Biogeosciences Discussions

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# Comment on bg-2020-469

Anonymous Referee #1

Referee comment on "Bioaerosols in the Amazon rain forest: temporal variations and vertical profiles of Eukarya, Bacteria, and Archaea" by Maria Prass et al., Biogeosciences Discuss., https://doi.org/10.5194/bg-2020-469-RC1, 2021

Prass et al. provide an analysis of the domain level diversity of bioaerosols from the Amazon rainforest. This dataset provides a window into an area of the atmosphere considered to be less affected by human pollution, which could help deconvolve what microbes are "naturally" in the atmosphere vs there by human-activities. It also provides a dataset that focuses on enact cells compared to sequencing methods that could also include eDNA.

**Major comments:**

1) The manuscript would be improved by more discussion of other bioaerosol-microbe focused papers and how they relate to the current findings, such as Souza et al. 2019 (referenced but not discussed), Stern et al. 2021; Env. Sci.&Tech. Zhen, Sci. Total Environ. 2017; Yamaguchi, N. Sci. Rep. 2012. What is known about the different domains and their potential ecosystem roles or residence times?

2) The study seems to pause right when something unique to FISH (the future work proposed at the end of page 10) could be presented. It is unclear why only FISH was utilized. The current standard for airborne microbiology appears to be sequencing based (see papers in point 1), which provides higher taxonomic resolution than the domain level FISH analysis conducted in this manuscript. 16S rRNA qPCR is more robust than microscopy for counting as well. The manuscript lacks an explanation why sequencing techniques were not applicable for this system (why wasn't FISH and sequencing done?) and should justify the decision to only look at domain level diversity (why weren't more FISH probes used?).

What is the standard microbial density of a given aggregate? Are all domains found in physical association? Separate? How are they dispersed on the aggregate? This would be

something a sequencing-only study could not provide and better justify the methods used. There are qualitative statements to this effect that could be expanded upon (pg 10 lns 13-16).

3) It is unclear why there is an improved understanding of bioaerosols from the number of bacteria present as opposed to total number of microbes present. For example, the paper states that these data provide constraints on mixing information, but it is not known if the bacteria are the same or different throughout. Is it the same population of bacteria that travel through the different heights? Or entirely different bacteria?

**Minor and specific comments:**

Methods - It is not clear how the determination for the genome size of all bacteria and archaea was made. Was this an average of all the genomes? How might this vary between cells?

The SD is very high compared to the average (Table 1). How many filters were counted? A supplemental table of each count conducted per time/height would be useful. It would be useful to know the variability in counting a given filter (variability in counts per field of view) separately from the deviation between filters counted for a given experimental filter (Table 1).

Man-made could be replaced with anthropogenic or human.

Figure 2 – why are there no "unknowns" for Mar 1 and Mar 2?