

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2021.004P** |  |
| **Short title:** Create one new species (*Anulavirus GLPV*)in the genus *Anulavirus (Martellivirales*: *Bromoviridae*) | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
|  |  |
| Elbeaino T, Demian E, Kontra L, Jaksa-Czotter N, Slimen AB, Fabian R, Lazar J, Tamisier L, Digiaro M, Massart S, Varallyay E | [elbeaino@iamb.it](mailto:elbeaino@iamb.it);  [emese.demian@gmail.com](mailto:emese.demian@gmail.com);  [Kontra.Levente@uni-mate.hu](mailto:Kontra.Levente@uni-mate.hu);  [Jaksa-Czotter.Nikoletta@uni-mate.hu](mailto:Jaksa-Czotter.Nikoletta@uni-mate.hu);  [b.slimen.a@gmail.com](mailto:b.slimen.a@gmail.com); [richard6fabi@gmail.com](mailto:richard6fabi@gmail.com); [lazar.janos@szbki.naik.hu](mailto:lazar.janos@szbki.naik.hu); [lucie.tamisier@uliege.be](mailto:lucie.tamisier@uliege.be);  [digiaro@iamb.it](mailto:digiaro@iamb.it); [sebastien.massart@uliege.be](mailto:sebastien.massart@uliege.be); Varallyay.Eva@uni-mate.hu; |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Istituto Agronomico Mediterraneo di Bari, Via Ceglie 9, 70010 Valenzano, (BA), Italy [ET, MD]  Hungarian University of Agriculture and Life Sciences, Pater K street 1, 2100, Godollo, Hungary [ED, LK, J-CN, RF, JL, EV]  Plant Pathology Laboratory, TERRA-Gembloux Agro-Bio Tech, University of Liège, Passage des Déportés, 2, 5030 Gembloux, Belgium [LT, SM] |

**Corresponding author**

|  |
| --- |
| Eva Varallyay, Varallyay.Eva@uni-mate.hu |

**List the ICTV Study Group(s) that have seen this proposal**

|  |
| --- |
| *Bromoviridae* Study Group |

**ICTV study group comments and response of proposer**

|  |
| --- |
|  |

**Authority to use the name of a living person**

|  |  |  |  |
| --- | --- | --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | | | N |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** | |
|  |  |  | |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 21-May-2021 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

NON

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2021.004P.A.v1.Anulavirus\_1ns.xlsx |

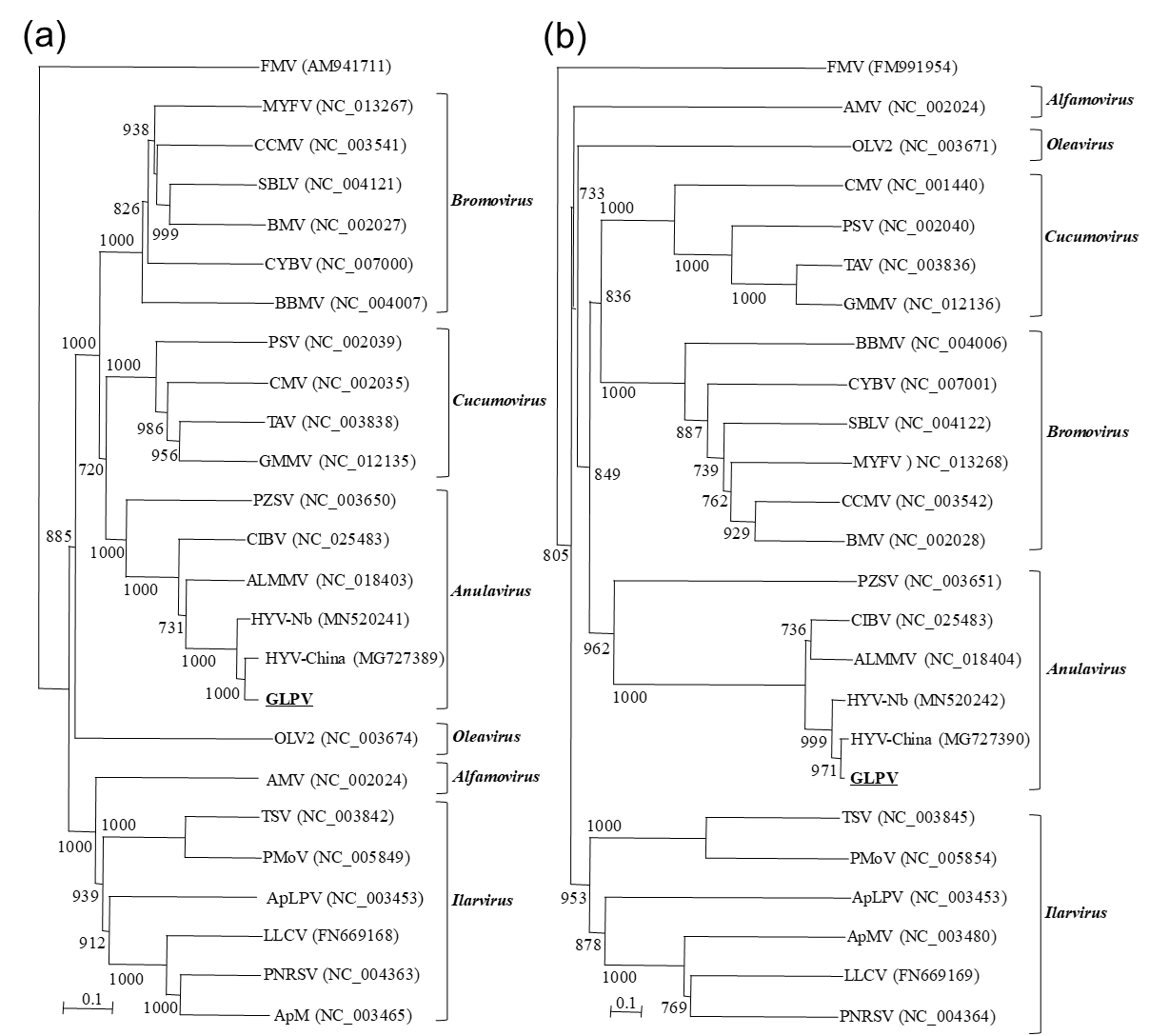
**Abstract**

|  |
| --- |
| Grapevine line pattern virus (GLPV) was first described 30 years ago in Hungary in grapevines showing line patterns and ringspots in their leaves. Three different high-throughput sequencing (HTS) protocols applied to a GLPV infected vine allowed the construction of the full genome sequence of this virus. The characteristics of its genome (i.e. the tripartite genome, the presence of a smaller 2a protein, the absence of the 2b protein encoding a VSR, a slightly larger RNA3 than RNA2) and the high nucleotide sequence identity to the genomes of other anulaviruses, confirmed that GLPV is a putative member of the genus *Anulavirus* in the family *Bromoviridae*. Based on the phylogenetic and sequence analyses we propose the creation of a new species, *Anulavirus GLPV,* that accommodates GLPV as the exemplar isolate. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | Sequences obtained from the high throughput sequencing and Sanger-sequencing of RT-PCR amplicons and 5′ and 3′ RACE clones, showed that the genome of GLPV is composed of three positive-sense (+), single-stranded (ss) RNA segments (RNA1 -MT319109, RNA2 - MT319110, RNA3 - MT319111), encoding four putative proteins: methyltransferase-helicase (1a), RNA-dependent RNA polymerase (2a), movement protein (3a) and coat protein (3b).  The 1a protein shares the highest aa identities (ranging from 47% to 82%) with the homologous protein of the two members (pelargonium zonate spot virus, PZSV, and amazon lily mild mottle virus, ALiMMV) and one tentative member (cassava Ivorian bacilliform virus, CIBV) of the genus *Anulavirus*. A BLAST search of the fully sequenced GLPV genome revealed a very high sequence identity (99%) with fully sequenced hop yellow virus (HYV), another tentative member of the *Anulavirus* genus not yet officially published and recognised. Two isolates from China, HYV-China (accession numbers: MG727388, MG727389 and MG727390) (C. Yu, unpublished) and HYV-Nb (MN520240, MN520241, MN520242) (Y. Lu, unpublished), are reported in GenBank, from hop (*Humulus lupulus* L.) and Thunberg fritillary (*Fritillaria thunbergii* Miq.), respectively. The 2a protein, encoding the viral RNA-depedent RNA polymerase (RdRP) shares amino acid (aa) identities of 92%–99%, 74%, 71% and 48%, with the homologous protein encoded by RNA2 of HYV (NB and China strains), CIBV, ALiMMV and PZSV, respectively. Similar to GLPV RNA1- and RNA2-encoded proteins, amino acid identities of the RNA3 encoded proteins showed that the MP (3a) and the CP (3b) of GLPV share the highest identity with anulavirus homologues, and in particular with the two Chinese isolates of HYV (97% and 95–98%, respectively) and the lowest with PZSV (45% and 28%). Phylogenetic trees based on alignments of the amino acid sequences of 2a and 3b (CP) also confirmed the relatedness of GLPV to the members of the genus *Anulavirus*, allocating it in one cluster together the HYV isolates in the recognized anulavirus clade.  The genome sequence of GLPV, almost 30 years after its first discovery is now available in GenBank. With this proposal we would like to request its official place as a viral species as well. The characteristics of its genome (i.e., tripartite, a smaller 2a protein, the absence of a putative 2b protein, and the larger-than-RNA2 RNA3) and the high nucleotide sequence identity with the genome of other anulaviruses, confirmed that GLPV is a member of the genus *Anulavirus*. Accordingly, GLPV should belong to the fourth species of this genus, which currently comprises only two officially recognized members: PZSV and ALiMMV, and a tentative member: CIBV. The GLPV properties revealed in the 1980s, i.e., disease characterization, shape of virus particle (polymorphic), suggested GLPV to be a possible member of the family *Bromoviridae* that infects the grapevine. Based on the molecular information now gained on the GLPV genome, together with the aforementioned attributes, we propose the generation of a novel species named *Anulavirus GLPV* in the genus *Anulavirus* to include GLPV as the exemplar isolate.  The molecular analysis conducted on its genome provides clear evidence that GLPV and HYV are two viruses of the same viral species. The sequences of the two isolates of HYV, detected from hop and Thunberg fritillary plants, are reported in GenBank, but, apart from the genome sequence, no other information is currently available for them. | |

**Supporting evidence**

****

**Figure 1.** Phylogenetic trees, generated by the “Neighbour-joining” method, constructed based on aa sequences of the (a) RdRP and the (b) CP of GLPV and members of six genera belonging to the family Bromoviridae: Alfamovirus [alfa mosaic virus, (AMV)], Anulavirus [Amazon Lily mild mottle virus (ALMMV), pelargonium zonate sport virus (PZSV), and the two putative members: hop yellow virus (HYV, isolates China and Nb) and cassava Ivorian bacilliform virus (CIBV)], Bromovirus [broad bean mottle virus (BBMV), brome mosaic virus (BMV), cassia yellow blotch virus (CYBV), cowpea chlorotic mottle virus (CCMV), melandrium yellow fleck virus (MYFV), spring beauty latent virus (SBLV)], Cucumovirus [cucumber mosaic virus (CMV), Ggyfeather mild mottle virus (GMMV), peanut stunt virus (PSV), tomato aspermy virus (TAV)], Ilarvirus [apple mosaic virus (ApMV), prunus necrotic ring spot virus (PNRSV), lilac leaf chlorosis virus (LLCV), apple line pattern virus (ApLPV), pepper mottle virus (PMoV), tobacco streak virus (TSV)] and Oleavirus [olive latent virus 2 (OLV2)]. Fig mosaic emaravirus (FMV) was used to root the trees. Accessions numbers of viruses used are reported within brackets. Numbers on branches indicate percentage of support out of 1000 bootstrap replications. Bootstrap values above 70% are shown. Scale bar represents 0.1 aa substitutions per site.

**References**

Elbeaino T, Kontra L, Demian E, Jaksa-Czotter N, Slimen AB, Fabian R, Lazar J, Tamisier L, Digiaro M, Massart S, Varallyay E. Complete Sequence, Genome Organization and Molecular Detection of Grapevine Line Pattern Virus, a New Putative Anulavirus Infecting Grapevine. Viruses. 2020; 12(6):602. <https://doi.org/10.3390/v12060602>. PMID: **32486454**