Interactive comment on "Regional-scale Simulations of Fungal Spore Aerosols Using an Emission Parameterization Adapted to Local Measurements of Fluorescent Biological Aerosol Particles" by M. Hummel et al.

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We thank the reviewer for his/her comments which have improved our manuscript. The comments are listed below in italics.

In general, the FBAP measurements measure all particles in the range of 2-4µm, however, it the authors assume these are fungal spores. Bacterial agglomerate, as well as giant bacteria and agglomerates of free proteins and amino acids could contribute to this fraction. In this case, the simulations, referring only to fungal spores would not represent this data well. This point should be further addressed and quantified, as the introduction generalizes this issue to the entire PBAP population.

It is not entirely clear what kind of biological particles dominate FBAP number concentrations. Several field and lab studies show that fungal spores and bacteria cells or bacteria agglomerates can contribute to FBAP concentrations in a size range of 2-4 µm (Huffman et al., 2010; Pöhlker et al., 2012; Gabey et al., 2013; Robinson et al., 2013; Healy et al., 2014). Taking previous studies into account, we conclude that FBAP concentrations shown in this study are dominated by fungal spores, but might also include to some extent contributions of other PBAP. A summary of recent WIBS and UV-APS measurements focusing on this issue is already included in section 2.4.

For readers not familiar with the measurement techniques, online measurements alone weaken the robustness of the study. If there are previously published works that validate this measurement with more traditional ways such as filters and genomics, please add them to show that this technique is robust and validated. If not – such validation is needed.

Additional references to previous studies that validate FBAP measurements with traditional techniques are included in section 2.4.

Text added: "At the costal site of Killarney, results of fluorescence and optical microscopy of impacted biological particles reveal that some PBAP, e.g. Spores of *Cladosporium spp.*, which have been frequently observed in many environments, were not correlated to the FBAP concentration (Healy et al., 2014). However, particle size modes of WIBS channel FL2_280 correlate with the concentration of airborne fungal spores commonly observed at the sampling site (Healy et al., 2014)."

In general, the authors should expend the experimental section for instrumentation and validations. For instance, what is the sensitivity of the instruments? This could lead to underestimation of biological particle detection.

Most FBAP measurement data is also shown elsewhere (Gabey et al., 2011; Schumacher et al., 2013; Toprak und Schnaiter, 2013) and some include information about the sensitivity of the instruments. This manuscript is already rather long and its focus is on the comparison of FBAP data to model

results. Additional information about the experimental part is contained in other studies (Gabey et al., 2010; Huffman et al., 2010; Pöhlker et al., 2012; Robinson et al., 2013).

P. 10, line 8: this sentence is inaccurate, as not all proteins will contain fluorphore-containing amino acids.

This issue is now taken into account and the sentence has been corrected as follows: "The region of excitation near 270 nm includes certain amino acids (e.g. tryptophan) contained in most proteins."

The Authors assume that there is no contribution from dust in this size range. Could the authors supply evidence (using back trajectory analysis for example) support this assumption?

Mineral dust also shows slight fluorescence signals which can result in a detected fluorescence fraction in WIBS instruments between <1% and 5.8% (Toprak und Schnaiter, 2013; Gallagher, 2014). It may therefore interfere with the FBAP signal (Gabey et al., 2011; Pöhlker et al., 2012). Contribution of mineral dust to FBAP concentration can only occur during dust events. For the investigated locations and time periods however, no contribution of desert dust is confirmed by using back trajectories (Figure 1 to Figure 3) by using HYSPLIT (Draxler und Rolph, 2013). All locations mostly show local contributions for the selected test cases. Contribution of soil dust may be part of particles from local sources. Soil dust can be internally mixed with fungal spores or other organic components.

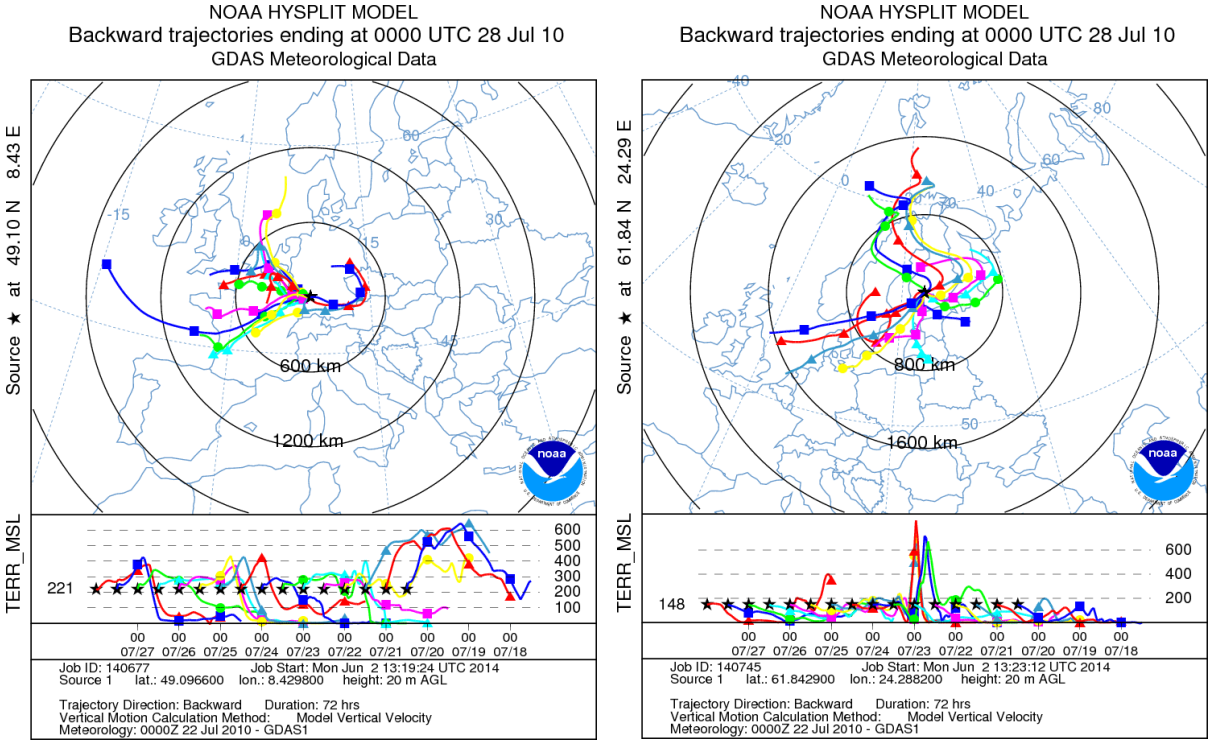

Figure 1. Back trajectories for the locations Karlsruhe and Hyytiälä at the simulation case during July 2010

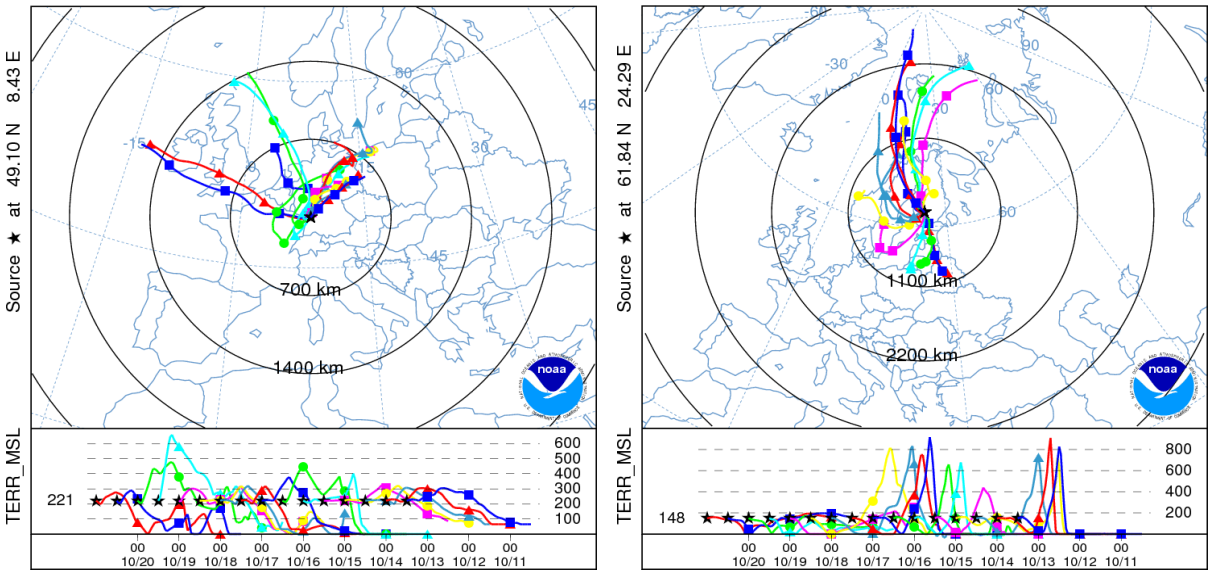

Figure 2. Back trajectories for the locations Karlsruhe and Hyytiälä at the simulation case during October 2010

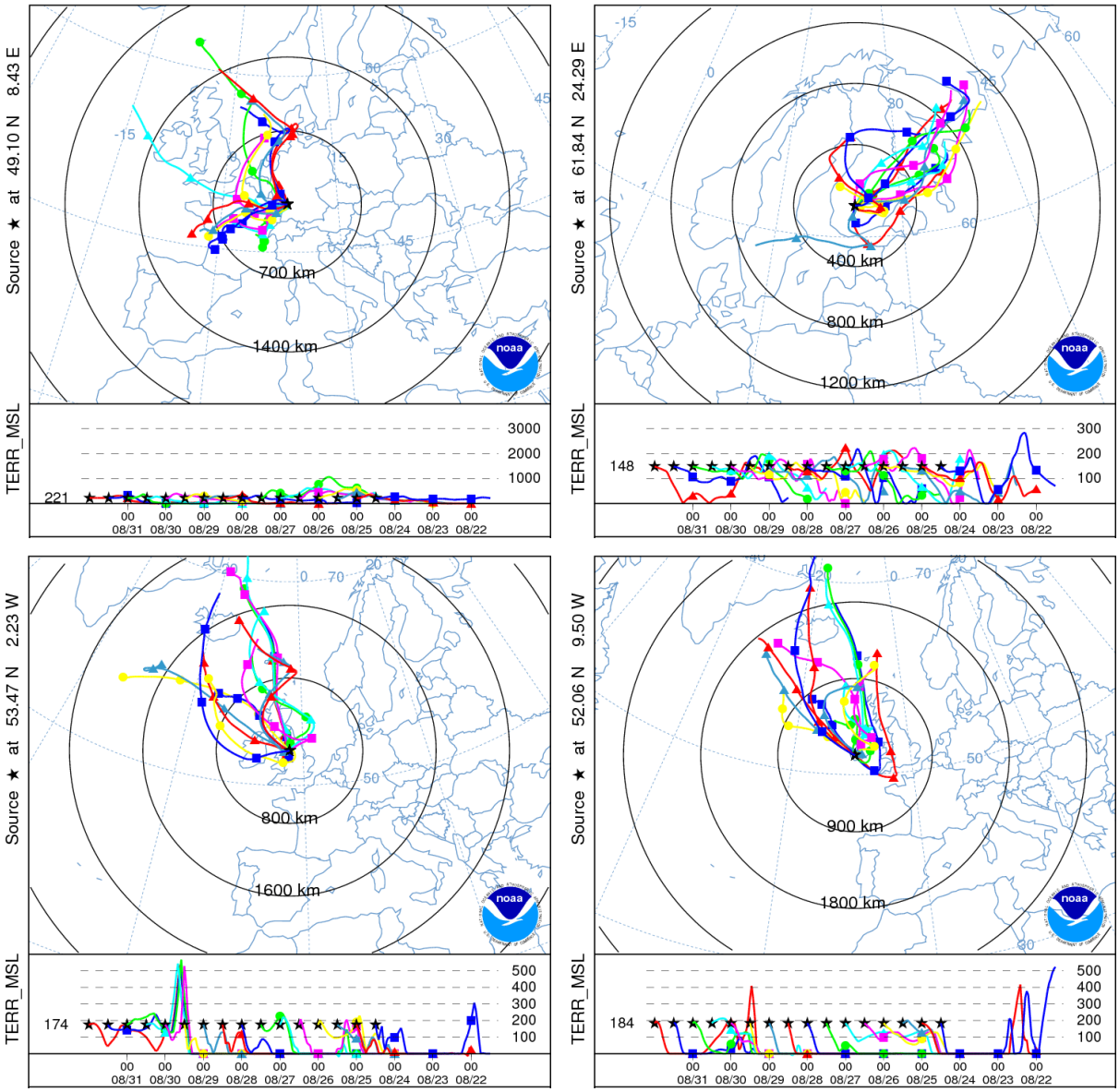

Figure 3. Back trajectories for the locations Karlsruhe, Hyytiälä, Manchester, and Killarney at the simulation case during August 2010

The two previously published models are based on manitol concentration, which can also indicate on other types of particles, such as vegetation in addition to fungal spores. This may lead to overestimation of bio aerosol loads. This should be mentioned and discussed as one of the factors influencing the difference between models and measurements.

Heald and Spracklen (2009) use mannitol concentrations that are compiled in Elbert et al. (2007) in order to estimate fungal spore emissions which best represent mean observed concentrations. Additional information about PBAP which are also containing mannitol (i.e. bacteria, algae, lichens, and plant fragments) is now added to the manuscript.

*The authors correct the spores suspension time in the atmosphere to be 4 ¾ [*hours*]. This significant claim needs to be validated before stated.*

In the updated manuscript version, this statement has been clarified. In order to calculate eq. 7, we need to assume a constant boundary layer residence time, previously called atmospheric lifetime. For a first shot, we used an approximation for atmospheric lifetime found in literature. A first model run with the new emission parameterization (calculated by using $\tau = 1$ day) revealed that the simulated fungal spore concentrations still underestimates the measured FBAP concentrations, although they are adapted to the measurements. We now calculated a corrected boundary layer residence time which is supposed to close the gap between simulated and measured concentrations. This was found to be $\tau = 4$ ¾ hours and is not directly comparable to an atmospheric suspension time or lifetime. Following sentences were also added to the manuscript: "All discrepancies between this boundary layer mixing time and a typical atmospheric lifetime are caused by assumptions which are done for eq. 7. This difference may be caused by deviations from a well-mixed constant concentration profile within the boundary layer (Figure 4), because source and removal processes in the simulation are not in equilibrium and fungal spores are continuously removed at the model boundaries.

However, using eq. 7 for calculating a potential FBAP emission flux is reasonable, because simulated fungal spore concentrations typically decrease rapidly near boundary layer height. This behavior is shown for an exemplary vertical profile in Figure 4."

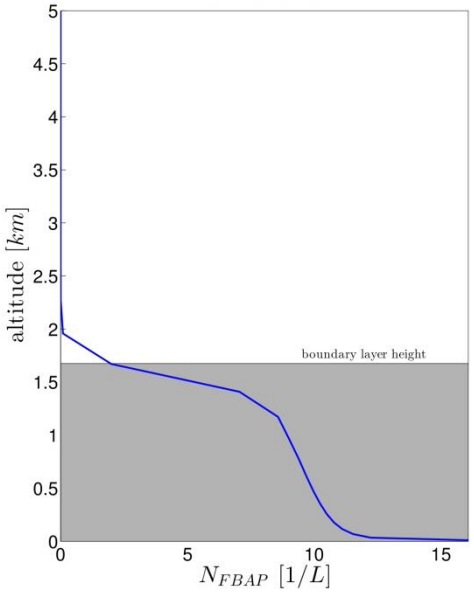

Figure 4. Exemplary vertical profile of simulated fungal spore concentration within and above the planetary boundary layer for Karlsruhe at 28 Aug 2010 14 UTC.

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