

CONFÉRENCE

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Proteomics for Organism Monitoring

The talk will focus on the new technology of MudPIT and community proteomics to measure microbial and plant protein expression in response to spatial and temporal environmental influences.

Previous research within our laboratory has been able to measure over 1000 synthesized proteins from bacterial, yeast and the plant *Arabidopsis* (from the photosynthetically active parts of the plant). This research uses a technology called MudPIT that uses whole cells samples processed through single tube cell lysis and protein digestion. Samples are analyzed through 2D nano-LC MS/MS system with a split-phase column (RP-SCX-RP) on a LTQ (mass spectrometer) with 22h runs per sample. All MS/MS spectra are searched with the SEQUEST (or similar) algorithm and filtered with DTASelect/Contrast. Tandem MS/MS spectra are searched against known annotated genome databases. From this research we have been able to measure many critical proteins required for organism growth including energy production, metabolism, transport and storage, secondary compound production, and stress response proteins. Our long term goal is to use the developing technology to enable understanding of viability within the growth environment and monitor communities, at a proteomic level, as they adapt to these variations. The ability to observe changes in protein synthesis and concentration will allow producers the ability to accurately monitor the growth, optimize production of secondary compounds and maximize yields.

Vendredi 2 novembre 2012 à 11 h 30
Pavillon Claire McNicoll, salle Z-300

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