

## ***Interactive comment on “Flux balance modelling to predict bacterial survival during pulsed activity events” by Nicholas A. Jose et al.***

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Dear Referee,

Thank you for your comments.

Out of 5265 putative genes, there are 1990 genes (37.8%) with unknown functions from initial automated annotation. The 858 genes currently in the model are picked from initial assignments via additional annotation via the ModelSEED pipeline and manual efforts.

The predicted fluxes compare well to the ones we measured in Rajeev et al (2013). In the light BSCs had a maximum uptake of approximately  $12 - 20 \mu\text{mol CO}_2 \text{ g}^{-1} \text{ hr}^{-1}$ , compared to the predicted average of  $11.9 \mu\text{mol CO}_2 \text{ g}^{-1} \text{ hr}^{-1}$ .

C1

had a maximum production of approximately  $12 - 20 \mu\text{mol CO}_2 \text{ g}^{-1} \text{ hr}^{-1}$ , compared to the predicted average of  $33.4 \mu\text{mol CO}_2 \text{ g}^{-1} \text{ hr}^{-1}$ . Although there is only a slight difference, the comparison is difficult to draw conclusions from because gene expression studies used BSC samples in field-like conditions, whereas our studies used *M. vaginatus* grown in isolation, constantly wetted in minimal media. In addition, because biomass was not used to normalize flux measurements in gene expression studies, an unknown biomass density needs to be assumed.

The biomass objective function is optimized. The function was initially obtained through ModelSEED, and was modified to include biopolymers in the light as a biomass requirement. The rate of total biomass accumulation was not measured, so that comparison could not be made. We do observe that the predicted growth rates scale with increasing light intensity and that in the absence of any light in the model the predicted growth rate is 0. Both of these observations are constant with the known growth patterns of *M. vaginatus*.

There are no experimental studies to our knowledge that have specifically investigated the ratio of day/night wetting events. The reason for such a simulation is more to demonstrate how this model could be used given the information we have determined—carbon fluxes at fixed time intervals in the light and dark. This was inspired by the previous studies of Belnap et al (2003) and Reed et al (2012), who showed that wetting frequency and season affect the carbon balance and production of pigments for radiation-protection. A follow-up study could explore this day/night ration and wetting frequency across seasons.

Upper and lower flux bounds were constrained by the average flux measurement in the dark. The description of Table 3 will be modified to include this clarification. Using an unconstrained flux boundary for resources (represented as positive and negative infinity for the upper and lower bound) would result in an unconstrained/infinite CO<sub>2</sub> flux. The purpose of constraining the FBA problem is to reduce the degrees of freedom to solve for a desired unknown flux.

C2

*M. vaginatus* certainly has mutualistic partners in nature (and in culture) that likely facilitate more rapid growth, but they are not essential for survival because *M. vaginatus* may be grown axenic. The naturally slow growth is also thought to be an evolved mechanism that allows survival in harsh arid environments. The “missing” of vital reactions is more a result of annotation, where key genes in *M. vaginatus* lack known homologs for functional assignment.

The suggested corrections will be added:

An SBML file (see attached) will be added to the supplementary information. Lines 67 and 249 will be corrected. Line 264: where for each day there is either a light or dark 12-hour wetting event.

Please also note the supplement to this comment:

<https://www.biogeosciences-discuss.net/bg-2017-403/bg-2017-403-AC1-supplement.zip>

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