

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

Anonymous Referee #3

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The manuscript describes an interesting approach to assess biological communities involved in the functioning of different ecosystems on the basis of their protein patterns. It is not clear to me what the intention of the author was when he wrote this paper. Is it meant to be a kind of opinion paper on this new methodology of environmental proteomics or is it an original research paper? To my opinion it is neither of these. The manuscript describes results of studies in which the approach to identify biological communities on the basis of protein patterns, is applied in different ecosystems, but the information provided in the manuscript does not allow for a proper evaluation of the results. The significance of the quantitative data on the occurrence and dynamics of the communities is not clear as a statistical analysis of the data is lacking. I realize that that is not always necessary, but the author mentions the existence of quantitative differences between samples and in that case a proper statistical analysis is required. The term proteomics and other “omics” terms are popular those days and are used frequently, and sometimes they are misused. The latter is also the case, here. Proteomics, at least in the definition that I know, is related to the study of the protein

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composition of an organism or a community (often referred to as metaproteomics) as directly related to the expression of the genome or large parts of the genome of an organism or the collective genome of a community. That is not the case here and therefore, the term “proteomics” is fully misused as is the reference to the metagenomic work of Venter and others (pg. 198). The methodology described here is similar to PFLA and associated methods developed and applied already for quite sometime to identify and assess the role of (microbial) communities in various ecosystems. It could well be that the methodology of analyzing protein patterns as described here adds a new and valuable technique to the existing tools for assessing biota and their functioning in natural ecosystems, but detailed information on the methodology and references for the assessment of the patterns of the different communities are missing and therefore the relevance of this paper can not be assessed properly. So, the remark that “the protein sequence derived from MS/MS spectra of tryptic peptides bears taxonomic information of the origin of the protein and are unique for a specific group of organisms or even single species” (pg. 200), should be supported by detailed information or by information from literature or otherwise it is inappropriate to mention this. The author does not show to be informed about the present knowledge on microbial ecology, when he mentions, that “bacteria are expected to be present in all environmental samples, but have not been recognized as such by ecologists” (pg. 200). I think that there is no ecologist that does not recognize the fact that bacteria are present in most if not all environments. The author does not clarify how the present method of analyzing enzymes differs from the vast array of techniques used for decades to detect enzymes in environmental samples and their functioning. If the present method only allows for the detection of the presence of an enzymatic structure (or a community of enzymes) within a sample, then how does that relate to the activity of the enzymes as determined by the many existing enzyme assays. It seems to me that the author was in a hurry when he wrote this paper as it contains several typing errors. Overall, I recommend to reject this manuscript for further publication.

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