

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

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| **Code assigned:** | ***2023.004F*** |  |
| **Short title:** Create a new genus in the family *Marseilleviridae* (*Pimascovirales*) and rename species in the family | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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

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| ICTV *Marseilleviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| *Marseilleviridae* | 3 | 0 | 0 |
|  |  |  |  |

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

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  | NA |
|  |  |  |
|  |  |  |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | 06-28-2023 |
| Date of this revision (if different to above) | 10-25-2023 |

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

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| Please change originally proposed name for the genus “*Lausannevirus*” as it is identical with previous species name and conflicts with the ICTV Rule 3.14.  Response:  We accept the suggestion and change the proposed name to “*Losannavirus*” which is sufficiently distinct from, but still reminiscent of the original nomenclature. |

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

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2023.004F.v2.Marseilleviridae\_1newgen\_spren.xlsx |

**Abstract**

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| In order to comply with recently adopted binomial system for species nomenclature, here we propose to create a new genus named “*Losannavirus*” to classify two currently unassigned species in the family and to rename all four currently recognized species of marseillevirids. |

**Text of proposal**

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| |  | | --- | | Following results of multiannual debate and consultations (1) the Ratification Vote held in March 2021, approved universal adoption of binomial format for species names across the ICTV framework of virus taxonomy (2).  According to the ratified original proposal “*2018.001G.R.binomial\_species*”, starting from 2021 all species names must follow new guidelines. This process is envisioned for completion in 2023.  Briefly, new rules indicate:  "A species name shall consist of only two distinct word components separated by a space. The first word component shall begin with a capital letter and be identical in spelling to the name of the genus to which the species belongs. The second word component shall not contain any suffixes specific for taxa of higher ranks. The entire species name (both word components) shall be italicized."  Hence, the new standards require renaming most of already recognized species. In 2021 and 2022, the new nomenclature was already applied to approximately 80% of current species. Therefore, in this document we propose renaming four species belonging to the family *Marseilleviridae* to fit new standards by adopting binomial species names.  In order to accomplish that, we propose creation of a new genus to classify two currently unassigned (“floating”) species in the family for which we propose the name “*Losannavirus*” (Table 1). The grouping of these two species in a new genus has already been supported in a number of published papers (originally in reference #4), based upon close evolutionary relatedness of a set of taxonomically-relevant proteins encoded by genomes of the known family members (Figure 1).  The two current species in the genus *Marseillevirus* are renamed to fit Linnaean (genus-species) format (Table 1) | |

**Supporting evidence**

**A screenshot of a computer screen

Description automatically generated**

**Figure 1.** Maximum Likelihood phylogenetic tree constructed on the alignment of concatenated amino acid sequences of VV-A18 and D5 helicases and the very late transcription factor (VLTF), the three proteins universally encoded by members of the family *Marseilleviridae*. The final dataset consisted of 1,270 positions. Tree was generated and visualized by MEGA v5 software (5). The numbers on branching points indicate percentage (%) bootstrap support. The original tree was published by Aherfi et al, 2014 (4).

**Table 1.** Current and proposed classification and species nomenclature in the family *Marseilleviridae.* Changes in species nomenclature only are highlighted in blue font, while changes in classification and nomenclature are reported in red.

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| **Current** |  | **Proposed** |
| **Family** *Marseilleviridae* |  | **Family** *Marseilleviridae* |
| **Genus**  *Marseillevirus* |  | **Genus** *Marseillevirus* |
| **Species** *Marseillevirus marseillevirus* |  | **Species** *Marseillevirus massiliense* |
| **Species** *Senegalvirus marseillevirus* |  | **Species** *Marseillevirus senegalense* |
| **Unassigned** |  | **Genus** “*Losannavirus*” |
| **Species** *Lausannevirus* |  | **Species “***Losannavirus lausannense”* |
| **Species** *Tunisvirus* |  | **Species “***Losannavirus tunisense”* |

**References**

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2. Walker PJ, Siddell SG, Lefkowitz EJ, Mushegian AR, Adriaenssens EM, Alfenas-Zerbini P, Davison AJ, Dempsey DM, Dutilh BE, Garcia ML, Harrach B, Harrison RL, Hendrickson RC, Junglen S, Knowles NJ, Krupovic M, Kuhn JH, Lambert AJ, Lobocka M, Nibert ML, Oksanen HM, Orton RJ, Robertson DL, Rubino L, Sabanadzovic S, Simmonds P, Smith DB, Suzuki N, Van Dooerslaer K, Vandamme AM, Varsani A, Zerbini FM (2021) Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). Arch Virol 166:2633–2648. DOI: [10.1007/s00705-021-05156-1](https://doi.org/10.1007/s00705-021-05156-1), PMID: 34231026
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4. Aherfi S, Boughalmi M, Pagnier I, Fournous G, La Scola B, Raoult D, Colson P (2014) Complete genome sequence of Tunisvirus, a new member of the proposed family *Marseilleviridae*. Arch Virol 159:2349-2358. DOI: [10.1007/s00705-014-2023-5](file:///Users/ss501/Downloads/ICTV%20Fungal%20and%20Protist%20Viruses%20Subcommittee%20Announcement%20of%20the%202023%20Taxonomic%20Proposal%20Season/10.1007/s00705-014-2023-5), PMID: 24770845
5. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S (2011) MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum par-simony methods. Mol Biol Evol 28:2731–2739. DOI: [10.1093/molbev/msr121](https://doi.org/10.1093/molbev/msr121), PMID: **21546353**