1. Please take this opportunity to thoroughly proofread the manuscript to ensure that there are no spelling or grammar issues.

Response 2: Thank you for your suggestion. We are sure that there are no spelling or grammar issues.

2. Please do not highlight notes for filming.

Response 2: Thank you for your suggestion. We have revised the highlighted part including no note.

3. Please do not abbreviate journal titles for all references.

Response 3: Thank you for your suggestion. All the journal titles have been corrected.

4. Step 1.1.2: How to measure and record? Please add more details to your protocol steps. Please ensure you answer the “how” question, i.e., how is the step performed?

Response 4: Thank you for your good question. More details were added to the step 1.1.2 as follow:

1.1.2) In total, measure and record 6 different particle size classes (0.3-0.5 μm, 0.5-0.7 μm, 0.7-2.5 μm, 2.5-5 μm, 5-10 μm and > 10 μm) simultaneously every 5 min. Also measure 4 other particle size classes (0.3-0.5 μm, 0.5-1 μm, 1-3 μm and ≥ 3 μm). Collect the air samples though the sampling hole on the top of the sampler and use the test modules inside the sampler to measure the particle size of each PM. Then the data was stored automatically. All the processes above can be performed automatically after the relative parameters, including sampling time and counting range, were set though the mini touching displayer of the airborne laser particle counter.

5. 4.2.1: What’s the centrifugation rate (in x g) and time?

Response 5: Thank you for your good question. Centrifuge the bacteria sample at 2000 x g for 5 min.

6. 4.2.5: What’s the centrifugation rate (in x g) and time?  
Response 6: Thank you for your good question. After brief centrifugation at 1000 x g for 30 s (no residues on the wall), put the centrifugal tube in 56 °C water for 10 min.  
  
**Reviewers' comments:**  
  
  
**Reviewer #1:**  
Manuscript Summary:  
The manuscript has been substantially improved by providing appropriate modification and other information to each comment.  
I recommend that the revised manuscript may be accepted without modifications.  
Response: Thank you very much for your comments and suggestions. We are looking forward to the publication of this manuscript.   
  
**Reviewer #2:**  
Manuscript Summary:  
This manuscript has revised in dependence on the comments of editor and reviewers. However, there are some remaining issues.  
I recommend publication after major revision.  
  
Major Concerns:  
1) The section of Materials and Methods is thought to be fragmented and does not include sufficient information about sampling methods.

Response 1: Thank you for your good question. More details were added to the step 1.1.2 as follow:

1.1.2) In total, measure and record 6 different particle size classes (0.3-0.5 μm, 0.5-0.7 μm, 0.7-2.5 μm, 2.5-5 μm, 5-10 μm and > 10 μm) simultaneously every 5 min. Also measure 4 other particle size classes (0.3-0.5 μm, 0.5-1 μm, 1-3 μm and ≥ 3 μm). Collect the air samples though the sampling hole on the top of the sampler and use the test modules inside the sampler to measure the particle size of each PM. Then the data was stored automatically. All the processes above can be performed automatically after the relative parameters, including sampling time and counting range, were set though the mini touching displayer of the airborne laser particle counter.

2) The description style for data results (taxonomic composition) has not reached to research article level, and now just data values are shown in the result section.

Response 2: Thank you very much for your comments and suggestions. According to your suggestion, we have shortened the description of the taxonomic composition results as follow:

The air samples were collected in four different types of piggeries by using an Andersen six-stage sampler and then cultured under suitable conditions. The whole-genome DNA of the culturable bacteria collected from each particle stage was extracted and detected by bacterial *16S rDNA* and fungal *ITS* region sequencing. A total of 91 genera and 158 species of bacteria were identified in the culturable bacteria in piggeries. The culturable bacteria community structures in four different types of piggeries, including farrowing house, pregnant sow house, fattening house and weaning house are shown in **Figure 4** with data from stage I to stage VI. The content of different predominant bacterial genera is not the same among different piggeries.

3) The aims of study also should be re-written for showing the comparison between liquid and filter sampling and between 16S and ITS.  
Response 3: Thank you very much for your comments and suggestions. We have added the relative description as follow:

In this study, we explored multiple types of analyses of bioaerosols, including PM number monitoring, bioaerosol collection and biological composition analysis. Air samples were collected by a cyclonic aerosol sampler, a high-volume air sampler with filters and an Andersen six-stage sampler. Then, the samples collected by these three samplers were analysed by biological analysis including bacterial *16S DNA* and fungal *ITS* sequencing to determine their biological compositions. Herein, we show representative results from the bioaerosol samples collected during Beijing hazy days and from livestock farms indicating that bioaerosols might have great impacts on human and animal health. The comparison between liquid and filter sampling methods were also explored in this study mainly based on the data from *16S DNA* and fungal *ITS* sequencing.

Minor Concerns:  
"16S rRNA genes" and "ITS" are not shown as italic letters.

Response: Thank you very much for your comments and suggestions. I have revised all the “16S rRNA” and “ITS”, all of them are italic letters in the revised manuscript.