

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

**Part 1a: Details of taxonomy proposals**

|  |  |  |
| --- | --- | --- |
| **Title:** | Create one new species in the genus *Velarivirus* (order *Martellivirales*, family *Closteroviridae*) | |
| **Code assigned:** | 2024.019P.A.v1.Closteroviridae\_1nsp |

|  |  |  |  |
| --- | --- | --- | --- |
| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** |
| Fontdevila N | Plant Pathology Laboratory, TERRA Gembloux Agro-Bio Tech, University of Liege, Belgium | nfpareta@gmail.com |  |
| Massart S | Plant Pathology Laboratory, TERRA Gembloux Agro-Bio Tech, University of Liege, Belgium | sebastien.massart@uliege.be | X |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |

**Part 1b: Taxonomy Proposal Submission**

|  |  |  |  |
| --- | --- | --- | --- |
| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses | **X** |
| Archaeal viruses |  | General |  |

|  |
| --- |
| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
|  |

|  |  |  |  |
| --- | --- | --- | --- |
| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

|  |  |
| --- | --- |
| **Submission date:** | 21/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

|  |  |
| --- | --- |
| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required | **X** |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

|  |
| --- |
| **Comments from the Executive Committee:** |
| Please include the edits highlighted in yellow and correct the “grapevine leafroll-associated 7 virus” to “grapevine leafroll-associated virus 7” in Figure 1. Alternatively, simply delete it from the figure, since the name is reported in the caption. |

**Part 1d: Revised Taxonomy Proposal Submission**

|  |
| --- |
| **Response of proposer:** |
|  |

|  |  |
| --- | --- |
| **Revision date:** | 07/10/2024 |

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

|  |
| --- |
| **Name of accompanying Excel module:** |
| 2024.019P.A.v1.Closteroviridae\_1nsp.xslx |

|  |  |  |  |
| --- | --- | --- | --- |
| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

|  |  |  |
| --- | --- | --- |
| **Is any taxon name used here derived from that of a living person:** | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
|  |  |  |
|  |  |  |
|  |  |  |

|  |
| --- |
| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Genus *Velarivirus* (order *Martellivirales,* family *Closteroviridae*)  *Description of current taxonomy*:  The family *Closteroviridae* comprises plant viruses with long, filamentous particles (650-2,200 nm in length) and large positive-sense RNA genomes (mono-, bi-, or tripartite). There are 57 recognized species in the family, classified in one of the seven existing genera (*Ampelovirus, Bluvavirus, Closterovirus, Crinivirus, Menthavirus, Olivavirus,* and *Velarivirus*). Within the genus *Velarivirus*, there are currently eight recognized species.  *Proposed* *taxonomic change(s):*  The authors propose adding a ninth species in the genus *Velarivirus,* named *Velarivirus gembloutense,* to classify recently identified virus Pyrus virus A (PyVA) in pear trees (*Pyrus communis* L.).  *Justification*:  Analysis of the genomic structure of this novel virus (PyVA) and subsequent phylogenetic analyses of the specific HSP70h gene placed PyVA as a novel member of the genus *Velarivirus* within the family *Closteroviridae*. |

|  |
| --- |
| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus *Velarivirus* (order *Martellivirales,* family *Closteroviridae*)  *Description of current taxonomy*:  The family *Closteroviridae* comprises plant viruses with long, filamentous particles (650-2,200 nm in length) and large positive-sense RNA genomes (mono-, bi-, or tripartite). Members of this family present a cellular HSP70 homolog (HSP70h) and a duplicated, diverged copy of the coat protein named minor coat protein (CPm). Moreover, their genome is expressed through a +1 ribosomal frameshift and sub-genomic messenger RNAs. There are 57 recognized species in the family, classified in one of the seven existing genera (*Ampelovirus, Bluvavirus, Closterovirus, Crinivirus, Menthavirus, Olivavirus,* and *Velarivirus*). Within the genus *Velarivirus*, there are currently eight recognized species.  *Proposed* *taxonomic change(s)*:  The authors propose adding a ninth species in the genus *Velarivirus ,* named *Velarivirus gembloutense,* to classify recently identified virus Pyrus virus A (PyVA) in pear trees (*Pyrus communis* L.).  *Demarcation criteria:*  The genus demarcation criteria in the genus include particle size, the size of the CP, serological specificity using discriminatory monoclonal or polyclonal antibodies, genome structure and organization, amino acid (aa) sequence of the relevant gene products (RdRp, CP, HSP70h) differing by more than 25%, the magnitude and specificity of their natural host range, and cytopathological features. The established demarcation criteria for the family *Closteroviridae* can be found in the ICTV Virus Taxonomy Profile of this family in the Journal of General Virology (Fuchs et al., 2020).  *Justification*:  Velariviruses (*Closteroviridae* family) present a large, linear, positive-sense, single-stranded RNA (+ssRNA) genome approximately 16,080 to 17,003 nucleotides (nt) in size. The members of this genus share several common features in their genomic organization. Briefly, they are comprised of nine open reading frames (ORFs) coding for the replication associated proteins (ORF 1a and ORF 1b), a small hydrophobic protein of *ca*. 4 to 8 kDa with a transmembrane domain, HSP70h, a protein of *ca*. 60 kDa, CP, CPm, and two additional proteins of, in most of the cases, 25 and 27 kDa, respectively (Figure 1).    Figure 1. Genome organization of grapevine leafroll-associated virus 7 (GLRaV-7), which is a member of the genus *Velarivirus* (Fuchs et al., 2020).  Moreover, velariviruses infect mainly woody hosts without inducing apparent symptoms. They are primarily transmitted by grafting and vegetative propagation, as no insect vector is known, and they are not transmitted through seed or mechanically.  Description of the new species candidate  The proposed novel velarivirus member (PyVA) was identified in pear trees during a virome scanning study with HTS. During the analysis of the data, two genomes containing all coding regions were assembled. The two isolates, namely isolate 621-BE (GenBank accession No. OR887736) and 224-BE (OR887735), have a length of 17,061 and 17,142 nt, respectively. The difference in size between the two isolates is due to the incomplete sequencing of the 5’ and 3’ untranslated regions (UTRs), which, although attempted, could not be fully assembled.  The two genomes encode nine putative ORFs (Figure 2A) and have a genomic organization similar to other velariviruses, especially to that of its closes relative Malus domestica virus A (MdoVA). In addition, the electron microscopy of purified viral particles showed them to have an approximate length of 2,000 nm (Figure 2B). The newly identified virus fits the demarcation criteria, as well as the distinguishing properties, for viruses belonging to the genus *Velarivirus* and family *Closteroviridae*. PyVA shows 75% aa identity in the RdRp, 60% in the HSP70h, and 41% in the CP (Table 1).  Moreover, a maximum likelihood phylogenetic tree (1,000 bootstrap replicates) using the HSP70h amino acid sequences of known members of the *Closteroviridae* family was constructed. The phylogenetic analysis showed that PyVA was grouped within the *Velarivirus* genus.  Regarding its host range, PyVA was successfully transmitted by grafting to healthy plants of of *Pyronia veitchii* (*Cydonia oblonga* x *Pyrus communis*) and to different pear cultivars (Beurré Hardy, Williams, A20, and Jules d’Airoles). On the other hand, there was no transmission to Virginia crab apple, Lord Lambourne (*Malus domestica*), C7/1 (*Cydonia oblonga*), Pyrodwarf (*Pyrus communis*), M9 (*Malus domestica*), St. Julien (*Prunus domestica*), and Gisela® 5 (*Prunus cerasus* x *Prunus canescens*).  Given that PyVA shows a narrow host range, presents amino acid identity levels below the species demarcation criteria, and has a virion size and genome organization similar to other members of the genus *Velarivirus*, the authors propose PyVA to be classified in a newly created species *Velarivirus gembloutense.* The specific epithet chosen derives from the place of isolation of the virus (Gembloux). |

|  |
| --- |
| **References:** |
| Fontdevila Pareta, N., Gailly, C., Blouin, A.G., Buchmann, B., Buenter, M., Candresse, T., Dubuis, N., Kutnjak, D., Lateur, M., Pecman, A., Steyer, S., Massart, S., in publication. Virome scanning of pear germplasm collections identifies a new Velarivirus and extends the geographical spread of three other pear viruses. Phytobiomes J.  Fuchs, M., Bar-Joseph, M., Candresse, T., Maree, H.J., Martelli, G.P., Melzer, M.J., Menzel, W., Minafra, A., Sabanadzovic, S., Report Consortium, I., 2020. ICTV Virus Taxonomy Profile: Closteroviridae. J. Gen. Virol. https://doi.org/10.1099/jgv.0.001397 |

|  |
| --- |
| **Tables, Figures:** |

A screen shot of a television screen

Description automatically generated

**Figure 2. A)** Graphic representation of the genomic organization of the novel velarivirus (PyVA, isolate 621-BE), with each box representing a predicted open reading frame (ORF) and the protein domains highlighted in different colors. The names in italics represent the products of the ORFs, the polyprotein 1a/1b complex, and the hypothetical proteins p4, p9, p25, and p26. The coverage of reads mapped to the genome of PyVA is shown in blue below the genome structure (maximum coverage = 1,051X). Abbreviations: methyltransferase (Mtr), helicase (Hel), RNA-dependent RNA polymerase (RdRp), heat-shock protein 70 homolog (HSP70h), heat-shock protein 90 homolog (HSP90h), capsid protein (CP), and minor capsid protein (CPm). **B)** Electron micrograph of three viral particles of the PyVA, marked with a black arrow. Figure taken from Fontdevila Pareta et al., (in publication) under an open access license.

Escala de tiempo

Descripción generada automáticamente con confianza media

**Figure 3.** Maximum likelihood phylogenetic tree (rtREV+F+I+G4 substitution model, MAFFT alignment, 1000 bootstraps) based on the alignment of HSP70h amino acid (aa) sequences of members of the *Closteroviridae* family and of PyVA (highlighted in red). The phylogenetic analysis was performed using the Galaxy server and visualized using the iTOL v6.8 tool. The HSP70 sequence of Arabidopsis thaliana was used as outgroup to root the tree. Bootstrap values are shown for each branch, and colored labels represent the genus that each virus belongs to as shown in the legend on the left. Figure taken from Fontdevila Pareta et al., (in publication) under an open access license.

**Table 1.** Percentages of amino acid (aa) identity of 10 proteins between the novel velarivirus (PyVA) and other members of the genus *Velarivirus*, obtained using a multiple sequence alignment tool (MAFFT). The genomes of cordyline viruses 2, 3, and 4 had partial sequences of the ORF 1a, and the genome of little cherry virus 1 did not have an annotation for p9. Thus, they were not used for the comparison. Table taken from Fontdevila Pareta et al., (in publication) under an open access license.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genbank nº | Virus | 1a | 1b | p4 | HSP70h | p9 | HSP90h | CP | CPm | p25 | p26 |
| NC\_027121 | Areca palm velarivirus 1 (APV-1) | 22% | 56% | 26% | 40% | 13% | 23% | 23% | 13% | 15% | 11% |
| NC\_038421 | Cordyline virus 1 (CoV-1) | 22% | 55% | 36% | 43% | 14% | 28% | 30% | 14% | 15% | 12% |
| NC\_043453 | Cordyline virus 2 (CoV-2) | - | 54% | 24% | 44% | 24% | 31% | 31% | 17% | 15% | 14% |
| NC\_043107 | Cordyline virus 3 (CoV-3) | - | 57% | 15% | 46% | 26% | 31% | 27% | 13% | 17% | 9% |
| NC\_043108 | Cordyline virus 4 (CoV-4) | - | 56% | 16% | 44% | 25% | 26% | 30% | 15% | 21% | 12% |
| NC\_016436 | Grapevine leafroll-associated virus 7 (GLRaV-7) | 23% | 55% | 18% | 42% | 20% | 28% | 26% | 11% | 14% | 10% |
| NC\_001836 | Little cherry virus 1 (LChV-1) | 30% | 60% | 21% | 48% | - | 34% | 21% | 19% | 13% | 15% |
| NC\_055599 | Malus domestica virus A (MdoVA) | 46% | 75% | 61% | 60% | 49% | 52% | 41% | 26% | 32% | 27% |