



*Letter to the Editor*

## **Accurate description of phages and their genomes - *Genet. Mol. Res.* 14 (1): 190-198 “Bioinformatic analysis of phage AB3, a phiKMV-like virus infecting *Acinetobacter baumannii*”**

**A.M. Kropinski**

Ontario Veterinary College, University of Guelph, Guelph, ON, Canada

Corresponding author: A.M. Kropinski

E-mail: [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com)

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Dear Editor,

By way of introduction, I have been reviewing bacteriophage manuscripts for 40 years, I am a RefSeq Genome Advisor (phages) to NCBI, and the current chair of the Bacterial and Archaeal Viruses Subcommittee of the International Committee on Viruses Taxonomy. Therefore, I am very interested in accurate published descriptions of phages and their genomes.

You recently published a manuscript entitled “Bioinformatic analysis of phage AB3, a phiKMV-like virus infecting *Acinetobacter baumannii*” (<http://www.geneticsmr.com/articles/3896>), which I regret to inform you contains significant problems:

a) The genome size is significantly smaller at 31,185 bp than its genomic homologs: *Acinetobacter* phages Fri1 (41,805 bp), vB\_AbaP\_PD-AB9 (40,938 bp), Abp1 (42,185 bp), vB\_AbaP\_PD-6A3 (41,563 bp), and IME-200 (41,243 bp).

Examination of the “missing region” suggests that it is highly unlikely that this is a naturally occurring deletion mutant.

b) The orientation of the genome is inconsistent with membership in the *Phikmvlikevirus* genus. Furthermore, one of the characteristic features of this type of phage is that it possesses terminal repeats on the genome, which are absent in the case of AB3.

c) The putative “DNA maturase B” (AB3\_001) does not have a stop codon; and at 489 amino acids all of its homologs are longer: DNA maturase Bs of *Acinetobacter* phages phiAB1, Abp1, vB\_AbaP\_PD-6A3, and IME-200. These phages all encode proteins with 645-amino acid residues.

d) The “putative DNA helicase” (AB3\_0027) at 128 amino acids is significantly shorter than its homologs - DNA helicases from *Acinetobacter* phages phiAB1, IME-200, vB\_AbaP\_PD-6A3, and Fri1 are 432 amino acids long.

e) There is no such thing as a “T7 phage family”. The family is *Podoviridae*, subfamily is *Autographivirinae* and genus is *Phikmvlikevirus*.

f) Figure 1 is of poor quality; and, no size is given in the text. The phage is indicated with a black not a white arrow. I have copied this letter to Dr. Hans- Wolfgang Ackermann who is the world expert on phage morphology in the hope that he may add a few comments.

g) Figure 2 lacks a scale bar.

h) *Acinetobacter* phage YMC/09/02/B1251 ABA BP is actually written YMC/09/02/B1251\_ABA\_BP.

i) Figure 4 is meaningless, and its “results” could have been reported in the text as “the genome of AB3 shows no significant sequence relatedness to ...”

j) The rho-independent terminator and the promoters are not indicated in the GenBank file.

I would strongly recommend in future that you use a reviewer who is thoroughly familiar with phage genomes to review this type of manuscript; and, I urge the authors to resubmit a correct version of their phage sequence to GenBank.