated 3 (PMWaV-3, DQ399259), plum bark necrosis stem pitting-associated virus (PMNSPaV, EF546442), raspberry leaf mottle virus (RLMoV, DQ357218), rose leaf rosette-associated virus (RLRaV, KJ7488003), strawberry chlorotic fleck-associated virus (SCFaV, DQ860839), potato yellow vein virus (PYVV, AJ557128), strawberry pallidosis-associated virus (SPaV, AY488138), sweet potato chlorotic stunt virus (SPCSV, AJ428554), tetterwort vein chlorosis virus (TwVSV, KR002687), tobacco virus 1 (TV1, KT203917), tomato chlorosis virus (ToCV, AY903447), and tomato infectious chlorosis virus (TICV, FJ815440).

|  |
| --- |
| **References:** |
|  |
| Edgar, R. C. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res 32:1792-1797.  Guindon, S., Dufayard, J.F., Lefort, V., Anisimova, M., Hordijk, W., Gascuel, O., 2010. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Systematic Biology 59:307-321.  Ito, R. and Nakaune, R. (2016). Molecular characterization of a novel putative ampelovirus tentatively named grapevine leafroll-associated virus 13. Archives of Virology 161:2555-2559.  Martelli, G.P., Abou Ghanem-Sabanadzovic, N., Agranowsky, A.A, Al Rawhanih, M., Dolja, V.V., Dovas, C.I., Fuchs, M., Gugerli, P., Hu, J.S., Jelkmann, W., Katis, N., Maliogka, V.I., Melzer, M.J., Menzel, W., Minafra, A., Rott, M.E., Rowhani, A., Sabanadzovic, S. and Saldarelli, P. (2012a). Taxonomic revision of the family *Closteroviridae* with special reference to the grapevine leafroll-associated members of the genus *Ampelovirus* and the putative species unassigned to the family. Journal of Plant Pathology 94:7-19.  Martelli, G.P., Agranowski, A.A., Bar-Joseph, M., Boscia, D., Candresse, T., Couts, R.H.A., Dolja, V.V., Hu, J.S., Jelkmann, W., Karasev, A.V., Martin R.R., Minafra, A., Namba, S., Vetten H.J. (2012b). Family *Closteroviridae*. In: King A., Adams, M.J., Carstens, E.B., Lefkowitz, E. (Eds.). Virus Taxonomy: Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier-Academic Press, San Diego, pp. 987-1001. |

|  |
| --- |
| **Annex:**  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. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **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. |