

Interactive comment on “Environment Gradient related Dissimilatory Nitrate Reduction to Ammonium in Huangmao Sea Estuary: Rates and Community Diversity” by Ran Jiang et al.

Anonymous Referee #2

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The authors examined the potential rates of dissimilatory nitrate reduction to ammonium (DNRA) using time-series incubations with supplemental $^{15}\text{N-NO}_3^-$, and applied high-throughput Illumina sequencing technology to assess the distribution and diversity of the nitrate ammonifiers *nrfA* genes in the surface sediments collected from the Huangmao Sea Estuary (HSE) continental shelf. There are many too bad problems in this manuscript. The data and analysis are too rough. The potential rates of DNRA are not reliable. I am not convinced for its publication in BG and even BGD.

1) The English of the paper needs an overhaul. Most of the sentences are wrong, unclear, lacking logic, or misleading. Some references cited in the main text are missing

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in the list.

2) The methods were not described clearly. Many key details are missing. For example, the one-year observations were not stated; the biogeochemical parameters (temperature, salinity, nutrient concentrations, etc.) measurements are missing; the procedure of the high-throughput sequencing of the *nrfA* gene is incomplete. . .

3) The method on time-series incubations with supplemental $^{15}\text{N-NO}_3^-$ to examine potential rates of DNRA needs to clarify the cross-feeding effect since heterotrophic bacteria can uptake $^{15}\text{N-NO}_3^-$ and release $^{15}\text{N-NH}_4^+$ to the experiment system.

4) There is no statistical analysis in this manuscript. All statements and conclusions on the control of environmental parameters on communities are not supported by any specific analysis or statistical test.

5) The whole paragraph of “2.4 Rate calculations” (Page 4, Line 22-30) was plagiarized from the literature. Also, some statements in the Introduction section (Page 2, Line 17-22) were from the literature directly.

6) Very few discussion was made in the Results and discussion section. And the descriptions are not logical and distracted!

7) The authors did NOT analyze RNA but used “transcripts” to describe the gene copy abundances throughout the manuscript.

8) All figures were unclear. There are Chinese characters in Figure 2. The phylogenetic tree is too rough..

I cannot list line-by-line specific comments because of too many wrong/problems throughout the manuscript.

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