The study by Angermeyer and colleagues surveys the response of salt marsh sediment bacterial communities to a large reciprocal transplant experiment between several marshes. They find that the communities are resistant to transplantation which may suggest limited dispersal of the communities.

This study is well-written, interesting, and the results are generally clear but do need some clarification at spots. Below I list some major comments and then below I detail some more specific comments relevant to the text.

Major comment: what ecotype of *Spartina* was selected for this study? Was it short or tall? This ultimately has important implications for their study and the interpretation of the data due to the starkly different habitats that the to ecotypes reside in. If this is the tall ecotype of *Spartina* then the plants are experiencing tidal flooding every day, whereas the short ecotype only sees flooding 1/3 of the month (e.g. Johnson et al. 2016, Ecol Appl).

Given this, if tall was selected the authors are likely seeing full integration of the transplanted soil into the local conditions of the new marsh. If short was selected, then I do not believe the transplanted soil fully experienced the abiotic conditions of the marsh itself (e.g. Balser and Firestone 2005, Biogeochem) and the small change in temperature between sites (17-24C) likely not enough of a push to drive changes. If the short ecotype was selected the authors would need to demonstrate the exposure of the transplanted sediments to the new conditions with some measurements of the soil abiotic conditions to convincingly demonstrate the efficacy of the transplant.

Related to this, I wonder how much exposure to new conditions sediment 20cm deep in marsh sediment receives. Unless these are bottom up flooding marshes (like many in New England are), these sediments likely wouldn't see that drastic of change in their abiotic conditions in particular because the biggest deciding factor here (air temperature) likely isn't all that differ 20cm deep.

Title: temperature is just one component of what makes up the gradient sampled here, especially in terms of the soil chemistry. I would suggest revising the title to reflect this. Also, population is the wrong word here, community is more appropriate. Something like "Salt marsh bacteria communities maintain structure despite transplantation'.

Methods

General comment: the authors should probably remove Chloroplasts from this analysis. V4 is generally terrible for this group of taxa and the short-read length makes meaningful identification of these eukaryotes difficult at best. Also, why mantel tests in lieu of something like a PERMANOVA/PERMDISP/ANOSIM?

Line 139: did this include a plant(s) or was it just bare sediment?

Line 140: it would be helpful to know a bit more about where in the marsh they were transplanted. Things like height relative mean sea level, tidal inundation, distance from the creek bank, and a bit more about the marshes themselves to better interpret the experimental design.

Line 151: I assume this is just something like cheese cloth, but it would be helpful to know the mesh size here.

Line 155: So the authors bored 20cm into the sediment with a spatula? How are they sure they reached the desired depth and didn't get mixing of higher layers? The sampling says 20cm, but was it around 20cm (e.g. 19-21cm)?

Line 178: why the DNA/RNA kit when only DNA is presented?

Line 188: delete 'Benchtop'.

Line 190: I would find it helpful for the authors to just include what they did instead of having to go to GitHub/another paper.

Line 192: data was rarefied before OTU picking? This seems odd and potentially biasing OTU clustering by removal of diversity. Can the authors please clarify?

Line 193: OTU picking method? Closed pick? De novo pick?

Line 222: this is on rarefied data, no? Absolute abundances in this instance seem to be perfectly viable over relativized abundance.

Line 237: It would also seem more appropriate to use a ANCOVA for the environmental variables and OTUs, holding origin and site as effects. Given that the variables change as a function of site and covary, this should be taken into account in the regression model.

Line 241: Bonferroni corrections are notoriously overly conservative, did the authors try another p-adjustment technique like Benjamini-Hochberg?

Results

Line 250: remove 'host'

Line 251: I also assume no roots entered the cores as well?

Line 258: Was anoxia measured? Creek bank sediment is only usually anoxic during flooding.

Line 275-276: is this information about DNA mass needed?

Line 283: this paragraph could be strengthened with some statistics (e.g. Kruskal-Wallis test w/p-correction).

Line 284: Drop the 's' from the end of 'compositions'.

Line 287: not a requirement, but oligotyping would be interesting for this Vibrio OTU.

Line 314 (and in methods too): is there a reason the ordination would need to be done with all OTUs and then again with the top ten most abundant taxa? Bray-Curtis is most strongly influenced by the top taxa and given that the ordinations look very similar, I question whether it is needed because the authors do not do anything with these top ten taxa.

Line 321: indicator OTUs is misleading here. This implies that they are indicator species, as determined by that specific test. I don't disagree with how the authors determined these four OTUs, however I'm surprised that only 4 of the 21k OTUs were significantly correlated.

Discussion

Line 336: this paragraph rehashes the introduction.

Line 345: one thing that's hard to tell about this experiment is whether dispersal, due to tidal flooding, occurred especially at the depth sampled. Do the authors have data about the sediment chemistry outside

Line 346: this is not just a temperature gradient; many things change along the eastern US coast.

Line 350-352: without presenting more data about the sites (e.g. porewater chemistry, ocean water chemistry, variations in abiotic conditions, ect), this is a hard claim to make. The physical properties of the sediments themselves, as noted in the methods/results, suggest these sites are very different.

Line 355: this implies that sampling didn't disrupt the communities, not that the methods were effective at excambing the question. Which ultimately is a strength given the likely release of carbon via severing marsh roots.

Line 362: while this intuitively makes sense, the authors lack the resolution in terms of measured variables to really parse out the driving factors here.

Line 365: remove 'host'.

Lines 368-370: this sentence is confusing, I'd rephrase or remove it because the next sentence says all that's needed.

Line 378: one thing about this paragraph that the authors do not discuss is the idea of no mixing of the local conditions. This has been discussed by several papers (e.g. Balser and Firestone 2005, Soil Biochem; Hughes and Martiny 2013, ISME J; Gasol et al. 2002, Limnol Oceano). Given this, it is likely that their results show no mixing. In addition, a recent paper about dispersal in soil systems would also be appropriate for discussion (Evans et al 2017, ISME J).

Line 402: while Vibrio do bloom in the summer, the authors sampled in October. Work by Bowen et al 2009, ISMEJ showed seasonal patterns in the microbial communities in marshes, which was also show in the active communities by Kearns et al. 2016, Nat Commun. Given this, how confident can we be that at the end of the season samplings are reflective of the warmer temperatures?

Further, given the lack of change in transplanted cores it suggests its likely something about the soil chemistry instead of the temperature. This may be reflective of the sandy nature of southern marshes relative to the high carbon marshes in the north.

Line 438: the presence of Vibrio regardless of temperature suggests lack of mixing, which may be why the persist. I also think that the idea of resistance, which has been shown a few times for marsh communities (Bowen et al. 2009, 2011, ISME; Kearns et al. 2016, Nat Commun; Angell et al. 2018, Front Micro), is an interesting talking point here.

Line 458: while I find this paragraph interesting, I question how applicable it is to this study given that the majority of studies in this area of plant-microbe interactions, outside of the work of Bowen and colleagues, shows the environment overrides plant genetic effects every time. Further, based on the sampling, it appears this study would be independent of the plant itself since the authors do not mention roots and the rhizosphere effect only extending a few millimeters from the root surface.

One other point about this is that *Phragmites* is hardly a salt marsh plant as its home range is in brackish (<10ppt) to freshwater environments, which all *Spartina* would be unable to compete in.

Figures

Fig 1: looks good. Perhaps scale bar?

Fig 2: I would recommend removing the failed samples, its not needed and it distracts from the figure. Also the size of the text could be improved.

Fig 3: the shape/letter makes these hard to interpret at first site. Perhaps color them?

Fig 4: I would add a legend, it's a pint to look back and forth between this figure and figure 2.

Table 1: are these averages over the course of the experiment or just a one time point measurement? If an average, please include the SE or SD.