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Biogeosciences Discussions

Interactive comment on "Detection and phylogenetic analysis of coastal bioaerosols using culture dependent and independent techniques" *by* R. Urbano et al.

Anonymous Referee #1

Received and published: 20 September 2010

General comments The study reports on the composition of bacteria and eukaryotes on aerosols obtained from a pier in Southern California. The most interesting result is that the bacteria/fungi in the aerosols did not seem to originate from seawater. While I like the setup and idea behind the work, I have concerns when it comes to the data and the manuscript. The amount of data (sequences) presented is very low, and I consider it to be at the very edge of what can actually be published. A minimum requirement is that the authors explicitly in the abstract and in the text highlight the low number of sequences on which their conclusions are drawn. Since the authors retrieved plenty of DNA (35->500 ng) it is a mystery to me why so few clones were sequenced. This needs to be addressed. Despite that the idea behind the study seems very clear-

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cut, the manuscript is not very clear. Introduction, Results and Discussion appear lengthy and are not written in a concise manner. Several sections, especially in the Introduction, appear review-like and need focus. A thorough make-over as well as general shortening of the complete text would benefit this work.

Specific comments 1. 1, 8-9. You did not investigate the exchange of airborne microorganisms at the air-sea interface. Please, remove. 2. 1, 11. Given the limited number of clones and isolates, you are not "determining the microbial diversity". Rephrase to e.g. "get insights into microbial community composition". Moreover, the number of clones and isolates obtained should be evident from the abstract. 3. 2, 17. or instead of and 4. 2, 25. To help readers not familiar with this subject, please explain what 0.7-0.11% means. 5. 3, 29. influenced 6. 4, 19. Please, insert the answer to that question. 7. 4, 22. What were the filter diameters? 8. 4, 25. In centimeters, please. 9. 5, 3. It is unclear what is meant by control filters. What was exactly done? Were they just blank filters run in parallel? Did you try to PCR amplify from these control extracts? It appears so from 8, 17. This needs to be carefully described. 10. 5, 10. Delete "all" 11. 5, 11. pH? 12. 5,21. 18s rRNA gene amplification. This needs to be corrected throughout the manuscript. You are not working with 18S/16S rRNA or 18S/16S, but with 18S/16S rRNA genes. 13. 5, 24 + 6. It is important for the reader to know the fragment sizes you're working with. Please insert position in association with the primer specifications. 14. 7, 5. Primers, not probes. 15. 7, 9-10. What is meant by all data? 16. 7, 13-14. This is self evident. I suggest deleting this sentence 17. 7. The obtained sequences need to be submitted to GenBank and accession numbers given here. 18. The Results section should be consistently in past tence. The whole section needs a complete make-over when comes to language and content. It looks very preliminary and I suspect that the corresponding author did not put effort into this section. That is indeed needed and required to make the text readable, non-redundant, and only contain appropriate information. 19. 7, 22. Delete methods 20. 7, 23. These are isolates and not clones. Revise this throughout the ms. 21. 8,16-17. Exactly how were these tests performed? 22. 9, 13. R.? 23. 9, 14. Unclear. Please clarify. 24.

BGD

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9,22-26. Revise sentence. It appears as if you expect fungi sequences by Scripps Pier because they have been found in the tropical rainforest, which doesn't make sence. 25. 9, 22. phylum 26. 10, 7-9. In principle it is extremely limited what you can say about the composition of bacteria/fungi in the aerosols based on the total of about 40 sequences obtained from isolates and clones. It needs to be highlighted in the text that the conclusions of this work is based on a very small dataset – and the authors need to be very careful with the conclusions drawn. 27. The discussion appears lengthy and could be written in a more concise manner.. For instance, I suggest deleting 11, 3-10 28. Since sequences representative of common marine bacterioplankton species were not found, the authors suggest that fungi and bacteria in the aerosols originate from the sandy beaches. The logic question is then, which bacteria/fungi are known from sandy beaches? I'm sure there are many references to choose from. The authors should make this comparison. Without it the suggestion is just unsubstantiated speculation that should be removed.

I think it would be appropriate to cite the following study, which to me appears very relevant to the present study: Camilla Fahlgren, Åke Hagström, Douglas Nilsson, and Ulla Li Zweifel Annual Variations in the Diversity, Viability, and Origin of Airborne Bacteria Appl. Envir. Microbiol., May 1, 2010; 76: 3015 - 3025 . Figures Figures 2 and 3. Accession numbers for GenBank sequences should be given in the trees. It is very unclear what the designations mean: A, DF, C, D, D7(H), B/C+, B – please, describe this clearly somewhere in the ms.

Interactive comment on Biogeosciences Discuss., 7, 5931, 2010.