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Atmospheric Chemistry and Physics Discussions

Interactive comment on "Global modeling of fungal spores with the EMAC chemistryclimate model: uncertainties in emission parametrizations and observations" *by* Meryem Tanarhte et al.

Anonymous Referee #2

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A. Summary:

This study presents and compares the results of three published parameterizations of fungal spore emissions against available PBAP observations from the literature. I find this work useful in exploring the impact of different parameterizations on the emission strength and the atmospheric burden of fungal spores in global models. This work also provides a nice compilation of recent FPAB observations database. However, a number of issues have to be addressed before the final publication in ACP.

B. Major comments:

1) As it is stated in the manuscript, fungal spores (and bacteria) are simulated as "pas-

sive" tracers. However, the dry deposition, the sedimentation and the wet scavenging parameterizations in the model are not presented. The authors have to be more specific on the PBAP removal parameterizations in the model and not just refer to previous publications. Moreover, taking also into account that PBAPs are present mostly in the coarse mode, the sedimentation should be a significant process for their atmospheric lifetime. For this removal parameterizations of PBAP in the model should be presented and discussed in more details in the manuscript.

2) The authors present the different fungal spores' parameterizations without any further explanation of the factors considered. Although these formulations are already published, in a manuscript like this, they should be at least discussed in some details: e.g., if the constants used in the fungal spore emission parameterizations resulted by "a best fit" of the respective modelling studies, how do the authors justify that they can be also be applied successfully in their model domain? Can the authors further propose and present an updated parameterization (especially focused on the constants used; e.g., the 500 m-2 s-1 or 2315 m-2 s-1) that may fit better with their observation database? If, yes, please provide an additional (sensitivity) simulation and compare with observations.

3) The authors show that the simulated bacteria concentrations are dominated against the fungal spores in the model. However, the bacteria emission (and removal) parameterizations are hardly (or not at all) presented in the manuscript. For completeness, please add bacteria model (emission and removal) parameterizations, rather than just referring to previous publications.

4) The authors do not state anything on how they treat PBAPs solubility in emissions (or in the atmosphere). Do you consider both bacteria and fungal spores as totally insoluble in emissions? As far as I can understand, you consider all PBAPs as insoluble tracers and you probably do not apply any atmospheric aging (e.g., see Sesartic et al., ACP, 2012, doi: 10.5194/acp-12-8645-2012, for bacteria). Thus, the model overestimation compared to observation may be also due to the fact that you treat them as

total insoluble and you underestimate wet scavenging. Please explain and discuss.

5) In the manuscript, it is stated that "laboratory-based observations have shown that the WIBS FL3 channel utilized here is less efficient at detecting bacteria". It is, somehow, confusing the reason for including the bacteria simulated concentrations in the FBAP comparison with measurements: e.g., on one hand, it is stated that "modeled bacteria-containing and fungal spores particles considered in this study are consistent with this observed size range of peak FBAP concentrations ($1 - 4$ μm), enabling a more accurate comparison" and on the other hand the authors limit the WIBS comparison only on FL3 which is less efficient in bacteria. Moreover, it is stated that observations it is likely to also contain pollen. Since the authors present mean FBAP number concentrations integrated either to 0.8 μm - 15 μm or 1.0 μm - 20 μm, why they do not also consider pollen in their comparison? Note that, according to Després et al., Tellus B, 2012 (doi: 10.3402/tellusb.v64i0.15598) and Jacobson and Streets, JGR, 2009 (doi: 10.1029/2008JD011476), the pollen grains may vary in size between 10 up to $\sim$100 μm, thus they may contribute on FPAB observations. Please explain and discuss.

C. Minor comments:

1) The authors state that "the SD derived fungal concentrations are the least comparable to observations (page 9, line 22-23)" probably, due to the different ecosystem database. It would be useful for the reader to present and discuss more on the differences of the two datasets (e.g., in the supplement) to justify their conclusions; or even perform an additional simulation with the current set-up of the model (i.e., also for the bacteria emissions). Should the constants for each ecosystem used in the PBAP emission parameterization need to be recalculated in case of changing an ecosystem database? Please discuss.

2) P.7 line 27. Please explain what FL3 channel stands for. What other channels exist? Where they are used and how?

3) The authors state that "discrepancies between model results and observations

may be explained by the rate of removal by dry and wet deposition". Please add the dry/sedimentation/wet deposition budget terms (separately) as calculated by the model, in Table 1.

4) Page 10; lines 8-9. This is not clear. Do the authors mean the results on the comparison with observations? Why present only the 2 formulations since in the manuscript the authors discuss at least the 3? Please clarify.

5) The authors state that a strong difference between non-urban and urban observations on model simulations (page 10; lines 22-28). Since the HO formulations take into account only the LAI and specific humidity (q) as variables, isn't it expected at least in urban locations, that the simulated fungal spores will be better correlated with q rather than LAI? Please discuss more your conclusion.

6) Page 13; lines 24-25: "Most bacteria are not strongly fluorescent in the applied wavelength channels and are therefore underestimated. This might explain the differences when we expect high bacterial counts, e.g. Savage et al. (2017)": why, then, the authors consider bacteria in their validations? Please explain.

7) It is hard to understand, in general, when the authors discuss PBAPs (as a sum) and when just for fungal spores. Especially in the validation part, it is not always obvious the importance of the different fungal spores' emission parameterizations on the PBAP concentrations.

D. Technical comments:

1) An outlook paragraph at the end of Sect. 1 will help the reader.

2) In page 9, there is a repetition of lines 1-2 in lines 26-28.

3) Please provide the respective equations of the modified normalized mean bias (MNMB) and the fractional gross error (FGE) in the manuscript (p.9; Sect. 3.2)

4) It is obvious from the manuscript that both PBAP observations and modelling include

significant uncertainty. It would be nice the model to observation comparisons to be presented with error bars to highlight this uncertainty.

5) P. 11; line 32: 'Therefore, the differentiation between HO5 and HO3 fungal spore concentrations is relevant in the comparison.' Please rephrase or explain better.

6) Table 2: The values in bold are not obvious.

7) Figure 2c: Mask emission fluxes over ocean.

8) Figure 3: Please correct the colorbar max value.

9) Figure 3 and Fig. 4: Please recalculate fungal spore concentrations for the HU parameterization based on corrected HU emissions. Although most of the observations are over land, model concentrations near the coastlines may be overestimated due to the long-range transport of the "false oceanic" fungal spores emissions.

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