

Interactive comment on “Determining the hierarchical order by which the variables of sampling season, dust outbreaks occurrence, and sampling location, can shape the airborne bacterial communities in the Mediterranean basin” by Riccardo Rosselli et al.

Riccardo Rosselli et al.

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Youssef Yanni (Referee) yanni244@yahoo.com Received and published: 11 February 2021 This is a track changes version of the text containing some notes and corrections that can improve the quality of the abstract and can through light of the revision needed for the entire parts of the context. I hope that they can assist production of a revised version suitable for publication. The revised text is also attached to the email for just in

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case the following text is not fully informative!

Abstract. An NGS-based taxonomic analysis was carried out on airborne bacteria sampled at ground level in two periods (May and September, XXXX) and two opposite localities on the North-South axis of the Sardinia Island (Between Latitudes XXXXXX to XXXXXX). Located around their central position of the Mediterranean basin, Sardinia constitutes a suitable outpost to reveal possible immigration of bacterial taxa during transcontinental particle discharge between Africa and Europe. With the aim of verifying relative effects of dust outbreaks, sampling period and sampling site, on the immigrating airborne bacterial community compositions, we compared the bacterial loads of air collected during dust-carrying meteorological events to that coming from wind regimes not associated to long-distance particle lifting. Results indicated that: (a) a higher microbial diversity (genera or sp.) (118 orders vs. 65) and increased community evenness were observed in the campaign carried out in September in comparison to the one of May, irrespective of the place of collection and of the presence or absence of dust outbreaks. (b) During the period of standard wind regimes without transcontinental synchronous outbreaks a synchronous, concerted succession of bacterial communities across distant locations of the same island, accompanied as mentioned by a parallel rise in bacterial diversity and community evenness appears to have occurred. (c) changes in wind provenance could transiently change community composition in the sampling locality placed on the coast facing the incoming wind, but not in the one located at the opposite side of the island; for this reason thus, (d) the community changes brought from dust outbreaks of African origin were observed only in the sampling station exposed to the south; (e) the same wind outbreak, once proceeding over land appears to uplift bacteria belonging to a common core already present over the region, which diluted or replaced those that were associated with the air coming from the sea or conveyed by the dust particulate, explaining the two prior points. (f) the hierarchy of the variables tested in determining bacterial assemblage composition results are: sampling period > ongoing meteorological events > sampling location within the island. Interactive comment on Biogeosciences Discuss.,

<https://doi.org/10.5194/bg-2020-324>, 2020.

ANSWER: We thank the Reviewer for these suggestions marked on the abstract. Apparently the tracked changes ended up mixed with the text, including the one that was meant to be substituted. As consequence, there are a number of typos scattered through the text that the Reviewer has sent, which make many points not easy to interpret. However, if we understood correctly the reviewer's words, these inputs were meant to suggest details to be expanded in the manuscript and we tried to follow these recommendations. Specifically, the geographical coordinates of sampling stations are shown in section 2.1 The year and other temporal details are in section 3.1.

Interactive comment on Biogeosciences Discuss., <https://doi.org/10.5194/bg-2020-324>, 2020.

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