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Interactive comment on "Regulators of coastal wetland methane production and responses to simulated global change" *by* Carmella Vizza et al.

M. Scranton

mary.scranton@stonybrook.edu

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Vizza et al: "Regulators of coastal wetland methane production and responses to simulated global change" Biogeosciences Discussions doi:10.5194/bg-2016-314

This paper describes a number of measurements and experiments made on Copper River Delta sediment with the goal of determining whether methane production from these sediments is enhanced by factors which could be influenced by climate change (in particular sea level rise and increased input of presumably labile organic matter). Unfortunately I do not think the authors make a good case that their results add much to the discussion.

The basic premise on which the authors base their study is that methane production depends on substrates produced during fermentation of organic matter and that

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methane production and sulfate reduction usually do not occur in the same sediment, presumably because of competition for these substrates. The authors mimic sea level rise by adding brackish water to their samples (which ignores the possible importance of increased water logging and decreased oxygen in the sediments). All incubations are done after vials are flushed with nitrogen although the natural sediments apparently all had some level of oxygen present in situ. Values for nitrate (another potential substrate for carbon remineralizing organisms) and for acetate (the putative important substrate for methanogens) were measured but data were apparently quite variable and are not reported. No measurements were made of H2, another potential substrate for methanogens and methanogens were not examined to see whether they were actually acetoclastic or hydrogenoclastic. The data for the dsrA and mcrA genes are again not presented and in the results section appear to contract the conclusions made about their abundance. The authors also ignore the fact that numbers of genes do not directly relate either to number of cells (a cell can have more than one copy of a gene) or to gene activity. Finally the authors use natural organic matter to enrich their incubations but do not indicate the amount of carbon added or the relative lability of that carbon. (Clearly a gram of sucrose and a gram of twigs would not be expected to stimulate microbial activity to the same extent).

Below I provide a number of specific comments

P2 Line 6ff: I do not like the term green house compensation point. It is not widely used and does not directly relate to what you are measuring (as you say nothing about carbon sequestration in this system). You do not mention carbon fertilization again, and there is no indication in the text of whether any increases in carbon production in the CRD system would be due to warming or to carbon fertilization. I think you hurt yourself by trying to draw connections to too many issues. I would recommend drastic simplification of this section and sticking to the facts.

P2 Line 16: redox conditions are only indirectly related to climate change. You seem to imply the mere presence of nitrate or sulfate changes redox conditions but this is not

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true, especially if oxygen is present. In fact there can be a lot of nitrate and sulfate in oxic surface sediments. Did you ever have sulfide in your samples? Does oxygen penetration vary with ecosystem? How far below the surface were the samples collected?

P2 Line 23: I don't think an "abundant supply of organic matter can reduce competition for methanogens by increasing substrate availability". Try instead "abundant supply of organic matter can increase substrate availability"

P2 Line 28: replace "are likely results of" with "may be influenced by"

P3 lines 7 and 10. Use same unit for sealevel rise (100 and 170 cm)

P3 line 15: Numbers of methanogens not as important as whether or not the methanogens are active.

P4 line4: The range of physicochemical parameters in table 1 are actually pretty small for most measurements. Perhaps more important is whether the intertidal sediments are exposed to the atmosphere at low tide (tidal range?). How long are they submerged? What is the water content? Again it matters how far below the surface these sediments were collected. From the table it must be shallow since there was more O2 in these sediments than the freshwater wetlands.

P4 line 26: Were no replicates run for sediments from a single site? How can you tell if observed variability is just typical of replicate samples? I would also think you MUST indicate how much macrophyte tissue you added (probably in terms of gC/g sediment or something like that) to even know if these treatments were similar since the lability of the carbon is likely not the same.

P5 Line 6: You mean incubation temperature not ambient temperature?

P5 line 8: Purging with nitrogen will likely have a bigger effect than incubating at a few degrees cooler than the actual sediment. I would expect stimulation by this as you allow more anaerobic processes to occur. Were any blanks or controls run?

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P5 line 12: "flame ionization" not "flame ionizing" detector

P5 line 20: You report that only sulfate was detectable in the water column. Did you present any water column data? Do they mean anything? What are detection limits for pore waters? Present nitrate and acetate data for sediments as well as sulfate.

P5 line 27: the method you describe is typically called “loss on ignition” and represents a loss of organic matter. Did you convert to organic C? Is this data reported anywhere in the paper? Was DOC measured the same way? Blanks? Detection limit?

P6 line 2: I would use the word “converted” rather than “scaled”

P6 line 5: I couldn’t tell what this composite sediment was used for. Were incubations for each site or was all sediment made into a composite? Why do this? It seems that then the averages for the genes refer to different samples than the physiochemical properties. Can you properly do statistics comparing the combined samples in one parameter to the individual samples in one parameter?

P7 line 2: move “log transformed” to immediately follow “four factors”

P7 line 26ff: You use a lot of significant figures for something that is so variable. Maybe you are justified in two significant figures but not 3 or more. Again blanks and detection limits need to be mentioned as your averages are pretty close to zero (or at least almost include zero). I would like to see these data associated with specific samples.

P8 line 14: This paragraph seemed very odd. You seem to contradict yourself a lot. For intertidal samples, three had no dsrA but this was found in all freshwater AND the dsrA was independent of ecosystem type. This seems to contradict your hypothesis which you nevertheless cling to. Remember the presence of a gene doesn’t mean the organisms are doing anything at the moment and the number of genes does not necessarily indicate the number of cells of a particular organisms.

P8 line 27ff: I really don’t like your equating sealevel rise purely with sulfate concentration. It is ok to say that sealevel rise will flood current intertidal areas, but the vegetation

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will change and the water will be permanently water logged rather than periodically exposed to air. You have no data on estuarine wetlands to compare to the freshwater wetlands (although others have done this comparison in other systems). I would guess the reason you see no effect here is that you are mimicking the process the wrong way. You are really looking at increased sulfate levels, not sealevel rise.

P10, line 2: The sentence beginning "our study also demonstrates. . ." seems to directly contradict your own data as you said before that dsrA did not correlate with ecosystem type

P10 line 13ff and next paragraph: These two sections are wild speculation with absolutely no data behind them. There are a lot of other factors that might be important that you haven't included.

P11 line14: This whole section is hurt by the fact that you don't characterize the macrophytes at all in terms of potential lability. Did you add a constant amount of C or organic N? Or just dry mass? Or just a "chunk" of leaves? Again much of this section is speculation without more facts

P12 line19: You have no idea whether there are hydrogen utilizing methanogens around or how much hydrogen there might be. You can reiterate what other people have said in other papers but I don't see you connecting these to your system with any facts.

Modeling: I didn't really understand the models. If you are making linear equations including various parameters and then constant factors for each, I would like to see more detail on how this worked. If you have a lot of variables, you can fit most data but figure 6 is completely mysterious and doesn't convince me of the value of your model. I also didn't understand the columns in tables 2 and 3. I have never heard of an AIC before, for example. Explain the statistics a bit to an audience that may include non-biologists.

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