

TITLE: A METHOD FOR IDENTIFY MISCLASSIFICATIONS OF VIRUSES SPECIES

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ABSTRACT:

The International Code of Virus Classification and Nomenclature (ICVCN) states that an objective of the International Committee on Taxonomy of Viruses (ICTV) is to maintain an Index of agreed names of virus taxa, namely the Master Species List (MSL). Two of the essential principles of the ICVCN principles of nomenclature are: to aim for stability and to avoid the unnecessary creation of names. Thus, the occurrence of duplicates is a misclassification. The MSL released on May 18th, 2021 addresses the GenBank accession KT321317 as the exemplar virus of two different accepted species names that are classified on two different genera of the subfamily *Rothmandenesvirinae*, characterizing a misclassification. Therefore, our objective was to propose a reclassification of this species by analyzing which species name was valid. We developed an R code to check the MSL for duplicated exemplar viruses. After finding KT321317, we started by looking at the proposal of both species on ICTV to find when the duplicated species was proposed. We also downloaded the genomes of all accepted species of the upper valid taxon, *Rothmandenesvirinae*, to perform analysis of intergenomic similarities with VIRIDIC and of cluster orthology with OrthoVenn2 to determine the classification of the species. We found that on June 8th, 2017 the genus *Jwalphavirus* was accepted with two new species *Achromobacter virus JWAlpha* and *Achromobacter virus Axp3*. In July 2020, was created the subfamily *Rothmandenesvirinae* comprising three new genus and *Jwalphavirus*. On their proposal, the movement of the *Achromobacter virus Axp3* wasn't made clear. It resulted in the creation of the synonymous species *Achromobacter virus phiAxp3*, that wasn't according to the ICVCN, since the use of transliterated Greek letters in the naming of new prokaryotic virus genera was discontinued in 2016. The intergenomic similarities on VIRIDIC showed that the *Achromobacter virus Axp3* is more than 89% similar to the *Dongdastvirus* and less than 60% to the other genera on *Rothmandenesvirinae*, indicating that this species belongs to this genus. This is reinforced by the cluster orthology analysis that showed us that *Achromobacter virus Axp3* share 75 protein clusters with the other *Dongdastvirus*, while sharing less than 58 with the other genera of *Rothmandenesvirinae*. Therefore, the valid species name for the Achromobacter phage phiAxp-3 is *Achromobacter virus Axp3* that is classified on the genus *Dongdastvirus*.

Keywords: Synonym; Duplicate; Bacteriophage; Virus; Classification.

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