

## **THE ROLE OF MASS SPECTROMETRY IN HIGH THROUGHPUT PROTEOMICS: CONQUERING NEW FRONTIERS OR GIVING FALSE HOPE?**

*Peter G Hains, Derek van Dyk, Angela Connolly, Nicole Verrills and Bradley J Walsh.*

Australian Proteome Analysis Facility, Macquarie University, Herring Road, North Ryde, 2109, Australia.

Mass spectrometry has developed an integral role in proteomics with MALDI-TOF MS playing an essential role in high throughput proteomics, due to the power of peptide mass fingerprinting (PMF) for protein identification. The facile data interpretation along with ease of automation, of both sample preparation and database searching, make this technique ideal for this application. More recently, hybrid ESI-QqTOF instruments have been used extensively for proteomic work. These machines can be adapted to automated LC-MS/MS applications and database searching or used for manual data acquisition to allow for high confidence *de novo* sequencing of peptides.

Here we present data acquired with a Micromass TOFSPEC 2E MALDI-TOF MS or Micromass Q-TOF ESI-TOF MS and relate the "MS dream" to the reality of the situation. Specifically, we examine how the efficacy of PMF is limited by the species being studied, the effectiveness of cross-species matching and how useful MALDI data is for high confidence identification of post translational modifications. Does the type of stain used affect the final outcome of the analysis? What is the practical limit of sensitivity? Additionally, data is presented detailing our experiences with the Q-TOF for protein identification, *de novo* sequencing and PTM identification. This data is then related back to the overall success rate of the project goals and the time frame involved for analysis.

The aim of the presentation is to address the question as to whether mass spectrometry is meeting the expectations originally proposed when the technique was being widely adopted in the proteomics field from a high throughput perspective.

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