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Biogeosciences Discussions

Interactive comment on "Molecular genetics and diversity of primary biogenic aerosol particles in urban, rural, and high-alpine air" *by* V. Després et al.

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MS-NR: bgd-2007-0010 Title: Molecular analysis and diversity of primary biogenic aerosol particles in urban, rural, and high-alpine air Author(s): V. Despres, J. Nowoisky, M. Klose, R. Conrad, M. Andreae, and U. Pöschl

General comments This paper describes an initial broad survey of DNA in aerosol particles from a variety of sources to cover almost all classes of potential biogenic aerosol. The one omission is viral NA but I am not aware of any simple way to obtain coverage of this group as a whole. Sampling was performed in 3 very different sites and the paper demonstrates the power of molecular methods to characterise biogenic aerosols

and contains useful information regarding the levels and sources of DNA in aerosol particles. The identification of the same two sequences at all sampling locations is intriguing and may prove to be the most important finding. This could indicate selection for particular bacteria in the atmosphere and gives further circumstantial evidence for an atmospheric ecosystem. It suffers in some respects in that there were different types of filters used, that they were stored for different lengths of time and that blanks were not available for all filter types. However full analysis was only carried out were filters had been decontaminated prior to sampling. It does demonstrate the range of filter types which can be used for this type of work although an indication of which was the easiest to set up and process would have been useful. A rather limited number of clones were analysed which reduces the impact of the paper. The fact that TRFLP apparently covers more of the diversity is, I think, a consequence of this.

This initial pilot has shown the wide range of biogenic aerosol particles which can be detected and possibly quantified using molecular approaches. It invites a larger more controlled analysis where some of the technical variability can be eliminated and by increasing the amount of sequence data obtain a greater insight into the nature of biogenic aerosols.

Specific comments

p 355 It appears that only a single PCR was carried out for each analysis and that 35 cycles were used. I feel bias would be reduced if several replica reactions were pooled prior to analysis and if the number of cycles were reduced, particularly if inferences about abundances are to be made.

p 363 lines 1-3 I found this a bit confusing. It is not clear to me how many clones were taken for each PCR reaction and how these relate to the table 3. Were 7 products obtained for a single PCR? This needs clarification.

p 365 The tentative tying together of the TRFLP data and the sequence data is of interest and I wonder if greater confidence would be obtained by labelling both primers

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with different fluorophores. If fragments from both ends correspond to a particular sequence this would be a more rigorous test of a match. p 367 line 12 In discussing the differences between different studies this is more likely to be a combination of both aerosol variability and technical points as aerosols are thought to be highly variable in time and space and this would be exacerbated by variation in techniques.

p 367 line 20-21 I feel a bit more explanation or at least a reference regarding the sequence data being “biased by the cloning procedure” is required.

Technical corrections p 352 line 5 insert fragment between restriction and length. Table 1 complete blanks with ND (not determined) if appropriate. Table 5 complete unknown row with 0 if appropriate.

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