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Atmospheric Chemistry and Physics Discussions

Interactive comment on "A next generation sequencing of Arctic bacteria in snow and frost flowers: identification, abundance and freezing nucleation" *by* R. Mortazavi et al.

Anonymous Referee #2

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The General Notes In this study, the authors applied a combination of culture-dependent and independent methods in order to characterize the microbial community structure of five different snow types and frost flowers and discuss their potential role in freezing and melting processes. Climate change is frequently linked to the increasing number of dust storms, which can lead to the transport of microbes to unrelated climate zones. Within those climate zones microbes may survive, propagate, and lead to an overall shift in microbial metabolic potential and ecosystem multi-functioning. Thus, this manuscript potentially represents a significant contribution to atmospheric science in general and particularly to the field of microbial ecology. However, the lack of biological

replicates (each of five snow types represented by a single observation) are a significant weakness of the study. Due to the lack of biological replicates, my suggestion is to focus mainly on community structure comparisons based on diversity parameters (alpha and beta diversity parameters) between the five snow types. Moreover, I suggest to remove frost flowers from this study based on the following reason: bacterial community structure mainly represents a phyllosphere bacterial community that is heavily influenced by a host (plant species) and that is normally exhibits a significant reduction in bacteria diversity (Fig A1). The author should provide a list of accession numbers for both the isolates and the pyrosequencing data. The authors present their results in a very confusing way: (i) Figure 1. In the diagrams, the axes and their values are unreadable; (ii) Figure 2. The legends are also unreadable; (iii) Figure 4 A. The bars are merged and unreadable.

The Specific Notes Page 1 Line 8: "the great majority of sequences (12.3–83.1 %) belonging to one of the five major phyla". Please rephrase to “a majority of sequences (12.3-83.1%)” Page 4 Line 9: "Xant/zomonas" should be Xanthomonas Page 7 Line 20: Please indicate names of 16S universal primers and their concentration in the PCR reactions. Please also provide nucleotide and enzyme concentrations in the PCR reactions Page 8 Line 4: Please provide the accession numbers for characterized isolates Page 8 Line 5: Please separate the "454 Pyrosequencing, and Electron microscopy analysis" section into two sections: (i) 454 Pyrosequencing and sequence analysis (ii) Electron microscopy analysis Page 8 Line 6: Please describe the DNA extraction protocol Page 8 Line 25: Please provide quality filtering parameters (Q values, sequences minimal and maximal lengths); taxonomic assignment algorithm and its parameters. Page 9 Line 2: Please provide the accession number for Pyrosequencing data Page 10 Line 7: Please justify the choice of Chao1 diversity index. The Chao 1 index is based upon the number of rare classes (i.e. OTUs) found in a sample, if your samples were filtered to eliminate singletons, then this estimation is not appropriate. Moreover, in order to conduct an inter-sample analysis using Chao1, the comparisons in your library must be equal in size. My suggestion is to use a Shannon diversity index that is

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much more robust. Page 17 Line 12: "the great majority of sequences (12.3–83.1 %) belonging to one of the five major phyla" Please rephrase to “a majority of sequences (12.3-83.1%)”.

Interactive comment on Atmos. Chem. Phys. Discuss., 14, 32093, 2014.

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