

Interactive comment on “Microbial functional signature in the atmospheric boundary layer” by Romie Tignat-Perrier et al.

Anonymous Referee #2

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General comments. This is an interesting study with a metagenomic analysis of a large amount of air samples from different parts of the world. The resulting metabolic signatures are attempted to correlate with other environments, both aqueous and terrestrial. The metabolic functions related to stress and resistance are analyzed and a predominance of those of fungi is observed. As a main conclusion, it is said that there is no specific atmospheric signature, but correlations with underlying ecosystems can be established. The great merit of this work is to develop a metagenomic study from air samples. In aerobiology, low biomass and low efficiency of the samplers make the application of molecular methodologies very complex. On the other hand, having been able to analyze samples in different parts of the world and different environments, is also a great success of this study, although that makes the results difficult to follow, es-

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pecially when rpuntos about the underlying ecosystems, whose results do not appear clearly. Specific comments. - My main comment is regarding the underlying ecosystems. I have not found data on how the samples were sampled or how they were processed. It is also not clear to me where they came from. Some data are given in table S2, but it is not clear where they come from and why the samples are selected. On the other hand, are they exactly underlying ecosystems? That is, did the soils, sea waters or snow samples correspond to the sites where air samples were being collected? It is interesting to introduce soil samples far from the air sampling sites, but also to analyze those closer. The same applies to snow or sea. - On the other hand, much importance is given to fungi, but little is said about bacterial metabolic activities. - Didn't they consider the possibility of analyzing other eukaryotes or archaea as well? - L108-112. In aerobiology controls are vital. In this study, it is commented that control filters were taken based on previous studies (Dommergue et al. 2019). Can you give more details about these controls? Were they processed together with the rest of the samples? What results did they give? - L242. The qPCR data are said to be from a previous paper and are summarized in table S4, but it hardly presents any data, most of the sampling points do not appear. - In general, the legends and characters on the charts are difficult to read, especially those on the supplementary material.

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