

Interactive comment on “Ecosystem–atmosphere exchange of microorganisms in a Mediterranean grassland: new insights into microbial flux through a combined experimental-modeling approach” by Federico Carotenuto et al.

Anonymous Referee #2

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The manuscript presents analysis of flux measurements and development of a model to simulate the emissions of culturable microbes from Mediterranean pasture. High uncertainties exist in the knowledge about the emissions and abundance of primary biological particles in the atmosphere and the development of an emission model for microbes is a step forward in closing this gap. The strength of the model is its ability to simulate the dynamics of the microbial population in the vegetation, and use that information together with meteorological factors to simulate the emissions to the atmosphere. However, the model currently has a few shortcomings, also admitted by the

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authors, that make it not immediately useful for large scale applications. Firstly, the model is calibrated using the observations of culturable microorganisms. However, this is not what is needed for the most probable uses of the model mentioned by the authors in the abstract. Studying the spread of pathogenic species needs emissions of those pathogenic single species, while most applications in biogeochemistry would require the emissions of total biogenic aerosol, not only the culturable species. Secondly, the model has only been calibrated for Mediterranean grassland. However, this is still a big step forward in the field of modelling microbial emissions, so although further development is needed before the model becomes usable as an emission module for large scale atmospheric dispersion models, I fully support this work to be published in ACP.

I have a few comments and questions.

Discussion: Please include comparison between the PLANET estimates and the previous studies, e.g. the Burrows et al, (2009b) and microbial flux observations from other locations, for instance using the same scaling factor to total microbes as Burrows et al. (2009a) used for grasslands (302).

Page 11, first paragraph suggests that obtaining a scaling factor to total microorganisms from the culturable fraction requires flux measurements of the total microorganisms. Why cannot the scaling factor be estimated from lower temporal resolution concentration measurements of both total microbes and the culturable fraction in the same site the flux measurements are made?

Page 11, lines13-18: Culturable and viable are not necessarily the same thing (see e.g Burrows et al, 2009a)

Minor remarks: Page 2, line 20-23: "In the past, only few attempts have been made to quantify the flux of microorganisms from plant canopies (Lindemann et al., 1982; Lindemann and Upper, 1985; Lighthart and Shaffer, 1994) covering only some periods and some land uses." This is confusing, as later the authors themselves reference several other studies that have tried to quantify the fluxes using various methodology.

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Please specify that this sentence refers to direct measurements of bacterial fluxes.

Page 4, line 23-24 "The experimental field for these previous campaigns was covered with similar herbaceous species such as cocksfoot (*Dactylis glomerata*), ryegrass, tall fescue (*Festuca arundinacea*) and alfalfa (*Medicago sativa*).” The list of species for the other field on the previous page only included clover and ryegrass, so how similar was the vegetation on these fields?

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