This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

**Code(s) assigned:** *2008.075B* (to be completed by ICTV officers)

**Short title:** create species named VPV262 to be unassigned in the family Podoviridae
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

| | |
|---|---|
| **Modules attached**<br>(please check all that apply): | **1** ☐ **2** ☐ **3** ☐ **4** ☐ **5** ☒<br>**6** ☐ **7** ☐ |

**Author(s) with e-mail address(es) of the proposer:**

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**ICTV-EC or Study Group comments and response of the proposer:**

# MODULE 5: **NEW SPECIES**

| | | |
|---|---|---|
| Code | ***2008.075B*** | (assigned by ICTV officers) |

**To create new species assigned as follows:**

| | |
|---|---|
| Genus: | **unassigned** |
| Subfamily: | |
| Family: | ***Podoviridae*** |
| Order: | ***Caudovirales*** |

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

## Name(s) of proposed new species:

*Vibrio* phage VpV262

## Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

The VpV262 sequence (NC_003907; 46,012nt, 49%GC) reveals that it is a distant relative of marine Roseophage SIO1, and an even more distant relative of coliphage T7. VpV262 and SIO1 appear to represent a widespread marine phage group that lacks an RNA polymerase gene and is ancestral to the *Autographivirinae*. VpV262 carries a different replicative module than SIO1 and the T7-related phages.

## References:

** Hardies SC, Comeau AM, Serwer P, Suttle CA. (2003) The complete sequence of marine bacteriophage VpV262 infecting vibrio parahaemolyticus indicates that an ancestral component of a T7 viral supergroup is widespread in the marine environment. Virology. 5;310(2):359-71

## Annexes:

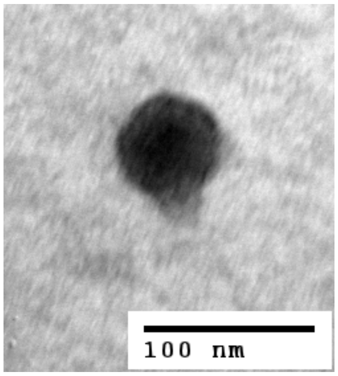

Figure 1: preliminary EM image for VpV262