**Reviewer #1**

Note: Line numbers correspond to the documents with tracked changes. Removing tracked changes in Word changes the line numbers.

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| **Reviewer comment** | **Author response** |
| Some important references in the field are missing. For instance: Pasic et al. 2009 on the metagenomics islands of Salinibacter ruber, Martin-Cuadrado et al. 2015 on the metagenomics islands of Haloquadratum walsbyi, Ghai et al on the Nanohaloarchaea, papers about viral metagenomes and single cell genomics compared with metagenomics, etc. In fact, the impact of metagenomics islands/hypervariable regions on genome recovering should be addressed in the new version. | This is a good point, and we included the suggested references from Pasic, Martin-Cuadrado and Ghai. We also discuss the fact that genomic islands can add to the heterogeneous nature of halophiles genomes (lines 303-305). |
| Metagenomes in hypersaline environments do not always have a high GC content. Indeed, both Haloquadratum and the Nanohaloarchaea have rather low GC genomes. This has to be discussed in the text. | Our phrasing was indeed inaccurate; we fixed this on lines 306 by saying that a majority of halophiles have high GC. |
| When discussing about MAG recovery, maybe the authors would like to mention the usefulness of subsampling. | We added some clarifications of this topic at lines 499-503. With recent advances in assembly with metaSPAdes and MegaHIT, subsampling is not typically recommended, and assembly quality does not drop off with increased coverage as It did with early metagenomic assemblers. Assembly of grouped or individual samples could still benefit the recovery of highly-abundant heterogeneous organisms, however. |

**Reviewer #2**

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| **Reviewer comment** | **Author response** |
| The title and introduction indicate the goal of the review is describing how advances in genome-resolved metagenomics have explained halophilic genomes. However, the review is simply an overview of different methods of genome sequencing and analysis, and does not offer any data on how these have been applied to halophiles and what new data they have uncovered. I recommend either including data on halophilic genome research to the review, or altering the title to describe the review as it currently is: a review of genome based analyses, which is not specific to halophiles. | We agree that the original manuscript contained only general discussion about the benefits of WMGS for halophile research. We expanded this significantly, adding numerous specific examples of how this technology has been used in a variety of high-salt environments. This also ties in Figure 1 and Table 1. See examples in lines 124-129, 131-134, 138-142, 143-148, 155-156, 161-250, and 257-267. Given these extensive changes we though it appropriate to keep the original title of the manuscript. |
| Figure 1 does not really represent the text | We added references to the figure throughout the text when giving specific examples of discoveries from the respective halophilic environments. See lines 124-129, 131-134, 138-142, 143-148, 155-156, 161-250, and 257-267. |
| Figure 1: identify where these images were taken. The bottom left panel does not really represent a deep sea halocline. | The sources for all images are indicated under the figure. All images (except for the halite photo, which is ours) are not copy-righted and are labeled as “free to use and modify, even commercially”. Most come from the free-to-use Wikimedia Commons database. We provided the editor with this information and asked for guidance on how to reference such sources for publication and whether this is appropriate for the journal. We replaced the ocean image with a non-copyrighted halocline image. |
| Table 1 and the entire section from line 87 – 176 are not very useful. The text and table just state that MAG discovery and WMGS have led to novel discoveries in hypersaline environments, but offers no details on what these discoveries are | We agree with this assessment, and added numerous examples of *specific* discoveries enabled by shotgun metagenomics in various high-salt environments to give the readers better context of what this technology offers for their research. See lines 124-129, 131-134, 138-142, 143-148, 155-156, 161-250, and 257-267. |

**Reviewer #3:**

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| **Reviewer comment** | **Author response** |
| Grammatical/textual/syntax errors  1. On page 1 line 21 (Abstract), please correct the misspelling of "no" to "not".  2. On page 1 line 24 (Abstract), please correct the misspelling of "halophiles" to "halophile" (or "halophilic").  3. On page 2 line 47 (Introduction), please correct the misspelling of "functioning" to "function".  4. On page 2 line 75, I would suggest that the authors change the word "lowly-" to "less" as the word 'lowly' is used to describe hierarchy, while I believe the authors here are preferring instead to amount/abundance.  5. On page 2 line 89, a sequencing approach, or any protocol, cannot 'interrogate'. Please change from "interrogates" to "reveals".  6. On page 3 line 111, please change "functioning" to "metabolic function".  7. On page 4 Figure 1 caption, please correct the misspelling of "commonly studies" to "commonly-studied".  8. On page 5 Table 1 title, please change the table title to "A short list of studies..."  9. On page 5 line 189, please correct "1088" to "1,088".  10. On page 5 line 201, please change "These new progress..." to "These new analytical methods..."  11. On page 5 line 205, change to "multiple shallowly-sequenced samples" and also change to "a few deeply-sequenced samples".  12. On page 6 line 213, please change "interrogated" to "investigated".  13. On page 6 line 215, change "enhance" to "enhances".  14. On page 6 line 258, please change "microbiome" to "microbiomes".  15. On page 7 line 272, once again, halophilic metagenomes cannot be interrogated. Please change "interrogating" to "analyzing".  16. On page 7 line 274, please change "specifically trained on/or intended for animal microbiomes" to "specifically designed for animal microbiomes".  17. On page 7 line 282, change "for specific types of microbial community types" to "specific microbial community types".  18. On page 9 line 342, please change "for not only sequencing" to "not only sequencing".  19. On page 9 line 352, please change "lowly" to "less".  20. On page 9 lines 358-359, change to "was successfully applied in 2017 to microbiomes to improve binning predictions (101)."  21. On page 9 line 361, change "extra-chromosomic" to "extra-chromosomal".  22. On page 9 line 367, please change "have" to "has".  23. On page 9 line 381, change "made" to "has made".  24. On page 9 line 385, change "further" to "has further". | All typos and errors have been fixed as suggested. The detailed proof-reading is much appreciated! |
| On page 1 line 28, the formatting of the manuscript is strange. There is an Arabic numeral "1." to denote the "Introduction" section, but then in the rest of the paper, there are no other numbered sections--no "2." or "3.", etc. Please correct and maintain consistency in the formatting by removing the number "1." on this line and just leave the subheading as "Introduction", since all the other subheadings throughout the manuscript are also not numbered. | The numbering was added by the journal's editor. We removed the "1" for now, but cannot control the formating changes that may be made during the editorial process. |
| On page 4 lines 164-169, the authors provide URLs as image credits; however, it would be more proper and correct to cite the actual person or entity that took the image as that would be the correct way to cite copyright. Can the authors please go back and find the individual person's source, even if it is a moniker; but a website that posts an image (e.g., Wikipedia, Wikimedia, etc) is not the copyright owner of the image. | The sources for all images are indicated under the figure (except for the halite photo, which is ours). All images are not copy-righted and are labeled as “free to use and modify, even commercially”. Most come from the free-to-use Wikimedia Commons – a media database specifically for non-copyrighted images free to be used for any purpose. We provided the editor with this information and asked them for guidance on whether this is appropriate for the journal. |
| On page 5 line 189, what is the reference citation for the number of halophile genomes in all databases? | Added reference Loukas 2018 on lines 313 and 507 |
| On page 1 line 8 (Abstract), the authors state that shotgun metagenomic sequencing of microbial life has taken place "In the past decade"; however, metagenomics in general, and shotgun sequencing in particular, has been going on for longer than that--for approximately two decades (twenty years). | Changed to “past decades” to be more inclusive, line 8 |
| The authors may wish to review the following article and citations therein, which date back to at least 2004: Christian S. Riesenfeld, Patrick D. Schloss, and Jo Handelsman. Metagenomics: Genomic Analysis of Microbial Communities. Annual Review of Genetics. Vol. 38:525-552 (Volume publication date December 2004) | We added reference to introduction at line 70 |
| On page 2 line 54, the authors refer to 2008 as a timeline regarding high-throughput DNA sequencing. Please see my earlier comment for line 8 on page 1 (Abstract). | Changed to early 2000s, with suggested reference, line 68 |
| On page 2 line 60, the authors may wish to cite earlier ground-breaking work that pre-date 2016. | We thank the reviewer the suggested 2004 review, which we added to this point in the text. Indeed, the Riesenfeld review describes the early potential of metagenomic sequencing, and serves as a perfect reference. Further more detailed references follow throughout the rest of the review. Line 74. |
| On page 3 lines 99-108, once again, the authors have left out some significant citations, namely the first ever complete metagenomics assembly of two hypersaline viruses, EHP-1 and EHP-2. I understand that the focus of this manuscript is not comprehensive, but since the  authors are discussing the breakthroughs achieved by WMGS in halophilic research, including haloviruses, then they would be remiss to exclude these two citations (Santos, et al, 2007 and Santos, et al, 2010), as well as the other haloviral metagenomics studies by the Anton group. I think it would be best for the authors of this manuscript to review and cite other previous works regarding WMGS of haloviruses. | The studies in the two suggested citations use fosmid libraries to perform the sequencing, and thus do not fit this review’s scope of covering shotgun approaches. However, we added these references when talking about pre-shotgun research era in regards to metaviromes (lines 137). |
| On page 8 line 288, the authors state that as of 2018, there are only 942 published complete halophilic genomes in NCBI; however, on page 5 line 189, the authors state that in 2018 there are 1,088 sugh genomes in all databases. Is there a mistake here? My understanding is that the three primary genomic databases (DDBJ-Japan, ENA-Europe, and GenBank-USA) all synchronize their data. So, if there are 942 complete halophilic genomes in GenBank (NCBI), then those same sequences will show up in DDBJ and ENA. So, why is there a discrepancy between these two numbers--1,088 versus 942--on pages 5 and 8? | We recognize that this was confusing – there are 942 genomes in NCBI, but if you include some periphery databases outlined in Loukas 2018, there are 1088. We simplified this by only referencing the 942 number and explicitly stating that it is in NCBI. Lines 313 and 507 |