

## ***Interactive comment on “Effects of Sea Animal Colonization on the Coupling between Dynamics and Activity of Soil Ammonia-oxidizing Bacteria and Archaea in Maritime Antarctica” by Qing Wang et al.***

### **Anonymous Referee #2**

Received and published: 7 June 2019

The manuscript entitled “Effects of sea animal colonization on the coupling between dynamics and activity of soil ammonia-oxidizing bacteria and archaea in maritime Antarctica” by Wang et al. describes the effect of sea animal colonization on the community composition of ammonia oxidizers. The subject matter is interesting and the work in general is technically sound, however, my main concern is that the authors make claims about the relationship between nitrification rates and ammonia-oxidizer dynamics. Furthermore, there are some inconsistencies within the environmental parameter data, as well as very speculative parts in the discussion which need to be addressed.

C1

General comments: The authors measured potential ammonia oxidation rates by adding 1mM NH<sub>4</sub>Cl and incubating the samples at 15 degrees, which seems to be very artificial and far from in situ rates. It is highly speculative to comment on in-situ ammonia oxidation rates based in these measurements. Hence, assessing the relative contribution of AOA and AOB to nitrification rates based on the presented measurements is highly speculative and can only be suggested based on the differences in abundance between those two groups. Further, the authors talk about “inhibition” of AOA due to seal and penguin activities (e.g., lines 312-313, line 344), however, the presented data simply suggests a higher abundance of AOB over AOA. While the environmental conditions might be more favorable for AOB, it is highly speculative to assume that this is caused by inhibition and should be phrased more carefully.

The ammonia concentrations of the 5 samples within the same site are sometimes extremely variable (e.g. 650 vs 0.1 in the STS site). How far were the different sampling points apart? Some of the data in Table 1 seems surprising or/and might be not well represented, e.g. the sum of the percentage of total carbon, nitrogen and sulfur makes up e.g. only 0.5%. What are the other 99.5%? Reporting total carbon, nitrogen and sulfur in mg/kg might be more useful as well. Additionally, the abbreviations of the sites are not very intuitive and easy to confuse.

Specific comments: Line 25: Nitrosospira are AOB and Nitrososphaera are AOA, needs to be switched. Line 32-33: “The results provide insights into the mechanism how microbes drive nitrification in maritime Antarctica”, here again the authors make claims that are not supported by the presented data. The mechanisms of nitrification are not studied. Line 37: “biogeochemical nitrogen cycle” instead of “biogeochemical cycle for nitrogen” Line 40: AOB were discovered much earlier than 2015, please chose a different reference Line 41: comammox should be spelled out Line 46: Are you referring to the marine water column or sediments? Please specify (instead of mentioning “marine layers”) and add the appropriate references. Line 93: “daily mean range” is contradictory, please correct. Line 101: “A great many” should probably read

C2

“A great majority” Line 346: typo in “reported” Lines 378-380: This statement is not necessarily correct. There might be more diversity within Km’s of AOA that differ from that of *N. maritimus*. Making such a claim based on a single organism is very speculative. Lines 393-397: The connection with comammox is not very intuitive. Did you detect comammox? Also, the reference of Santoro 2016 does not fit here because it measures actual rates (instead of potential rates) using stable isotopes in marine environments where no comammox has been found thus far. Lines 417-420: Why does a high organic carbon favor AOA over AOB? So far most studies have shown that AOA are inhibited by complex organic substrates (Stieglmeier et al 2011, Qin et al 2017, etc). Lines 430-433: This statement is highly speculative and likely wrong. Why would the presence of an *amoA* gene be an ancestral remnant that is not active? There is no data presented supporting such claims. Lines 446-455: this section does not discuss the data and should be moved to results

---

Interactive comment on Biogeosciences Discuss., <https://doi.org/10.5194/bg-2019-114>, 2019.