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Atmospheric Chemistry and Physics Discussions

Interactive comment on "Characterization of free amino acids, bacteria and fungi in size-segregated atmospheric aerosols in boreal forest: seasonal patterns, abundances and size distributions" *by* Aku Helin et al.

Anonymous Referee #2

Received and published: 23 August 2017

General comments

In this study, DNA and free amino acids (FAA) were analyzed using quantitative polymerase chain reaction (qPCR) and liquid chromatography-tandem mass spectrometry techniques, respectively, in order to characterize particulate matter of biological origin (bioaerosols). In qPCR, two target specific amplicons and one genus specific amplicon were chosen to quantify bacterial and fungal DNA and DNA of the genus Pseudomonas. For each sampling interval covering several days, two sets of size segre-

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Discussion paper

gated (<1.0, 1-2.5, 2.5-10 and > 10µm) aerosol samples were collected consecutively for the two analysis methods in a boreal forest at the SMEAR II station in Hyytiälä, Finland. Data sets ranging from February to October 2014 were complemented with meteorological and atmospheric gas data from the same site. FAA and microorganisms concentrations derived from qPCR results were analyzed for correlation to meteorological data and their seasonal trends interpreted together with backward air mass trajectories calculated with the HYSPLIT model from NOAA Air Resources Laboratory. FAA and DNA showed high abundances during the spring pollinating season and in autumn corresponding to concentration maxima of bacteria and fungi, respectively. Their distribution over size fractions provided information on contributing dispersion mechanisms. Also rainfall was shown to correlate to bioaerosol abundances.

The analysis methods proposed in this paper represent a substantial progress in the ability to track sources of biological aerosol particles as target groups or genus specific abundances. Linear correlations from (multivariate) variance analysis of FAA and DNA abundances also supported interpreting interactions of aerosol sources with meterological parameters. The manuscript outlines appropriately background information on bioaerosols including an extensive list of references followed by the experimental section which is kept compact and fluent by moving details to the Supporting Information (SI). Assumptions and estimations necessary for quantification such as the calculation of cell concentrations are described clearly and backed by references. The extensive SI includes detailed descriptions not only of the sample set collected as well as the materials and analysis procedures used, but also information on testing and validation measures taken to verify critical parameters affecting data quality such as blanks, recovery and selectivity. Results and interpretations are described clearly, taking into account related work. Also, limitations of the current work and an outlook on future research exploiting higher time resolution and long term measurements are pointed out. Considering the above, I therefore recommend the manuscript to be accepted subject to a few technical corrections.

Specific comments

As already pointed out by referee #1, the use of the term primary biological aerosol particles (PBAPs) defined in detail in one of the references (Despres et al., 2012) may be considered instead of bioaerosols. At the end of page S21 in the supplementary information it is already in use without prior definition.

Technical corrections

line 97 word 9: weighted → weighed

line 121 end: primers pairs → primer pairs

line 586: Ozler → Özler

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