EGUsphere, referee comment RC1
https://doi.org/10.5194/egusphere-2022-689-RC1, 2022

Comment on egusphere-2022-689

Anonymous Referee #1

Referee comment on "Soil depth as a driver of microbial and carbon dynamics in a planted forest (*Pinus radiata*) pumice soil" by Alexa K. Byers et al., EGUsphere, https://doi.org/10.5194/egusphere-2022-689-RC1, 2022

General comments

The authors examine an important topic: what is the size and age and variability of soil organic carbon (SOC) in deeper portions of the soil profile (30 -100 cm in depth e.g. subsoil), and how do these quantities vary across space? The authors description of SOC and soil microbe composition changes along the soil profile will inform ongoing scientific discussions of soils and their ability to store carbon (C). This question and the findings of this study are also relevant for the growing number of projects (public and private) hoping to mitigate climate change through increasing SOC pools via soil amendments or ecological restoration.

The methods used by the authors are appropriate for investigating this topic. I am also pleased by their use of multiple estimates of SOC age - which gives confidence to their findings. I found the manuscript to be well written, maintaining a healthy balance of thoroughness and interest throughout the text.

Specific comments

To understand and generalize from these dynamics, I (and I assume readers) would be interested to know the average and range of pH in the soils of this planted forest. I would add this information to the description of this site (which is otherwise fairly

comprehensive).

The authors need to pay attention to the notation that they use and keep this consistent throughout the text and figures. At times they switch between percent and permille for 14C (Fig. 2). Figure axis titles should also be the appropriate symbol, and not %o for permille.

CRA is not defined in the text. Please do so before introducing this as a measurement.

My understanding of Fig. 5 is that C and D are replots of A and B, but just now with the environmental vectors overlaid. These replots with the environmental vectors don't allow me to interpret the shifts in your data points (the data is too scrunched near 0,0). I suggest either removing C and D or re-scaling the vectors (divided by 10 maybe) and replot A and B with these rescaled vectors so that readers can see how these environmental variables are affecting your estimated microbial compositions.

Fig. 6 has some bizarre mispellings of names (Sebciunkles instead of Sebacinales) and I would standardize the names to remove the trailing '_ unk' artifacts of taxonomic clustering

Line 175 - McMurdie not Mcmurdie

It's not clear to me why you exclude negative interactions from the network analysis. If you can justify this briefly, do so in the text.

Line 414/415- you didn't examine microbial biomass though, you quantified DNA and you've stated that you did not partition between viable and nonviable cells/hyphae. While DNA abundances can be used as a proxy for biomass in controlled systems of relatively short age I don't agree with claiming this as biomass here, as much of the DNA you sampled from these lower depths may actually be relictual. Best refer to it as something neutral like 'DNA abundance'

I found it interesting that Bray P did not correlate with other factors (Fig. 4). In the text you mention that you also measured total soil P, however it looks like this wasn't included in analyses. Was this estimate just not variable? I noticed that the soils are very young (from a recent volcanic eruption even), so I'm assuming that the microbes and vegetation are more N limited while P is abundantly available? If it's not too much trouble I'd add general P and N abundance or availability at this site in the site description (plant-microbe people love this). Total P should atleast show up in the supplemental materials along with total C and N(e.g. Table A2)