Fast nondestructive Raman spectroscopic detection of minerals and biomolecules for exobiological studies

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Raman spectroscopy has been established as a potential field method of detection of minerals, which is not only important for applications in geosciences but also in exobiology. For planetary exploration, two different approaches can be identified, namely, telescopic Raman remote measurements methods or Raman detection *in situ*, close to the outcrops using miniaturised field instruments.

In this study, numerous rock-forming and secondary minerals [1, 2] were detected unequivocally using their most intense Raman bands, which were found at their previously reported correct Raman peak positions. Few organic minerals and biomolecules were successfully detected as well. Excellent reliability and satisfactory spectral resolution was observed for portable instrumentation in the wavelenght range 200 – 2000 cm^{-1}. Portable Raman instruments can be recommended for the fast and robust detection of minerals in the field. These results are important because of planned incorporation of Raman instruments in rovers for future NASA and ESA missions to Mars. In this context especially organic minerals and biomolecules detection represents a challenge.

[1] Jehlicka *et al*. (2009) *Spectrochimica Acta Part A* **73** (in press, doi:10.1016/j.saa.2008.09.004). [2] Jehlicka *et al*. (2009) *Journal of Raman Spectroscopy* (in press, DOI 10.1002/jrs.2246).

SIP goes Proteomics - Elucidation of structure and function of microbial communities

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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. Approaches based on genetics do reveal information about potential capacities but only proteome based experiments can show the acute activities. We have developed a method to analyse the specific metabolic activity of a single species within a consortium making use of a ^{13}C containing substrates 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, as well as their ^{13}C content as an indicator for function and activity of the host organism. By this approach we could distinguish which species is metabolically active within a consortium with a sensitivity of ^{13}C incorporation of 5%. With less sensitivity this method can also be used with 15N containing substrates. Thereby we present the technology to follow the carbon and nitrogen flux within microbial communities.