

Peer-Review Record:

Viruses of Haloarchaea

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First Round of Evaluation

Round 1: Reviewer 1 Report and Author Response

The review of Luk *et al.* on Viruses of Haloarchaea is well-written, comprehensive and could be published after minor revision after answering points mentioned below:

- (1) The authors do not distinguish between the described and hypothetical virus species. Nearly half of the viruses listed in Table 1 have not been described in any sufficient detail. For about half of them, no genomic information is available (according to the ICTV regulations, availability of genome sequence is obligatory for a virus species) and another half is represented only with hypothetical genomes, assembled from metaviromes, which may not even represent viruses with archaeal hosts. All these putative “viruses” should be excluded from the table. They may be presented in a supplementary table. It would be highly appropriate to indicate in Table 1 families to which the listed viruses are assigned.

Response: Table 1 is a key resource of the review summarising the characteristics of haloarchaeoviruses. Many of the viruses listed without genomes, or with hypothetical genomes are referred to in the main text. Consistent with the progress of technologies used to assess microbial ecology, and in this case, viruses of haloarchaea, descriptions about viruses are being gleaned from environmental genomic

studies. Through such discovery science, knowledge of haloarchaeovirus diversity has been greatly expanded. Rather than detracting or providing misleading information, such studies invigorate and prompt subsequent analyses, including providing strong leads for isolation attempts of novel viruses.

To improve the table, we made a number of changes. HTV-1 and CGΦ46 were removed as they have significantly less information supporting their assignment than the other viruses. It would be redundant to state for each virus whether it was cultured and isolated or studied genetically, as it should be obvious from the data available in the table. Moreover, the viruses are arranged according to their stated morphology. To highlight the viruses which have been studied in more detail, they are now in bolded font, with a footnote to clarify. Similarly, since each morphotype corresponds to one viral family, it would be redundant to list the families in a separate column. Again, the footnotes now provide further clarification.

The “virus” column footnote states: “Viruses in bold have been studied in more detail, with both culture-dependent and culture-independent methods”.

The “host” column footnote states: “Proposed viral families were assigned based on morphology, with head-tailed (contractile), head-tailed (non-contractile), head-tailed (short), pleomorphic, spherical and spindle morphotypes assigned to Myoviridae, Siphoviridae, Podoviridae, Pleolipoviridae, Sphaerolipoviridae and Fuselloviridae, respectively. Pleolipoviridae and Sphaerolipoviridae families, and the classification of many haloarchaeoviruses into existing families, have not yet been formally accepted by the International Committee on Taxonomy of Viruses”.

Also note that the clarification about formal acceptance by the International Committee on Taxonomy of Viruses is stated in the legend for Figure 1.

- (2) The references to the number of known haloarchaeal viruses should be revised—much less of them have been described than is mentioned throughout the text.

Response: The total numbers of haloarchaeoviruses mentioned previously have now been changed to more accurately reflect the actual number of confirmed viruses.

- (3) On Page 3, Lines 97–99, the authors erroneously refer to the paper by Bamford 2003 (*Res. Microbiol.* 154: 231–236) as a source of the statement that “... all viruses had a common ancestor that diverged into different viral lineages...”; in the above-mentioned paper it is clearly stated that “... virus origins are polyphyletic, as opposed to the idea of a monophyletic origin of cellular life”.

Response: This section has been rewritten to appropriately cite references and develop possible views about viral lineages.

- (4) In addition to the hypothesis that caudoviruses were introduced to Archaea by cross-domain spreading from Bacteria, mentioned on page 11, Lines 76–78, an hypothesis was also recently proposed about the existence of caudovirus ancestors prior to the divergence between Bacteria and Archaea (e.g., Prangishvili 2013, *Ann. Rev. Microbiol.* 67: 565–585, Krupovic *et al.*, 2011. *Biochem. Soc. Trans.* 39: 82–88).

Response: A section has been added to include the proposed ideas.

Round 1: Reviewer 2 Report and Author Response

The review manuscript “Viruses of Haloarchaea” offered by Alison W.S. Luk *et al.* is a very unique, comprehensive and extremely valuable overview presenting the unexpectedly big world of the fascinating haloarchaeoviruses. As the authors state under 2.1 Viral Lineages, the virus/host systems and their scientific examination is underpinning a phylogenetic web of lateral and vertical inheritance, rather than supporting a coherent phylogenetic tree of the viruses. This will remind evolution biologists of the necessity to widen the horizon and adapt theories and postulations when appropriate. The review is very well investigated concerning literature. Discussions are well integrated into the respective chapters. The chapters of the review cover all kinds of relevant scientific key issues that play a role in phage/virus research nowadays. Comparisons to “usual” phages are conducted. The special life modus of a persistent infection characteristic for representative haloarchaeoviruses is well documented and highlighted in the manuscript. Although electron micrographs are represented as rather small in Figure 1, the morphotypes with their structural principles are documented. Additional micromorphological depictions might increase the already striking appeal of this manuscript. It might be an additional point of scientific interest for the future to investigate a random profile sample aimed at the “free-living” (planctonic) phage/virus diversity in these habitats. I have not yet seen a review article on the haloarchaeoviruses with comparable quality and depth. The review focuses on a young research field but such old phylogenetic systems and highly specialised habitats.

There is a mistake regarding the phage/virus tail lengths under 3.1 Head-Tailed Caudoviruses (Page 11, Line 174): the Myoviridae have contractile tails whereas the Siphoviridae have non-contractile tails.

Response: The correction has been made.

Second Round of Evaluation

Round 2: Reviewer 2 Report and Author Response

The revised manuscript has improved, reviewers’ comments have been included. I trust all the references and reference modifications with their numbers as allocated have been carefully checked. The reference modifications are substantial so that it is a precondition to be sure they all have been cross-checked (again) before accepting the revised manuscript version.

I would have just one more suggestion: this is regarding the genus names abbreviations in Table 1: even if genus abbreviations are officially accepted, it would be easier to read the table if the full genus names would appear instead of the genus abbreviations in the 18 cases where isolates are represented by “sp.” designation (genus abbreviation plus sp.). The reason is that not all readers are experts with respect to these genera.

Response: The references had indeed been checked throughout.

A footnote disclosing all currently accepted abbreviations for haloarchaea genera has been cited in the footnote to the Table with abbreviations retained in the table. The decision to take this approach was achieved in consultation with the publisher to account for journal style.

Genus name abbreviations used are based on those proposed by the subcommittee on the taxonomy of the family Halobacteriaceae; the complete list: Haladaptatus (Hap.), Halalkalicoccus (Hac.), Haloarcula (Har.), Halobacterium (Hbt.), Halobaculum (Hbl.), Halobiforma (Hbf.), Halococcus (Hcc.), Haloferax (Hfx.), Halogeometricum (Hgm.), Halomicrobium (Hmc.), Halopiger (Hpg.), Haloplanus (Hpn.), Haloquadratum (Hqr.), Halorhabdus (Hrd.), Halorubrum (Hrr.), Halosimplex (Hsx.), Halostagnicola (Hst.), Haloterrigena (Htg.), Halovivax (Hvx.), Natrialba (Nab.), Natrinema (Nnm.), Natronobacterium (Nbt.), Natronococcus (Ncc.), Natronolimnobius (Nln.), Natronomonas (Nmn.), Natronorubrum (Nrr.) [80].

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