**Biogeosciences
Discussions**

Interactive comment on "Activity and abundance of denitrifying bacteria in the subsurface biosphere of diffuse hydrothermal vents of the Juan de Fuca Ridge" *by* A. Bourbonnais et al.

Anonymous Referee #2

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This is a nice paper presenting their data on nitrogen transformation in particular nitrogen loss at deep-sea diffuse vents. Through their data, they could determine the potential rates of denitrification, annamox, and DNRA using 15N paired isotope techniques. Their result suggested that bacterial denitrification is the dominant nitrogen elimination process in sulfidic hydrothermal vent waters. In combination with data from other sites, the authors estimated that nitrogen loss in the subsurface biosphere of vents, represent a small but significant fraction of the total marine N loss.

The paper is overall well written, my only argument is for the bacterial community analysis and q-PCR. I am afraid that the 16S rRNA gene library analysis performed in

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this study is weak. Only very limited clones were sequenced from the five bacterial 16S rDNA clone libraries, for example, only 27 clones from library of Phang were sequenced, thus the coverages of the libraries were low, mostly around 50-60%. Therefore, the compositional analysis of different bacterial groups in the environments were not convincing at all. I understand that one of the main focuses of this paper is to determine the relative contributions of different Nitrogen elimination processes (i.e. denitrification, annamox, and DNRA) in the diffuse vents, thus the authors didn't make enough efforts for community analysis. Then I would recommend the authors just to make a brief description of the bacterial community analysis, in my opinion, it's almost worthless to calculate the percentage of different groups using so limited data, Fig.4 could be eliminated from the text. And actually I couldn't understand why the authors only did Q-PCR for SUP05, based on the fact that SUP05 is actually not the main players in the samples, why not do quantitative analysis of the epsilonproteobacteria?

Other comments: 1, The rates presented in this study were measured at ambient pressure, possible influences by high pressure on the activities were ignored. The authors already discussed and assumed that the depths encountered in this study (1500-2200m) may not change bacterial metabolisms from those at atmospheric pressures. I make an argument here that pressure of $\sim$ 20 MPa may have significant influences on bacterial metabolic rates and growth rates, therefore, in-situ measurements were needed to prove or disapprove the assumptions. 2, Fig.2 is difficult to read, need some modifications. And I could not find numbers in brackets. 3, Fig. 5 could be used as a supplementary Figure. 4, Introduction, second paragraph, need to add refs

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