

## ***Interactive comment on “Characteristics of bacterial community in fog water at Mt. Tai: similarity and disparity under polluted and non-polluted fog episodes” by Min Wei et al.***

### **Anonymous Referee #2**

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The authors investigated the differences in bacterial community structures from fog water droplet samples collected from Mt. Tai in North Plain of China including those clear and polluted days in July and August of 2014. They performed sequence analysis of the samples, and also investigated the effects of environmental factors on the bacterial community structure. Overall, it is interesting to study the bacteria in the fog water samples, especially in higher altitude from a ground. The information developed is useful to understanding the microbial transport and possible roles in atmospheric pollutant transformation. The authors provided a number of different analyses of their results and derived some valuable information. Nonetheless, this reviewer does observe the following drawbacks that need the authors' attention:

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1. From their work, it seems they only had one day with higher PM2.5 pollution level, i.e., exceeding 100  $\mu\text{g}/\text{m}^3$ , and they had more samples from clear days with much lower PM2.5 levels. In their work, they compared them and further derived relevant information. I think the authors have to carefully make their conclusions regarding their limited set of data from a single polluted day. Probably, they can use the 24-hour backward trajectories to discuss more on them.
2. It seems they did not clearly define what level of PM2.5 for which a day can be classified as a polluted day in their method section. Also they should clearly define what those symbols such as "FE" stand for? although I guess it should be "Fog Episode", but they should appear in all figure captions so that readers can easily understand the figures. They should describe that the characteristics of each Fog Episode are shown in relevant Tables in each Figure.
3. be aware that they only performed genus level sequence and they cannot derive any particular bacterial species, especially when they discuss about pathogens. For certain genera, not all of their species are pathogens or opportunistic pathogens.
4. I did not see any concentration levels for the total bacteria in their fog water droplet samples? Did they perform qPCR for total bacteria for their samples?
5. It would be great if they can provide data for fungal spores. I guess there will be some fungal spores in the fog water droplets.
6. For certain bacteria, when they are stored at 4 degree C, they can still grow. How long did it elapse between the collection and their actual analysis?

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