



Interactive comment on "Environmental proteomics – what proteins from soil and surface water can tell us: a perspective" *by* W. Schulze

Anonymous Referee #4

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Proteomics is a rapidly developing and technology-driven discipline with high potential. Environmental proteomics concerns the study of proteins and peptides found in water, sediment, soils, etc. Environmental proteomics has potential to further our knowledge on e.g. function, cellular location, post-translational modification and source of proteins found in environmental samples. Proteomics complements genomics (i.e. nucleic acid based) approaches to study micro-organisms activity and diversity. This subject of this paper is therefore highly relevant for biogeosciences and might be of interest to a very broad community.

However, the present version of this manuscript needs at least a major overhaul before publication.

(1) This manuscript is not prepared with the utmost care. There are many typos and the wording is not always correct or concise. It appears that this manuscript has been submitted premature.

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- e. How quantitative is the approach adopted given differences in matrices among samples and yields that depend on mass and other factors? f. How were proteins extracted from plant material and detritus? g. The samples analyzed should be better documented. Interesting results are
 - presented, yet the background sample characteristics are not presented.
 - (3) A number of very interesting, new results are presented, but these are not discussed or put into context. For instance, how does protein size distribution compare with other environmental studies where they have analyzed protein size distributions? Some validation of this novel approach by comparing with established techniques would be very useful, perhaps a must to convince skeptical readers.
 - (4) The limitations of the chosen approach should be better communicated: i.e. study of solid samples requires extraction. Standard extraction procedures may work for organisms, but do the standard extraction protocols work for environmental samples? Work by Rick Keil and others on proteins and peptides at UW, Seattle might be incorporated. Some documentation why a (ESI)LC-MS-MS approach rather than MALDI-TOF MS has been used to study particulate materials.

- (2) This paper suffers by a lack of details and clarity regarding sampling, sample material and methodology. Some examples:
 - a. DOC is filtered through 0.45 micrometer so some bacteria and viruses (may) have passed the filter. This has direct consequences for the results (bacterial and viral proteins).
 - b. How were samples desalted?
 - c. How were samples purified: by one-D electrophoresis?
 - d. Is the purification (based on 1-D electroph.) enough to separate complex mixtures found in environmental samples?

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- (5) Figure 8 and related discussion are rather trivial: i.e. differences in relative importance of phylogenetic groups based on density (numbers), standing biomass and active biomass have been reported decades ago. Most biologist report organisms in terms of numbers and biomass: this is not specific to proteomics.
- (6) The author might also consider including studies on marine DOC and proteins in the ocean by E. Tanoue and colleagues (see refs below).
- (7) Organic geochemists studying soils, sediments, suspended particulate matter and dissolved organic matter are usually unable to characterize the entire pool of organic matter using HPLC, GC and pyrolysis based techniques. NMR studies have shown that proteins may account for a major fraction of the uncharacterized organic matter. Environmental proteomics may also offer new ways to address this old problem and it is a pity that the author did not elaborate this.
- (8) This paper should be rewritten to improve the readability. As written, there are significant doubts whether the intended audience will be reached. Most bio-geosciences readers will not be familiar with all the techniques, jargon and approaches within the proteomics community. This paper could have been a key one making the necessary link between environmental sciences and proteomics. However, the present version does not meet the quality standards of top journals in the field.

Detailed comments are not provided because there are too many and this manuscript needs at least another round of evaluation.

In conclusion, the topic is very interesting and novel, but the manuscript is not yet mature enough in terms of presentation and clarity to be published in biogeosciences.

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References:

Yamada, N. and Tanoue, E.: Detection and partial characterization of dissolved glycoproteins in oceanic waters, LIMNOLOGY AND OCEANOGRAPHY, 48 (3), 1037–1048, MAY 2003.

Suzuki, S., Kogure, K., and Tanoue, E.: Immunochemical detection of dissolved proteins and their source bacteria in marine environments, MARINE ECOLOGY-PROGRESS SERIES, 158, 1–9, 1997.

Tanoue, E.: Characterization of the particulate protein in Pacific surface waters, JOURNAL OF MARINE RESEARCH, 54 (5), 967–990, SEP 1996.

Tanoue, E., Ishii, M., and Midorikawa, T.: Discrete dissolved and particulate proteins in oceanic waters, LIMNOLOGY AND OCEANOGRAPHY, 41 (6), 1334– 1343, SEP 1996.

Interactive comment on Biogeosciences Discussions, 1, 195, 2004.

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1, S236–S239, 2004

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