

General comment:

The manuscript improved significantly after the previous revisions. Although insufficient sequence number of clone library is the major limitation of this study, addition of qPCR of some nifH phylotypes is helpful in compensating the limitation. As limited amount of relevant studies have been done in temperate regions of North Pacific Ocean, it is difficult for the authors to further elaborate and discuss with this set of data in a convincing way. On another hand, the data set could provide useful information for the related studies in the future. Therefore, I think this work can be accepted, after some minor revisions. There are some grammatical mistakes found in the manuscript, and the authors should do proof-reading more carefully.

Specific comments:

L.141, What does “when nitrogen fixation was not detected” mean? Did the authors mean “when nitrogen fixation was undetectable” or “not measured”? If the nitrogen fixation rate was not measured, the authors should not assume the missing data to be zero. The authors should clarify their meaning here.

L.199, “underestimates” should be “underestimated”.

L.401, “one or more the factors” should be “one or more factors”

L. 432, It is suggested to use “undetectable” to replace “disappear”

L.455-457, The logic here is not clear enough. Since the author did not use qPCR to quantify the *P. stutzeri*-like nifH gene, there is no reason to say “*P. stutzeri* could not be a major diazotroph in this study region”. Also, “ γ -24774A11 was not detected on that occasion by qPCR analysis” should not be the evident suggesting “ γ -24774A11 was not quantified as *P. stutzeri*”. The authors can simply compare the sequences of γ -24774A11 and *P. stutzeri* nifH gene recovered in this study.