

## **107e Interspecies Cyanobacterial Proteome Comparison and Characterization Using Two-Dimensional Gel Electrophoresis and Gel-Free Shotgun Proteomics**

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Much work in environmental genetics has focussed on the identity of the organisms that are present in a particular ecological niche, whether this is a natural biotope or a mixed consortium bioreactor. However, it has been recognised that what is more important is what these organisms are doing, rather than which are there. As the proteins are the functional molecules within an organism, it is important to develop functional phylogenetic relationships between groups of organisms so as to predict their potential biotechnological activities.

Cyanobacteria are a diverse group of photosynthetic prokaryotes, and are believed to be the ancestral origin of the higher plant chloroplast. With the completion of an increasing number of cyanobacterial genomic sequences, attention is now being focused on post-genomic understanding of these organisms. Here we have developed a novel 2DE method, supplemented by multidimensional liquid chromatography, to compare and contrast the proteomes for a range of cyanobacteria. The first goal was to analyse the proteomes from closely related organisms, and to compare the outcomes for sequenced (*Anabaena variabilis* ATCC29413) and unsequenced (*Anabaena ambigua* CCAP1403/7) species. Secondly, we extended this approach to the more distant organisms *Nostoc* sp. PCC7120 (sequenced), *Scytonema* sp. PCC7110 (unsequenced) and *Lyngbya majuscula* CCAP1446/4 (unsequenced). By use of image analysis, spot matching and electrospray ionization tandem mass spectrometry, together with protein-protein BLAST analysis, we have been able to develop functional phylogenetic relationships between these cyanobacteria to act as a guide for future biotechnological exploitation. This approach has important implications for environmental proteomics where the genome sequence of an organism is unknown or difficult/expensive to obtain.