

***Interactive comment on “Technical Note:
Community of bacteria attached on the PVDF MF
membrane surface fouled from drinking water
treatment, in Seoul, Korea” by Kyongmi Chon et al.***

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General comments

This technical note presents an interesting combination of organic characterization tools and bacterial community analysis to provide a qualitative analysis of membrane foulants. The aim of the research is not entirely clear, however. My main point is: how does bacterial community analysis provide better understanding of the biofouling *mechanism*, as was mentioned in the introduction section (page 66, lines 21-22)? It is clear that conclusions can be drawn about the quality of the source (oligotrophic), what does this tell us about the process of biofouling? How will these results be highly bene-

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ficial in the field of membrane fouling, as was emphasized in the last conclusion (page 71, lines 2-3), can these results be generalised? To provide insight in the biofouling mechanism, the following questions need to be addressed: are all bacteria filtered by the membrane, or a specific fraction? Does growth occur on the membrane?

Also, the structure of the text is not consistent. The logical order seems: first characterisation of the organic foulants to prove that the fouling has a microbial origin and second an analysis of the bacterial community.

Specific comments

1. page 66, line 18: I would refrain from using the term paradigm shift in this context. Otherwise, explain what the old view is and what is the new view; why is it a paradigm shift and not an ongoing change of insight?

2. page 67, lines 6-9: ‘Compared to . . . drinking water treatment has rarely been studied’ The one reference chosen here is on drinking water distribution. There are a few more recent publications on bacterial community analysis in drinking water distribution network. Moreover, there is a study on bacterial community dynamics of a whole drinking water supply system, definitely worth mentioning here: ‘Composition and dynamics of bacterial communities of a drinking water supply system as assessed by RNA- and DNA-based 16S rRNA gene fingerprinting (2006) Eichler, S., R. Christen, C. Hölzle, P. Westphal, J. Bötel, I. Brettar, A. Mehling and M.G. Höfle, Appl. Environ. Microbiol. 72:1858-1872.’

3. page 70, lines 23-25: One of the conclusions is: ‘however, specific bacteria found through genetic identification could not be directly compared to similar published results’, please explain this in the results section.

Technical corrections

1. page 66, line 2: change approximate’ to ‘approximately’

2. page 66, lines 12-13: ‘indicated that the they were most likely’ , remove ‘the’

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3. page 69, lines 3-4: 'The freeze dryer (Ilshin, Korea) was used to dry down the water samples into powders.', should be: 'A freeze dryer (Ilshin, Korea) was used to dessicate the water samples.'
4. page 69, lines 22-23: '..indicated that the Proteobacteria dominated on the membrane surface': remove 'on'
5. page 69, lines 8-12: 'Excitation and emission peaks measured from ... provided information on the peaks that was different from those of the humic substances ... and similar peaks for protein-like substances ...' should be 'Excitation and emission peaks measured from ... were different from those of humic substances ... and similar to those of protein-like substances ...'

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