

DMMC Course PROTEOMICS: METHODS & APPLICATIONS

1530, Tuesday 6 June 2006. UCD Conway Institute Lecture Theatre

Shotgun Proteomics & Quantitative Proteomics

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Abstract

Comprehensive proteome analysis requires efficient, robust, and practical methods for the identification and quantification of all proteins in complex biological samples. Although the identification of proteins using mass spectrometry is well established, technical challenges remain. Two-dimensional gel electrophoresis (2-DE) coupled with MS has traditionally been employed as a semi-quantitative proteomics tool. However, other separation strategies based on liquid chromatography now complement 2-DE as a central method for the analysis of proteins in complex biological systems. In this talk I will give an overview of LC based protein profiling and discuss the most promising methodological developments in this area with particular emphasis on labeling strategies for semi-quantitative LC-based expression profiling.

Biography

Connie Byrne has a honours degree in Food Science and Technology and obtained her PhD from University College Cork in 1998. She then worked at the University of Tuebingen, Germany as a Marie Curie Fellow on the separation and identification of proteins by high performance liquid chromatography (HPLC) and mass spectrometry (MS). She returned to Ireland in 2000 to join the Clinical Pharmacology Department at the Royal College of Surgeons in Ireland before spending a year in industry with HiberGen Ltd., as genotyping group leader, working on the identification of medically relevant genetic variation via capillary electrophoresis and MS. In 2004, Connie joined Gerard Cagney's Translational Proteomics Group as MS Group Leader at UCD Conway Institute.