

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

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| **Code assigned:** | **2020.009B** |  |
| **Short title:** Create two new species in the genus *Bottigliavirus* (*Ampullaviridae*) | | |
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**Author(s) and email address(es)**

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**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 |  |
| 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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| 2020.009B.R.Ampullaviridae.xlsx |

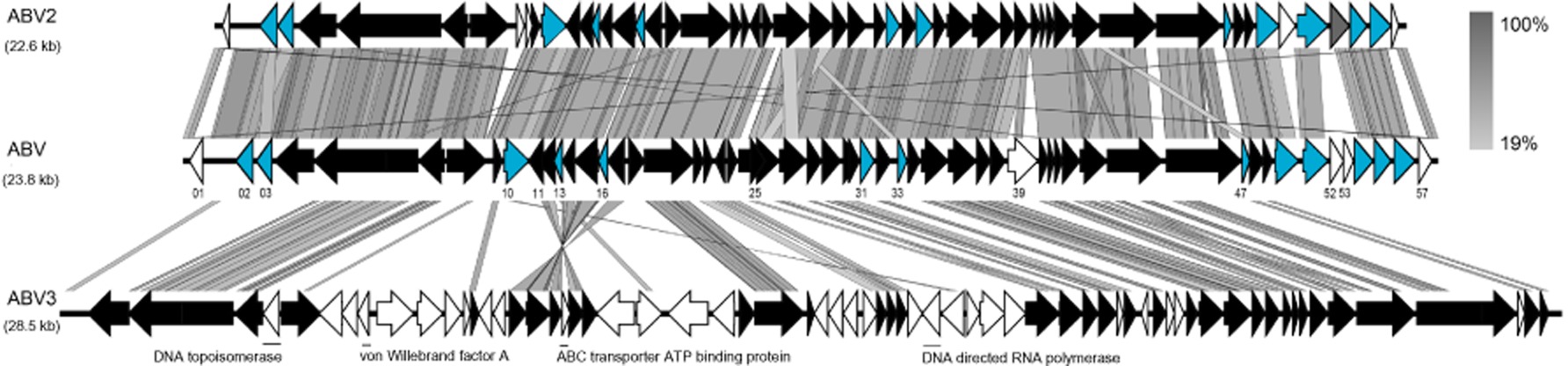
**Abstract**

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| Here I propose to create two new species, *Bottigliavirus ABV2* and *Bottigliavirus ABV3*, in the genus *Bottigliavirus* (former *Ampullavirus*) of the family *Ampullaviridae*, for classification of Acidianus bottle-shaped viruses 2 and 3. |

**Text of proposal**

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| |  | | --- | | The family *Ampullaviridae* includes a single species*, Acidianus bottle-shaped virus*, in the genus *Ampullavirus*. The only classified representative of the family, Acidianus bottle-shaped virus (ABV), infects a hyperthermophilic archaeon from the genus *Acidianus* and has a linear dsDNA genome of 23,814 bp with inverted terminal repeats (ITR). The virions have a unique champagne bottle-shaped morphology and consist of a nucleoprotein filament condensed into a cone-shaped core, which is encased by an envelope, with the base of the ‘bottle’ decorated with a ring of 20 filaments. Genome replication is presumably carried out by the virus-encoded protein-primed family B DNA polymerase [1]. Recently, two additional genomes showing similarity to that of ABV have been sequenced through metagenomics exploration of virus diversity in the acidic hot springs. These were named Acidianus bottle-shaped viruses 2 and 3 (ABV2 and ABV3, respectively) [2].  The ABV2 genome encodes 54 ORFs, with 5 ORFs having no significant sequence similarity to the ABV genome. The remaining 49 ORFs are homologous to ABV genes with an average amino acid identity of 70%, despite the fact that the genomes were retrieved from the same hot spring. On the other hand, five of the ABV genes (gp01, gp39, gp52, gp53 and gp57) have no homologue in ABV2 genome (Fig.1). The ITRs ABV2 show no sequence similarity to those of ABV.  The ABV3 genome contains 66 ORFs, 30 of which have no significant sequence similarity to the ABV genome, whereas the remaining 36 ORFs match ABV ORFs with an average amino acid sequence identity of 44%. Comparisons between the three ABV-like genomes revealed 36 core genes present in all (black arrows in Fig. 1) and a number of virus-specific genes (5 in ABV, 5 in ABV2 and 30 in ABV3; white arrows in Fig. 1). Phylogenetic analysis of the conserved protein-primed family B DNA polymerase shows that the three viruses form a monophyletic clade (Fig. 2). Thus, both genome comparisons and phylogenetic analysis support the classification of ABV2 and ABV3 into the family *Ampullaviridae*.  Species demarcation criteria have not been previously proposed, due to scarcity of available representatives. We propose to use a 95% global genome identity as a species demarcation criterion, to be consistent with the thresholds used for other prokaryotic viruses. ABV2 is more closely related to ABV, with 75% nucleotide sequence identity over 80% of the genome length. By contrast, ABV3 is more divergent, showing little nucleotide sequence similarity to either ABV or ABV2 (only ~14% of the ABV3 genome can be aligned to that of ABV). Thus, both ABV2 and ABV3 should be considered as new species.  I propose the following changes to the *Ampullaviridae* family:   1. Rename the genus *Ampullavirus* to *Bottigliavirus* (from Italian *bottiglia* for *bottle*), to avoid confusion due to the same stem in the family and genus names. 2. Rename the existing species, *Acidianus bottle-shaped virus*, to *Bottigliavirus ABV*, to match other proposed species. 3. Classify ABV2 and ABV3 into the species *Bottigliavirus ABV2* and *Bottigliavirus ABV3*, respectively. | |

**Supporting evidence**



**Figure 1.** Genome comparison between ABV, ABV2 and ABV3. Black arrows indicate ORFs conserved across all three genomes, whereas white arrows denote ORFs unique to each genome. Blue arrows denote ORFs conserved between ABV and ABV2. Predicted functions of genes exclusively found in ABV3 are listed below the respective ORF. The figure is reproduced from [2].

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**Figure 2.** Maximum likelihood phylogenetic analysis of protein-primed family B DNA polymerases from bacterial and archaeal viruses, and non-viral mobile genetic elements. In this tree, archaeal viruses comprise the following taxa: *Ampullaviridae*, *Halspiviridae*, *Ovaliviridae, Pleolipoviridae,* and *Thaspiviridae*. The clade including ampullaviruses is highlighted in blue. The sequences were aligned using MUSCLE [3]. Poorly aligned (low information content) positions were removed using trimAl v1.2 [4] with a gap threshold of 0.2. The final alignment contained 705 positions. The maximum likelihood phylogenetic tree was constructed using the PhyML program [5] with automatic selection of the best-fit substitution model for a given alignment. The best model identified by PhyML was VT+G+I+F. The tree was midpoint rooted for convenient visualisation. The branch support was assessed using aBayes implemented in PhyML.

**References**

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