Wang et al. - Review no. 2

After revision, the manuscript of Wang et al. increased a lot in readability, most of my suggestions and the ones from reviewer 1 were included into the revised manuscript. Most formal corrections and requests have been addressed.

Still, there are details that have to be addressed, such as the sequencing statistics. This is something that is visible from the raw sequencing files and can hardly been unseen. It is not credible that the authors do not have access to these data, while stating that they did the analysis on their own. I would thus like to see the sequence quality files as part of the fastq files or the sequence raw data. In addition, I have to insist on the information of the sequencing chemistry and protocol, as there are contradicting information even on the type of sequencer between what is given in the methods part and in the NCBI sequence read archive.

Response: thanks for this criticism. We split our data and made a statistic table using the sequencing data. Table S1 shows the details. There was a typo in the previous version. We used Illumina 2000, instead of Illumina 2500. Sorry for the mistake. The sequencing data for the anhydrite amplified DNA were 1.8Gb although we requested 2Gb as shown in the NCBI SRA. After quality control, 1.6Gb was left. After removal of MALBAC primers, we obtained 0.9Gb clean data for assembly and genomic binning. See 275-277 for the description of the data.

Further, I still do not believe the quantification of microbes based on traces of DNA, the quantitative aspect of the metagenomics dataset is not credible based on a not representative amount of DNA, which has likely been subject to different degradation processes. How much DNA has been isolated in total?

Response: There was a total of 500pg of raw DNA using 20g crystals. The quantification was done with a Quant-iT PicoGreen kit (Invitrogen, USA) (line 159). At present, DNA less than 1ng could not be used for library preparation for Illumina. The MALBAC can amplify DNA into fragments of small sizes between 400-2000bp, so degradation of DNA won't notably affect linear amplification of genomic DNA. The linear amplification of MALBAC has been demonstrated in our publication Acta Oceanol. Sin., 2016, Vol. 35, No. 2, P. 131–136 in the reference list. We admit that quantification of microbes was not accurate based on the low amount of DNA. At least, our result showed the compositional discrepancy between the communities in the crystals and the control.

Specific comments (track change version):

l. 102 remove second 'anhydrites', there are several repeated words down to line 128, please remove

Response: This was caused by PDF maker. I cannot find the problem in the final version.

l. 239 Rephrase: Using the classify.seqs command as part of the Mothur software package. Add a reference instead of a link

Response: yes. Done.

l. 247 replace 'in' by 'from'

Response: revised!

l. 393 I don't see genes indicating nitrogen fixation, here

Response: Sorry it was a typo. We revised the sentences in lines 325-328. Ammonia might be imported and assimilated into glutamate as depicted in figure 6.

l. 455 ‘propose’

Response: yes

810: **Response: the sentence was revised!**