

Interactive comment on “Global analysis of gene expression dynamics within the marine microbial community during the VAHINE mesocosm experiment in the South West Pacific” by Ulrike Pfreundt et al.

Anonymous Referee #2

Received and published: 21 March 2016

The data obtained in this study complements the results already published on the VAHINE mesocosm. The mesocosm experiment was designed to promote the growth of nitrogen-fixing microorganisms and analyze the fate of dissolved organic nitrogen.

While a lot of data was obtained in this study, the manuscript would greatly benefit from some revisions. The goal of authors was to link transcription of microbial taxa in the mesocosm to the chemical measurements, diazotrophic abundances and microbial composition shifts obtained by other researchers. Hence, the differential transcription between the treatment and the lagoon community has to be analyzed. While, in the be-

C1

ginning of Results and Discussion section, authors refer to the differentially expressed genes, it is not clear if these genes had differential transcription between the treatment (mesocosm) and the lagoon communities or among different time points within each of the mesocosm and lagoon. The figures show that the second comparison was most likely done. A clear description of the data analysis and a scheme of the analysis flow would help.

Overall, the major results and especially their significance are not clear from the analysis, figures and discussion as they are presented now. I suggest breaking down the Results and Discussion into sub-sections following experiment succession: for example, the authors differentiate samples into several clusters, mainly by the time of sampling, with the analysis of what is in these clusters. It would be easier to compare the transcription profiles to other measurements in this way. An alternative separation can be done by metabolism and cellular processes.

A comparative analysis between the mesocosm and lagoon communities with a focus on a few findings with major significance to understanding the processes in this experiment would improve this manuscript.

Interactive comment on Biogeosciences Discuss., doi:10.5194/bg-2015-564, 2016.

C2