Atmos. Chem. Phys. Discuss.,
https://doi.org/10.5194/acp-2020-569-RC3, 2020

Atmospheric Chemistry and Physics Discussions

Interactive comment on "Drivers of the fungal spore bioaerosol budget: observational analysis and global modelling" *by* Ruud H. H. Janssen et al.

Anonymous Referee #3

Received and published: 9 September 2020

Overall comments:

This manuscript presents the development of a new parameterization, suitable for use in regional and global atmospheric models, of the emissions of fungal spores to the atmosphere, as a function of meteorological and land surface parameters. The new parameterization is derived based on a large dataset of fungal spore counts from the American Academy of Allergy, Asthma and Immunology (AAAAI), which has previously not been exploited for this purpose. Since visual counts of fungal spores are widely understood to be the most reliable measurement of atmospheric fungal spore concentrations that is typically available (despite potential limitations), a parameterization based on this new data source can be expected to have greater reliability than previous parameterizations based on other proxy measurements (e.g., mannitol con-

centrations, and concentrations of fluorescent biological aerosol particles, FBAP). The new parameterization should especially be relevant within the region from which the observational data were obtained (North America), but has been developed on the basis of variables that are globally available from observational datasets and/or within atmospheric models.

In addition, the new parameterization uses an approach to estimating the relationship between fluxes and near-surface concentrations based in a simplified approach to modelling the convective boundary layer that involves some limitations and assumptions, but which is more sophisticated than (and likely an improvement upon) the approaches taken in the development of some earlier parameterizations for fungal spore emissions. The parameterization is selected via a regression model, which is similar to the approach taken in Heald and Spracklen (2009), but which considers more variables and uses an improved statistical approach for model selection (i.e. multiple linear regression with model selection via the Bayesian information criterion to select the best model while avoiding over-fitting). Also, a biological-growth-based model is proposed in addition to the statistical regression model. Finally, the new parameterization is evaluated by comparison with normalized FBAP measurements (seasonal cycles and vertical profiles), and several sensitivities of the model are discussed.

In summary, this paper represents a significant advance in emissions modelling of fungal spores, and is within the scope of Atmospheric Chemistry and Physics. Most of the questions I had are already addressed by the authors with appropriate caveats in the manuscript in its current form. The neglect of horizontal advection in the inference of emission fluxes is likely a meaningful limitation, but one that is not possible to address with the approach/framework used here. Diurnal cycles of emissions (and their interaction with the diurnal cycle of the convective boundary layer) are also not addressed, but it appear that the existing data do not have sufficient time resolution to allow investigation of these cycles.

Based on my evaluation, I recommend that it be published after the following questions

and comments are addressed.

General questions and comments:

1. The main question I had about this paper is regarding the equilibrium boundary layer approach used to derive the flux estimates. I was not entirely convinced that the prior use of this method for inferring CO2 fluxes is adequate justification for its use in inferring aerosol fluxes, since CO2 is considerably more well-mixed in the atmosphere and has fewer complicating removal processes (especially wet removal). The study by Perring et al. (2015) is cited as showing that FBAP concentrations decline with altitude within the PBL, which seems to contradict the reliance on the assumption of well-mixedness. The approach relies on the assumption that convection maintains a well-mixed boundary layer; this assumption will not always be met, and there are likely systematic relationships between the times when the assumption is violated and some of the model's predictor variables (e.g., near-surface temperature). Diurnal cycles in emissions could also complicate the validity of the approach.

I think some discussion/analysis of how frequently the underlying assumptions of this approach are likely to hold would be warranted – especially the assumption of a boundary layer that is well-mixed with respect to both scalars and aerosols.

2. It strikes me as almost slightly contradictory that the temperature plays such a small role in the statistical model obtained via linear regression (Figure 3), yet the threshold value in temperature is shown to have a large impact on simulated emissions, and temperature also is a key variable in the population model. A priori, I would expect that fungal spore growth has an important, but non-linear, dependence on temperature, where growth would be inhibited at colder temperatures that are sub-optimal for fungal spore growth (as is also embodied in the population growth model). I wonder if the model would show a dependency on T if the analysis were repeated with a different statistical (or machine learning) method that allows for potential nonlinear dependencies. I recognize that would entail a significant amount of work (essentially repeating

the entire study), which is not necessary (and might not lead to improvement!).

But here I think it would be helpful if the authors could comment on (1) whether such approaches were tried and discarded for some reason, and (2) whether there is any notable relationship between the model-data mismatches (in modelled versus derived emissions and likely predictor variables including T at 2m and 10m (as might be revealed by a scatterplot).

3. The normalization of FBAP to compare with the spore data is appropriate considering the limitations of both types of observations. However, I think the normalization factors should be reported, as it would be informative for readers to know how much scaling had to be applied and how consistent or different this was between the datasets. Additionally, for the normalized vertical profiles in Figure 10, I was unable to find an explanation in the text of how the normalization factor was determined (I think so that the largest value in each vertical profile is 1?).

4. A key difference between the new proposed scheme and the HS09 scheme, which I think is not discussed, is the geographic representativeness. The mannitol data used in the HS09 scheme (Elbert et al., 2007; Table A3) includes a large number of data points from tropical rainforests of Brazil, which are not represented in the AAAAI dataset, as well as some extratropical data, which are mostly from Europe. It should be pointed out explicitly to readers that the geographic sampling is quite different from the data used for the previous parameterization (in addition to the differences in the measurement type and assumed size distribution, which are already noted).

Minor and typographical comments: P 6, l. 18-19 and l. 23-24 are partially redundant. p. 7, l. 24: some commas missing here inside the parentheses

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