

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 #1

Received and published: 30 May 2016

This manuscript reports functional metatranscriptome sequences collected every two days from inside and outside a phosphorus-amended mesocosm in New Caledonia during a 3 week period. This work is complementary to a number of other studies undertaken at the same time, which have already been published. Major findings include identifying different community dynamics inside and outside the mesocosm, including a fast decline of *Synechococcus* cyanobacteria inside the mesocosm from the beginning, potentially caused by increased cyanophage lysis.

The authors also used transcript functional information to give hints about the bioge-

C1

chemical processes occurring inside and outside the mesocosm. In particular, regarding nitrogen requirements, the authors found that certain bacterial species expressed urease genes while others ammonium transporters and glutamine synthetase. Nitrogen fixation was dominated by 5 different cyanobacterial types, again showing temporal dynamics; little heterotrophic N-fixation was found.

Specific comments P 4, L29: sentence missing a word. Altermonadaceae à Ális misspelled throughout (should be Alteromonadaceae) P9, L29: add “but” after the references

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

C2