

4th International Conference on **Proteomics & Bioinformatics** August 04-06, 2014 Hilton-Chicago/Northbrook, Chicago, USA

Proteome analysis of toxic *Microcystisaeruginosa* via 2 dimentional gel separation and MALDI-ToF Mass-Spec

Frank Pierce and A Ouellette Oswego University of Newyork, USA

T oxic cyanobacterial blooms pose a number of significant ecological problems in eutrophic waterways, one of which is the release of toxins into the environment. Exposure to these toxins can be harmful or even fatal to a variety of organisms, including humans. This study was undertaken in an effort to compare two strains of Microcystisaeruginosa, one non-toxic (UTCC 124), and one very toxic (UTCC 299), in an effort to correlate protein expression and toxin production. Proteins isolated from Microcystisaeruginosa were separated via 2-D gel electrophoresis. These gels were scanned and analyzed via AmereshamImagemaster, with a correlation of ~17% between all gels run, and ~50% correlation within duplicates. Following separation, proteins were excised from the gels and digested with trypsin, then analyzed via MatrixAssisted Laser Desorption/ Ionization Time of Flight Mass Spectrometry. Spectra obtained were then run through the Mascot search engine. As of his admission,64 spots have been investigated and 13 proteins have been positively identified, including ATP synthase, allophycocyann, c-phycocyanin and four unnamed protein products.

fpierce@oswego.edu