Dear Dr Soininen,

We thank the reviewer and yourself for considering our revised manuscript entitled "What drives study-dependent differences in distance-decay relationships of microbial communities?". We are pleased to read that the reviewer approved of our revisions, and we appreciate the further constructive comments from the reviewer. We provide our point-by-point response to these comments below, along with a "clean" version of our manuscript.

Dr Dave Clark and Prof. Alex Dumbrell (on behalf of all authors)

Point-by-point response to reviewer comments. Editor.

"I am very happy to see your effort to improve the manuscript. Although the most critical issues have been addressed, I still have some minor request that will for sure improve the clarity of the findings."

- We thank the reviewer for kindly acknowledging our previous revisions, and for the further constructive suggestions.

"(1) I still lack a clear definition of what the authors call "strength". This is important given the multiplicity of interpretations such wording provide (e.g., strength as the rate of decay per unit distance, or strength as the variation of similarity around the slope, or strength as the correlation between similarity and distance as in mantel tests)

See Legendre et al. (2015) Should the Mantel test be used in spatial analysis?"

- We have now clarified our definition of distance-decay strength in the introduction to define strength as the degree to which community similarity and geographic distance are correlated (lines 71-72), and have added text elsewhere to further reinforce this definition (e.g. in hypotheses 1 and 2).

"(2) Page 14 Lines 32-38 - Isn't this sentence in discordance with Nekola & McGill 2014?

Nekola & McGill 2014 argue that distance decay is power law (log-log) at small scales, because there is no dispersal limitation, and environment drives community assembly. It is, of course, possible that Microorganisms are highly widespread and dispersal limitation plays a very small role in community assembly even at continental scales. This would explain why Martiny 2011 (cited by the authors) used log-log relationship at a continental spatial extent as we assume that log-log relationships describe deterministic community assembly processes (without effects of dispersal; Munoz 2008, Scheiner 2011). Therefore, I believe that the pattern described by the authors is size-dependent., this should be stated in the sentence.

Munoz, F., P. Couteron, and B. R. Ramesh. 2008. Beta diversity in spatially implicit neutral models: a new way to assess species migration. American Naturalist 172:116–127.

Scheiner, S. M., A. Chiarucci, G. A. Fox, M. R. Helmus, D. J. McGlinn, and M. R. Willig. 2011. The underpinnings of the relationship of species richness with space and time. Ecological Monographs 81: 195–213."

- We appreciate the reviewer's suggestion to reinterpret this sentence in the light of the work by Nekola and McGill (2014). We have therefore clarified that as the spatial extent of the study changes, so too does the form of the distance-decay relationship, inline with findings from Nekola and McGill, and that the scales at which distance-decay follows either of these forms may be organism-size dependent (lines 101-107).
- "(3) Legend of Table 2 should explain what "All" means the same way that Figure 1 explains."
 - We have added this detail to table 2 as a footnote to keep the table legend concise.
- "(4) The lack of relationship between the spatial extent and Mantel r seems a result of methodological choices (e.g. log-log vs log-linear, grain size, etc), not ecological. This is quite interesting result:). It was confusing to me whether the p-values and R² originated from full models or individual models. The authors should clarify this."
 - We apologise for the confusion caused. The p-values and R² stated are from individual models (e.g. including only spatial extent in the model rather than all contextual variables). We have clarified this by stating that we tested for relationships between distance-decay strength and continuous variables separately, and that p- and R² values were calculated for each term, within the methods section (lines 214-221).