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SIP goes Proteomics

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The function and activity of single species in microbial communities is a major question in environmental microbiology because microbial communities rather than single species are governing environmental relevant processes. It is still a challenge to assign specific metabolic capacities and activities to certain species in a microbial community. Therefore we have developed Protein-SIP, a method to analyse the specific metabolic activity of a single species within a consortium. It makes use of a 13C containing substrate for metabolic labelling of proteins. These can be separated by 2D gel electrophoresis or by LC and further analysed by mass spectrometry to characterise the identity of proteins. Concomitantly their 13C content as an indicator for function and activity of the host organism is analysed. By this approach we can distinguish which species is metabolically active within a consortium with a sensitivity of 13C incorporation of down to 2%. With less sensitivity this method can also be used with 15N containing substrates. With Protein-SIP it becomes possible to track the carbon and nitrogen flux within microbial communities.