

Review of: "Characterization and complete genome sequence of bacteriophage vB_Vc_SrVc2, a marine phage that infects *Vibrio campbellii*"

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Potential competing interests: The author(s) declared that no potential competing interests exist.

This MS describes some characterization of a bacteriophage vB_Vc_SrVc2 which infects *Vibrio campbellii*. Based on genome sequencing analysis, the bacteriophage vB_Vc_SrVc2 was identified as a member of Maculvirus, Autographiviridae, which has high lytic ability against *Vibrio* species. Bacterial reduction assay further showed that bacteriophage vB_Vc_SrVc2 inhibited the growth of *V. parahaemolyticus* CIBGEN-001, *V. campbellii* CIBGEN-002 and *V. alginolyticus* CIBGEN-004, but had no effect on *V. campbellii* CIBGEN-003. Additionally, the authors confirmed this bacteriophage has a high tolerance to environmental stresses including temperatures, salinity, UV radiation and chloroform. This study may have therapeutic potential to control *V. campbellii* infections in the aquaculture industry.

Specific comments are as follows:

1. (Figure 1) In the bacterial reduction assay, the bacteriophage vB_Vc_SrVc2 inhibited the growth of *V. campbellii* CIBGEN-002, but had no effect on *V. campbellii* CIBGEN-003. This is strange. What is the difference between these two *V. campbellii* strains? Why *V. campbellii* CIBGEN-003 appeared to be more resistant to the bacteriophage? These points should be discussed. In addition, the experiment should be carried out in triplicate.
2. (Figure 4) The survival rate of bacteriophage vB_Vc_SrVc2 dropped sharply to 40% at 20 ppt, but it survived very well at close salinity (15 ppt and 30 ppt, survival rate 100% and 80%). This result needs to be reconfirmed.
3. The major concern of this manuscript is novelty. Phage vB_Vc_SrVc2 has 99.99% identity and 100% query coverage to another phage vB_Vc_SrVc9 which had been reported by the same group (i.e. reference 14). The authors should clarify what is the significance of this report. At least the difference in the effects of these two bacteriophages on the growth of *Vibrio* species needs to be investigated by carrying out further experiments. How the 0.01% genome difference may account for the growth effects, if any, should be discussed.