



MEDIA RELEASE

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Significant advances in healthcare and agriculture through *proteogenomics and protein mapping* used to accurately identify drug targets and biomarkers

Proteomics International has published the results of proteogenomics and proteome mapping methodologies that clearly demonstrate that these techniques are powerful, rapid and economical ways to aid in the comprehension of genomic assemblies. The potential benefits of this technology are vast for the agri-biotech and pharmaceutical industries, molecular biologists and other scientists worldwide.

Proteins are the operational and executive molecules of life. Hence the goal of nearly all genome and proteome sequencing projects is to identify and characterise the expressed genes (proteins) within the organism.

In two recently completed studies using diverse technologies Proteomics International has achieved unsurpassed levels of proteome coverage.

The central dogma of biology states that genes encoded in the chromosomes are copied into RNA intermediates, which are in turn translated into proteins. These are known collectively as, respectively, the genome, the transcriptome and the proteome. The problem is that it is extremely difficult to determine the exact number of expressed genes (proteins). For example, when the human genome project was completed in 2003 there were thought to be 40,000 genes, but now that number is less than 25,000. This is because gene annotation underpins genome science, and it is not exact.

Proteomics International has joined a handful of groups pioneering a new way to improve this process. Proteomics, through mass spectrometry, provides the amino acid sequence of the protein, and can immediately identify the gene encoding it. This technique is called proteogenomics (using proteomic information to annotate the genome).

Working with a fungal pathogen as a model system, and in collaboration with the Australian National University, and the Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)(Murdoch University) results published on-line in BioMed Central Bioinformatics illustrate the power of the technology.

The group targeted *Stagonospora nodorum*, which is the causal agent of leaf blotch on wheat, and is responsible for \$60M (AUD) of crop loss in Australia each year. The genome sequence of this major pathogen was obtained in 2005, and despite a large amount of DNA data the number of estimated genes varied from 11,000 to 16,000 depending on the computational method used. A single proteogenomics run was carried out and successfully identified over 2,100 of the genes in a six week time frame. The proteomic analysis matched 1324 genes that were not directly supported by any transcriptomic (RNA) approaches.

The second approach used the more well-known iTRAQ technology (isobaric tags for relative and absolute quantification) to perform quantitative proteomic analysis of protein signalling in the same pathogen.

In this study, iTRAQ was combined with two-dimensional chromatography and rapid laser based mass spectrometry (LC-MALDI-MS/MS) to characterise protein expression changes in wild type and mutant strains. Results published in the journal "Proteomics" this month identify a total of 1336 proteins, a record for a fungus. The concentration of 4% of the proteins was significantly altered between the two strains, yielding information on important metabolic pathways of the pathogen and how it reproduces.

In combination the two approaches are a powerful, rapid and economical way to aid in the annotation of genomic assemblies, and the potential benefits of this technology are vast. The company already has plans to investigate a second model system thanks to a new \$255,000 grant from the Australian Research Council. In partnership with another multi-centred team, this time headed by the WHO Collaborating Centre for Parasitic Infections at Murdoch University, and including the Universities of Calgary, and Kent (UK), Proteomics International will study the functional proteomics of *Giardia*.

The team will apply the same proteome mapping and proteogenomic approaches to dissect and compare genes and their protein products associated with disease. This will identify new parasitic drug targets and diagnostic markers, and discover novel bioactive peptides and proteins from this evolutionary unique organism.

About Proteomics International Pty Ltd

Proteomics International is both a contract service provider and research and development company, focused on providing quality analytical services to the biological research market and on developing value from protein drug discovery. Proteomics International is the world's first ISO/IEC 17025 accredited proteomics services laboratory, and combines the most advanced high throughput mass spectrometry instrumentation (MALDI TOF-TOF and LC-MS/MS) and a team of qualified scientists with proven expertise in protein and peptide chemistry. The company has two focal research activities; analysis of venoms using its proprietary *Bioven* process, and the discovery and use of biomarkers from a variety of tissue sources. Skills developed from these research programs are incorporated into the sophisticated suite of specialist contract research techniques provided to clients such as iTRAQ, MRM, and *de novo* proteome mapping. High quality, fast and affordable protein identification, analytical and characterization services are routinely provided. Proteomics International is based in Perth, Western Australia and has established itself as an industry leader in the delivery of contract research and lead molecule discovery services in the Asia Pacific region. **Proteomics International is actively seeking distributors from many countries.**

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