The manuscript describes a study on the parameters affecting airborne microbial community composition, e.g., season, dust intrusion, geographic proximity to the dust source. These are important questions in the study of aerobiology, especially in the Mediterranean basin that is prone to increasing frequency of Saharan dust intrusions.

My specific remarks are:

L. 20: "…two opposite localities…" – should be "locations".

L. 26: "(118 vs. 65)" – should be moved towards the end of the sentence or removed altogether, at its current location it is unclear what it refers to.

L. 67-68: "Fungal taxa were also analyzed along with their and relationships…" – please correct this sentence.

L. 130-144: This added section describes the samples and their conditions fully and clearly.

L. 143-144: The term "flanking" is somewhat misleading here. The selected sampling events, on a chronological axis are: dust event, clear day, clear day, dust event. There are no samples before the first dust event or after the last one.

L. 147: There is a stray "." . Please remove.

L. 247: "collection during dust outbreaks under winds from Africa" – the phrasing "under winds" is not correct. Please rephrase.

L. 248: "collection upon under opposite…" – please correct.

L. 252: "add visual aids to each chart attributes" – please remove.

L.257: "their maxima were seen…" – does this refer to all core taxa mentioned, or only to Actinomycetales? Please clarify.

L. 273-274: abrupt line break, please correct.

Table 1: Please add standard deviation to mean values.

Table 2: According to the data presented in this table, the mean variance between the two halves of a single dust event was higher in Cagliari than in Sassari, this is opposed to the number of orders that showed a variance that surpassed the chosen threshold (Table 3). How do the authors interpret each observation?

Table 3: Why show the richness in orders? How is it better than showing the number of OTUs?

L. 377-392: ANOVA is an inadequate statistical test to determine differential abundance. I suggest following the approach presented in Gloor et al., 2017 (Front. Microbiol.), which the authors are familiar with (L. 467), yet for some reason chose not to follow.

L. 424-430: The authors' claim, that an air sample is a built-in average of XXX liters of changing atmosphere, is unreasonable. As the authors themselves state, there is a high day-to-day variability in atmospheric microbiome, yet the hour-by-hour changes

are gradual, as the authors themselves must have noticed when analyzing dust events on a 12h basis. When comparing samples that were obtained by 24h of sampling, it is still important to obtain sufficient replicates of the same scale, for statistical significance. Had one chosen to sample 10 liter of sea water, would it be acceptable to obtain a single sample to represent each condition, claiming that it is an average of 10000 ul of diverse microcosms? Avoiding adequate sampling design by suggesting that the samples themselves represent averages of smaller increments is unacceptable in aerobiology as it is in any environmental microbiome study.

Each environmental sample is somewhat different than its replicate, and some environmental conditions are difficult to replicate, such are dust events. This should encourage deeper and more extensive sampling, and not the opposite. The authors could make the effort to sample more times on clear days, which are not as rare, and their study would only benefit from this choice. In the lack of more samples, it is statistically irresponsible to compare 3 different variables.

L. 467: As the authors cite the problem well defined by Gloor et al. (2017), why not implement the suggested solution to their work? The cited paper gives adequate tools to overcome the compositional nature of sequencing data, yet the authors chose to ignore it altogether.