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Interactive comment on "Biogeochemical and plant trait mechanisms drive enhanced methane emissions in response to whole-ecosystem warming" *by* Genevieve L. Noyce and J. Patrick Megonigal

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Thank you for your thoughtful comments. Our responses are below in italicized text.

1) It would be nice to describe the statistical analysis of the data more in detail.

Data were log-transformed. Were they all normally distributed after log-transformation?

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Yes, the flux and porewater data were normally distributed after log-transformation. We will include a statement to that effect in the revision.

In my opinion you should use time series analysis because of your monthly measurements. You should consider the decrease of correlation between measurements with increasing time distance. With linear mixed models you can nicely separate growing seasons from other periods.

Our main research question was to understand the overall effects of temperature treatment and vegetation community on CH_4 emissions as summarized over the 4-year dataset. Our understanding of time series analysis is that it focuses on trends of one index over time, allowing for modeling and forecasting, but does not allow for comparison between treatments. However, we acknowledge the reviewer's concern that sampling the same plots each month could lead to autocorrelation in these data. In response, we have reanalyzed the data using linear mixed models with plot as a random effect and will include these updated statistics in the revision. This change does not alter any of the original significant findings. We will also describe all of our statistical analyses in more detail, as requested.

2) Did bulk density and mineral N (and maybe other soil characteristics e. g. pH etc.) differ between treatments. I think the authors should present these results since they may be major drivers of methane cycling.

This is a reasonable question that we can address partly with data from SMARTX and partly with data from the other long-term experiments at this site. We measure pH as part of the suite of porewater analyses, but there has been no effect of warming on porewater pH over the past 4 years. We did not measure bulk density but know from previous research that bulk density is very uniform throughout the soil profile and is also unresponsive to treatments because the fact that the soils are organic (80 % organic matter). When carbon is added to or removed from the soil profile the result is

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a change in soil elevation, not a change in bulk density. The near lack of soil minerals means that mineral nitrogen effects are negligible. We recognize that we only briefly touched on the organic nature of these soils in the site description and will expand on that when revising the discussion.

3) Why did the authors not measure acetate concentrations? It would have been nice to compare acetate concentrations between treatments to discuss potential changes in the ratio between hydrogenotrophically and aceticlastically produced CH_4. That would have improved the discussion about changing CH_4 emissions very much. The authors mention the role of acetate throughout the manuscript but do not mention the methanogenic pathways and their potential role for changing ecosystem methane emissions.

We agree that a discussion of methanogenic pathways is needed and thank the reviewer for pointing this out. Our revised paper will include a discussion of potential pathway shifts and their role in driving CH_4 emissions. As outlined in the initial manuscript, our working hypothesis (based on our data thus far) is that acetate availability is higher in the C_4-dominated areas, so those areas are also likely to have a high ratio of CH_4 derived from acetoclastic methanogenesis. We agree with the reviewer that the potential effect of shifting methanogenic pathways is clearly important to this topic and that concentration data for acetate would support the rest of this dataset. Our future plans include measuring low molecular weight organic compounds (including acetate), using stable isotopes to track methanogenic pathways, and looking at the composition of the microbial methanogen community to further support these initial findings.

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