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Protein fingerprint from soil samples

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Mass spectrometry based analysis of proteins is widely used to study cellular processes in model organisms. However, it has not yet been routinely applied in environmental research. Recent advances in mass spectrometry using nanoflow liquid chromatography coupled with mass spectrometry make such a large scale approach feasible (Aebersold and Mann 2003). Here we present the possible use of protein analysis in ecology and environmental sciences focusing on different terrestrial ecosystems. In contrast to DNA, which has been shown to remain bound to mineral particles in the soil, proteins present the reactive component of organisms. Furthermore proteins are assumed to have a higher turnover reflecting dynamics of organisms. Therefore protein characterization allows us to take a closer look at the potential catalytic capabilities in the soil and their taxonomic origin. In contrast to existing methods which focus on few taxonomic groups (e.g. fungi, bacteria), pioneer studies (Schulze et al. 2005) indicate that characterization of phylogenetic origin is possible across all major taxonomic groups. It could be shown that the contribution of different taxonomic units to the environmental protein pool is responsive to disturbance, seasons, soil depth, etc. However, the lack of sequenced genomes of soil organisms imposes limitations to the characterization of proteins at the level of single species. In summary, the analysis of proteins from soil samples opens a new area of research between the fields of microbiology and biogeochemistry.

References:

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