

***On the taxonomic resolution of Raman microspectroscopy:  
Identification within the highly related Bacillus subtilis group***

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Vibrational methods are recently presented as a powerful new technique for the identification of micro-organisms. Their multiple advantages, compared to more classical, chemotaxonomical and microbial tools, make them attractive to incorporate in modern microbiological laboratories. Since Raman spectra contain biochemical information regarding the complete molecular composition of the cells, the method combines discriminatory abilities of different phenotypic characterizations such as fatty acid content and composition (FAME), Polyamide acryl amide gel electrophoresis of whole cell proteins (PAGE) and metabolic tests (API, BIOLOG). Moreover, Raman spectroscopy is much less labor intensive and sample preparation is very simple. The overall information content and speed of analysis are interesting advantages for screening studies. Together these elements have set the stage for the development of Raman spectroscopy into a powerful tool for rapid and inexpensive routine microbial analysis. However, before this vibrational technique can be used in microbiological laboratories a good understanding of the taxonomic resolution of the technique is necessary.

*Bacillus mojavensis*, *Bacillus vallismortis*, *Bacillus amyloliquefaciens*, *Bacillus atrophaeus* and *Bacillus subtilis* all belonging to the *Bacillus subtilis*-group are difficult to discriminate by phenotypic approaches. Consequently, the *B. subtilis* group is an excellent starting point to study the fine taxonomic resolution of Raman spectroscopy. This study aims thus to determine this taxonomical resolution (species or strain level) and to explore its application for bacterial identification.

The presentation will discuss how to discriminate between different highly related species by considering each strain as an independent entity. The robustness of the proposed identification method will be finally assessed by a blind study.