

Review- Chen et al. 2020 BG

I read carefully read your ms. It seems that a lot of work has been done, however I think that the work is over simplified and needs to be more thorough and precise before it can be considered for publication.

**Major concerns:**

1) The main finding, as presented already in the title, is not novel. It has been shown in the last decade in many studies that there is an overlap between methane production and oxidation in marine and freshwater sediments. There are also studies that described the different layers of different AOM and methanogenesis pathways and overlaps, as you mention yourself (very nicely shown by He et al., 2019). Therefore, there is a problem in the novelty aspect of this study and fitting it to BG, as well as incorrect statements in the text (e.g L 31).

2) The occurrence of iron reducing bacteria and iron reduction above sulfate reduction, can be interpreted also as classic organoclastic iron reduction and not necessarily as iron-AOM.

3) The analytical methods are not detailed, partly explained and without any statistics. Please explain how did you measure exactly  $\delta^{13}C$  CO<sub>2</sub> (no measurement of DIC as written in Fig. 1?), NO<sub>2</sub><sup>-</sup>, TOC? What is the error on the symbols? I'm not sure I trust the NO<sub>2</sub> peaks you see in Fig 1 at 12 cm depth below the sulfate decrease. It seems to me like a constant very low value all along the sediment. I have concerns also reg. the methane profiles. Did you have duplicates for the geochemical and the biological parameters?

4) How do you explain that the AOM rates were higher than the production rates?

5) Fig. 5 can be explained also by changing the main mechanism for methanogenesis.

6) There is limited discussion on the microbial community, the types of methanogenesis, the controlling parameters etc.

**Based on the above I recommend:**

1) Showing the data with the statistics and the patterns considering this statistics

2) Changing the focus of the paper from this overlap and AOM to the complex microbial community and methane cycle in general (methanogenesis and AOM) considering the controlling parameters. Fig. 2 is nice (just check the AOM higher rates than meth) and the discussion should be expanded around this topic + the population (Fig. 3 and 4).

**More comments:**

5) Fig. 1, you don't need to put in each graph the same CH<sub>4</sub> profile, just add another graph of CH<sub>4</sub>.

6) Please edit the English. There are several typos (as in L. 226 –decreases and not decrease)

7) Why do you think you had less methanomicrobiales than methanosarcinales? Please explain, its not typical in fresh water sediments.