

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

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| **Code assigned:** | **2020.108B** |  |
| **Short title:** Create one new genus (*Myoalterovirus*) including one new species (*Caudovirales*: *Myoviridae*) | | |
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**Author(s) and email address(es)**

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| Gonzalez-Serrano R, Dunne M, Rosselli R, Martin-Cuadrado A-B, Grosboillot V, Zinsli LV, Roda-Garcia JJ, Loessner MJ, Rodriguez-Valera F | [rafael.gonzalezs@umh.es](mailto:rafael.gonzalezs@umh.es); [matthew.dunne@hest.ethz.ch](mailto:matthew.dunne@hest.ethz.ch);  [riccardo.rosselli@gmail.com](mailto:riccardo.rosselli@gmail.com);  [amartincuadrado@ua.es](mailto:amartincuadrado@ua.es); [virginie.grosboillot@hest.ethz.ch](mailto:virginie.grosboillot@hest.ethz.ch); [lea.zinsli@hest.ethz.ch](mailto:lea.zinsli@hest.ethz.ch); [jroda@umh.es](mailto:jroda@umh.es);  [martin.loessner@ethz.ch](mailto:martin.loessner@ethz.ch);  [frvalera@umh.es](mailto:frvalera@umh.es) |

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

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| --- |
| Universidad Miguel Hernández [RGS, JJRG, FRV]  ETH Zurich (MD, VG, LVZ, MJL)  NIOZ Royal Netherlands Institute for Sea Research and Utrecht University (RR)  Universidad de Alicante (ABMC) |

**Corresponding authors**

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| Gonzalez-Serrano R, Dunne M, Rodriguez-Valera F |

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

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| Bacterial and Archaeal Viruses Subcommittee |

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

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

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

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| Date first submitted to SC Chair | March 2020 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2020.108B.R.Myoalterovirus.xlsx |

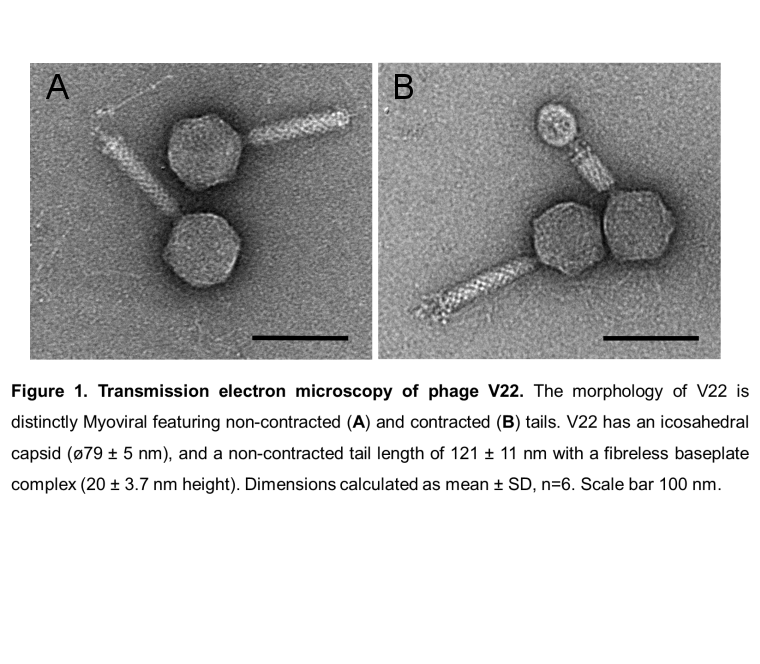
**Abstract**

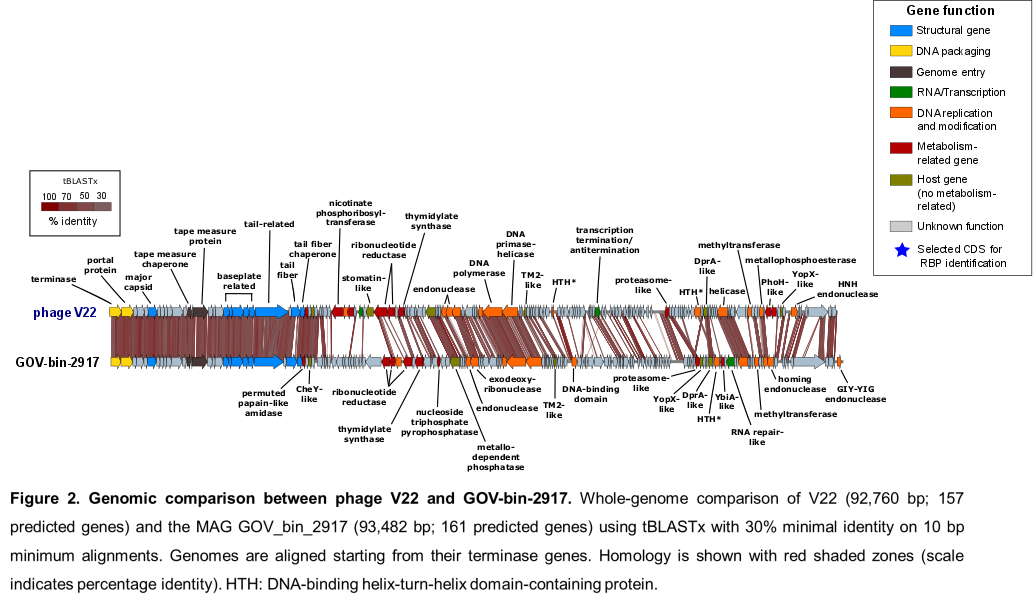
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| A new *Alteromonas* myovirus isolated from the Mediterranean Sea has been characterized and we propose the creation of a new species, called ***Alteromonas* virus PT11-V22**. The phage has been named **vB\_AmeM\_PT11-V22** (vB from bacterial virus; Ame from *Alteromonas mediterranea* (the host); M from the viral family identification code (*Myoviridae*); PT11 from the *A. mediterranea* strain; V from Villajoyosa (the sampling site); and 22 from the number of the sample).  We also propose to include the phage **vB\_AmeM\_PT11-V22** and its closest relative (the metagenome-assembled genome (MAG) **GOV-bin-2917**, found at NCBI non-redundant database) into a new genus within the *Myoviridae* family called ***Myoalterovirus***. After genomic comparative analysis with nr NCBI database, no other similar genome was found, so both vB\_AmeM\_PT11-V22 and GOV-bin-2917 cannot be included within any known viral genus. |

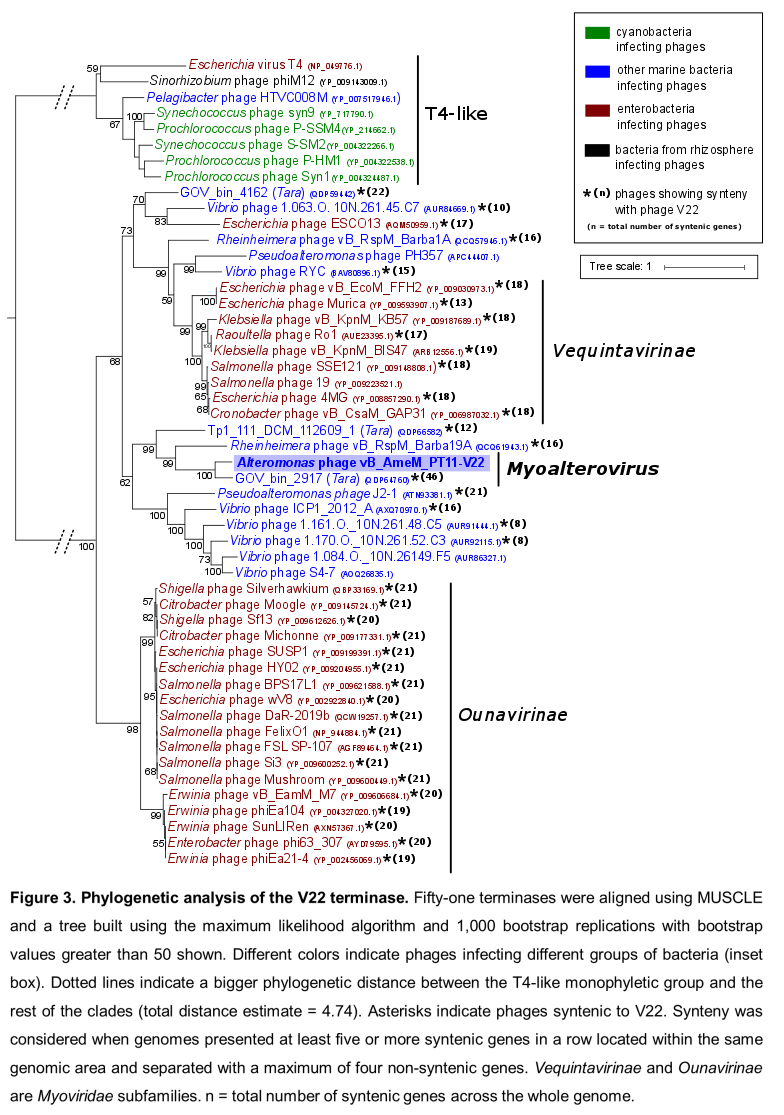
**Text of proposal**

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| |  | | --- | | Phage name assignation: *Alteromonas* virus vB\_AmeM\_PT11-V22 (herein, V22), was formulated according to the nomenclature described by Kropinski et al. (2009). TEM images (Fig. 1) allowed us to identify the family of the isolated phage, which showed the typical morphology for *Myoviridae* phages. Besides, the tail has a sheath able to contract throughout the long axis of the tail (Fig. 1B). This is the first myovirus infecting *Alteromonas* described so far.  The V22 genome was submitted for comparison against the non-redundant (nr) database at NCBI using BLASTn and results showed significant alignment (72.58% id., 45% query cover) with an undescribed and uncharacterized dsDNA virus (a metagenome assembled genome (MAG) named GOV-bin-2917 (GeneBank accession number MK892806) assembled from a viral metagenome sampled at the Indian Ocean during the 3-year *Tara* Oceans expedition (Karsenti et al., 2011; Roux et al., 2016) (Fig. 2 & Fig. 3). Considering the average nucleotide identity (ANI) value (71.13%) (see Adriaenssens and Brister, 2017) and the number of syntenic genes (46 in total) found between both genomes (see Figure 2), taking into consideration the big phylogenetic distance found between these two phages and the most closely related *Rheinheimera* phage vB\_RspM\_Barba19A (significant distance estimate of ca. 1.34) (see Figure 3), and also considering that we found a very low homology among them and other phages included into the *Myoviridae* family, we propose the creation of a new genus within the *Myoviridae* family called ***Myoalterovirus****.*  This new ***Myoalterovirus*** genus would include both the new species *Alteromonas* virus PT11-V22 (assigned as the type species) and the MAG GOV-bin-2917 as the only other known representative to date.  The phylogenetic tree shown in Figure 3 was built using the V22 terminase sequence and the 42 most similar terminase sequences from the NCBI nr database. It was generated using Maximum Likelihood and 1,000 bootstrap replications. Only bootstrap values greater than 50 are shown.  On 11th November, 2019 we were in contact with Dr Evelien Adriaenssens and, based on the information we provided her, she encouraged us to proceed with the submission of a new genus proposal based on our new isolate.  We recently submitted a manuscript to mSystems journal where we provide in-depth characterization of phage V22, as well as provide experimental evidence for the identification of its novel receptor-binding protein and associated intermolecular chaperone. We are currently waiting for the editor´s response.  GeneBank accession number for phage vB\_AmeM\_PT11-V22 is **MN877442**. | |

**Supporting evidence**







**References**

1. Kropinski, A. M., Prangishvili, D., & Lavigne, R. (2009). Position paper: the creation of a rational scheme for the nomenclature of viruses of *Bacteria* and *Archaea*. Environmental Microbiology, 11(11), 2775–2777. <https://doi.org/10.1111/j.1462-2920.2009.01970.x>
2. Karsenti, E., Acinas, S. G., Bork, P., Bowler, C., de Vargas, C., Raes, J. Sullivan, M., … & the *Tara* Consortium (2011). A holistic approach to marine eco-systems biology. PLoS Biology, 9(10), 7–11. <https://doi.org/10.1371/journal.pbio.1001177>
3. Roux, S., Brum, J. R., Dutilh, B. E., Sunagawa, S., Duhaime, M. B., Loy, A., … & Sullivan, M. B. (2016). Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. Nature, 537(7622), 689–693. <https://doi.org/10.1038/nature19366>
4. Adriaenssens, E. M., & Brister, J. R. (2017). How to name and classify your phage: an informal guide. Viruses, 9(4), 1–9. <https://doi.org/10.3390/v9040070>