

Response to Referee #3's Comments

General Comments

This paper examines atmospheric bioaerosols at three sites downwind of the Gobi Desert in the Dust-Bioaerosol 2016. The authors found that the number of bacteria and the diversity of the bacterial communities increased significantly during the dust events by microscopic observations made with DAPI staining and MiSeq sequencing analysis. In general, this is a well-written paper that presents interesting data. It will be of interest to readers of this Journal, particularly researchers in the field.

Response: We sincerely thank the reviewer for his suggestions. Those suggestions helped to improve the quality of this paper. The authors have taken the comments from reviewer seriously and addressed all comments in current revision. Below are our point-by-point responses to those comments.

Specific Comments

Page 2, line 6: "proteobacteria" should be capitalized.

Response: By following the reviewer's suggestion, we have corrected it.

Page 8: The description of the methods of MiSeq sequencing should be limited. It would help readers if the authors gave a more detailed explanation.

Response: We thank the reviewer for the helpful suggestion, and have revised section 2.4 as follow.

Original Text Pg.8 Ln.4: The genomic DNA (gDNA) was extracted from the atmospheric samples from Erenhot and Mongolia using the PC extraction/alcohol precipitation method. Two-step PCR amplification and product purification were then carried out according to the method of Maki (Maki et al., 2017). Two-step PCR has several advantages, such as increased reproducibility and the recovery of greater levels of genetic diversity during amplicon sequencing (Park et al., 2016). An Illumina MiSeq sequencing system (Illumina, CA, USA) and a MiSeq Reagent Kit V2 (Illumina, CA,

USA) were used to perform the sequencing, and an average read length of 270 bp was obtained. All the data obtained from MiSeq sequencing have been deposited in the DDBJ/EMBL/GenBank database, and the accession number of the submission is PRJNA413598.

Amended Text Pg.8 Ln.4: The genomic DNA (gDNA) was extracted from the atmospheric samples from Erenhot and Mongolia using the phenol chloroform extraction/ethanol precipitation method (Maki et al., 2017). Two-step PCR amplification and product purification were then carried out according to the method of Maki et al. (2017). Two-step PCR has several advantages, such as increased reproducibility and the recovery of greater levels of genetic diversity during amplicon sequencing (Park et al., 2016). During the first-step PCR amplification, fragments of 16S rRNA (which covered the variable region V4) were amplified from the extracted gDNA using the universal bacterial primers 515F (5'-Seq A-TGTGCCAGCMGCCGCGGTAA-3') and 806R (5'-Seq B-GGACTACHVGGGTWTCTAAT-3') (Caporaso et al., 2011), where Seq A and Seq B represent the nucleotide sequences bounded by the primer sets of second-step PCR. Detail process has been described by Maki et al. (2017). An Illumina MiSeq sequencing system (Illumina, CA, USA) and a MiSeq Reagent Kit V2 (Illumina, CA, USA) were used to perform the sequencing, and an average read length of 270 bp was obtained. All the data obtained from MiSeq sequencing have been deposited in the DDBJ/EMBL/GenBank database, and the accession number of the submission is PRJNA413598.

Page 10, line 18 to Page 11, lines 8, Fig. 6, and Table S1: The sample names contain a number of errors. Please check all sample names, including sampling information, and revise them accordingly.

Response: We thank the reviewer for the helpful suggestion, and have corrected all sample names throughout the manuscript and checked the sampling information in the supplement. In Pg.10 Ln.19, the sample name 'ER4_12' has been corrected to 'ER4_12D'.

Page 14, lines 11 and 14: "orders (and class level candidate taxa)" should be "orders (and order-level candidate taxa)".

Response: By following the reviewer's suggestion, we have corrected it.

Fig. 9: The authors should check the symbols in Fig. 9. "DAPI-stained bacteria" should be "Black particle" in Fig. 9 (a). In contrast, "Black particle" should be "DAPI-stained bacteria" in Fig. 9 (b).

Response: We thank the reviewer for the helpful suggestion, and have corrected the symbols in Fig. 9.