

## ***Interactive comment on “Protein analysis in dissolved organic matter: what free proteins from soil leachate and surface water can tell us – a perspective” by W. Schulze***

**Anonymous Referee #3**

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### General Comments

This paper deals with the application of proteomics in environmental samples. Yet, there are only rare examples in the utilization of this technique with this respect. While there are some data available within marine sciences, this concerns in particular terrestrial ecosystems. Here, W. Schulze tested whether proteomics can be used to deduce some processes involved in the microbial decomposition of plant residues and the mobilization and fate of dissolved organic matter (DOM) in the soil. She could clearly show the potential of this novel technique to distinguish not only the phylogenetic origin of proteins found in solid and dissolved organic matter but allows also to relate this information to relevant biogeochemical processes. I agree with her conclusion that with proteomics a powerful tool emerges in environmental sciences, in particular when used

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together with methods of molecular biology. It has also to be acknowledged that she relates the findings of proteomics to alternative methods and discusses critically the current limitations of this method.

### Specific Comments

Even though the overall goal of the paper, i.e. testing the suitability of proteomics in terrestrial biogeochemistry, is achieved, the manuscript lacks a little bit of the arbitrary choice of samples. This made it a little bit hard to test clear process-based hypotheses. But one may argue that this would be then the second step, and the ground is now ready for more detailed process-oriented work in follow-up papers.

However, for a better understanding of the samples and their context in the environment, a more straight forward description of samples is necessary. The same database should be given for the samples. This may include data about location, climate, parent material, vegetation, soil type and humus type (in case of the stream samples soil type representing the catchment), DOC concentration and in case of the soil-derived DOM samples total organic carbon and microbial activity. These parameters have been shown to strongly influence source, concentration, and composition of DOM. Such information may help to relate the results presented in this paper to older work on DOM dynamics using other methods.

In the Material and Methods and Results it would be more useful to present first the method / data of the decomposing plant litter (as a source of DOM), and then follow the water flux in the terrestrial ecosystem starting with the rain samples, followed by the soil DOM samples, and finally by the stream DOM samples.

Can there any speculation be done about the origin or composition of the 70% of the proteins not characterized?

In the discussion the author can make a little better use of the wealth of papers investigating DOM dynamics with alternative methods, mostly degradative and non-

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degradative chemical analyses.

Since for the Tura site the author is having information about the decomposing plant material (which is an important source of soil DOM), the DOM in the surface soil and the DOM leaving the soil (i.e., in the creek), I think that at this site the fate of DOM can be discussed a little bit deeper. This concerns e.g. the link of the solid and dissolved organic matter.

It is interesting to see that the three replicates taken at the Hainich site do not show significant differences in their protein composition. However, there is information in the literature using chemical and molecular approaches that soils are having an extreme small scale heterogeneity of their chemical and biological properties. In consequence, it looks like that the proteomics is a quite conservative method. However, since proteomics detects more the active part of the ecosystem, I can't believe this. This requires a comment. By the way, to assess the reproducibility of a method it would be better to do multiple analyses on the same sample.

When assessing the DOM composition of subsoil solution or stream samples, it would be always advantageous to know something about the water flow in the soil. At low soil water contents, when matric flow is occurring, DOM in the streams is mainly characterized by the results of sorption processes in subsoil horizon. In contrast, at high soil water contents DOM mobilized in the organic layers may pass the sorbing subsoil via preferential flow paths.

Sorption may be also a reason why no exoenzymes have been detected in the soil solution. Large and charged biomolecules do have a strong affinity to mineral surfaces and the organic substrates attached to these surfaces.

Technical Comments

The contents of chapter 2.2 can be moved to chapter 2.1.

The designation of the bacterial subgroups in Fig. 3B is hardly readable.

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Interactive comment on Biogeosciences Discussions, 1, 825, 2004.

**BGD**

1, S496–S499, 2004

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