Deciphering the Second Code of Life

with

Mass Spectrometry?

CRP; Faculties Club; Applied Biochemistry

Modification specific proteomics with emphasis on phosphorylation and glycosylation

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Sequencing of the human genome has revealed that the number of protein coding genes is approximately 25,000, i.e., only approximately twice as many as that of the fly or worm and five times that of yeast. This strongly implies that protein complexity and regulation in higher eukaryotes is governed by co- and post-translational modifications and splicing events. It is becoming increasing obvious in biological studies that numerous proteins and protein complexes are regulated by post-translational modifications. Several protein modifications have been documented and methods to systematically identify post-translational modifications during protein identification studies are being developed. We have developed an approach, which we term Modification Specific Proteomics, for specific detection of various types of protein modifications in proteomics. The detection of PTM's is very challenging because these are often transient and highly heterogeneous in terms of modified site (e.g. phosphorylation) as well as the modifying group (e.g. glycosylation). Our concept is based on specific detection of PTM's in the 2D-gel, by specific "pull-out" of modified proteins/peptides, or by selective detection of the specific type of PTM in the mass spectrometer. It will be illustrated by our recent attempts to perform phospho- and glyco-specific proteomics. These two types of modifications are found in more that 50 % of all proteins in higher organisms. Due to their implications on protein structure and function, studies of biological phenomena must include detailed elucidation of these two types of modifications on a sensitivity level compatible with proteomics studies.

Vorleufer::Seyed Tabaei; *Towards Ultrasonically Levitated Droplet Ion Sources for Mass Spectrometry* (15min)

Venue : BMC Building D Plan 15 Time: Wednesday 25 of April at 14^{00}

Välkomna; Christer Sjögren; Curt Reimann & Staffan Nilsson

Towards Ultrasonically Levitated Droplet Ion Sources for Mass Spectrometry

Seyed Tabaei

Abstract

The *Airborne system* is a miniaturized droplet manipulation system based on acoustic levitation, which has been developed for analytical, and bioanalytical chemistry applications. This system provides a way to avoid solid walls around the sample and hence eliminates adsorption of analyte at the walls of the vessel as well as contamination of the sample solution by desorption of substances from such walls. Several detection protocols such as fluorescent imaging, right-angle light scattering and Raman spectroscopy have been incorporated in the system.

The aim of this project was to study the feasibility of interfacing the *airborne system* directly to mass spectrometry equipment. By utilizing levitated droplets as an ion source for ESI-MS, it may be possible to realize online mass spectrometric monitoring of progressing chemistry in levitated microdroplets.