Manuscript: #49405v4

Title: Characteristics of planktonic and sediment bacterial communities in a heavily polluted urban river

General comments:

This study aims to investigate the spatiotemporal dynamics of both planktonic and sediment bacterial populations in the urban river and the associated environmental factors. The authors addressed previous comments and suggestions, which further strengthens the paper. However, there are still some issues that need to be addressed in the revised manuscript: (1) the construction and interpretation of the co-occurrence network was insufficient. MENA was used to construct the co-occurrence network. However, no details were provided for data preparation (did the authors use the entire dataset or a filtered dataset; was logarithm used or not; which similarity matrix was used for correlation analysis) and network properties. Also, I find it difficult to believe that water bacterial communities had more than 90% of negative correlations. Obviously, there will be competition and predation among species, but the majority of interactions will not consist of these factors. It would make more sense to have such a high percentage of positive correlations. Although the current network displays positive/negative interactions, I suggest that the authors upload an additional metadata table into Cytoscape where OTUs are colored according to phylum level. Observing positive/negative correlations between phyla in water and sediment communities will add great value to the study. (2) The Conclusion section is very short and can be elaborated to include more detail.

Specific comments (based on Word document manuscript)

Line 124: platform at
Line 184: the OTUs
Line 185: “46.7% of OTUs were identified in water and sediment samples”
Have to indicate that OTUs were shared between water and sediment samples
Line 186: Water samples contained 1273 unique OTUs that accounted for 14.0% of the total OTUs.
Line 235: with the water temperature
Line 325: The MENA network
Line 328: “The most abundant phylum”
Start new paragraph here
Line 370: between seasons mainly accounted
Line: 373: causes a “wash-out effect”
Line 374: found to be another key driver explaining
Line 393: “functional microorganisms”
Do the authors here refer to metabolically active microorganisms? What about antibiotic resistance studies in this river? Pollution is very high so it’s likely that antibiotic resistance microorganisms will be present.