

Metabolomics: Bridging the Phenotype–Genotype Gap

Guest Editorial

The ‘-omics’ technologies have been used to obtain a more holistic view of how biological systems work and underpin the fields of functional genomics and systems biology. They are also widely employed to identify biomarkers for use in the diagnosis and monitoring of human disease. While ‘-omics’ technologies such as transcriptomics and proteomics are now well established and widely used across the biological sciences, each has limitations and only provides part of the picture. This has led to increasing interest in metabolomics, a rapidly emerging ‘-omics’ approach that involves the analysis and quantitation of all low molecular weight (<1,500 daltons) metabolites in a biological sample. Metabolomics is clearly complementary to other ‘-omics’ approaches, but may have a special role in bridging the phenotype-genotype gap, since analysis of the metabolome can reflect the sum of all up-stream regulatory events, as well as direct inputs from the external environment. Metabolomic approaches can also provide unique insights into metabolic dynamics. Specifically, analysis of metabolite changes over time (rates of metabolite uptake/secretion) and stable isotope labelling experiments can be used to infer metabolic fluxes that cannot be deduced by any of the other ‘-omics’ methods. Analysis of the metabolome is daunting, not least because of the chemical diversity and dynamic range of cellular metabolites, as well as the redundancy of cellular metabolic pathways that complicate data interpretation. However, recent advances in analytical instrumentation, particularly mass spectroscopy, as well as bioinformatic and computational tools have made metabolomics much more accessible to investigators.

Metabolomics Australia (MA; <http://www.metabolomics.net.au>), comprising five research centres/nodes around Australia, was established in 2007 to provide a metabolomics

service to Australian researchers in academia, government research organisations and industry. MA is funded under NCRIS (National Collaborative Research Infrastructure Strategy) as part of Bioplatforms Australia Pty Ltd, which also incorporates Genomics Australia, Proteomics Australia and the Australian Bioinformatics Facility. In this Special Technical Feature, four research groups that have contributed to the development of MA provide an overview of the different facets of metabolomics, with a strong emphasis on technical issues and pitfalls. Robert Trengove and colleagues (Murdoch University, WA) review the use of different types of hyphenated mass spectroscopy to analyse polar metabolites in biological extracts. Peter Meikle and colleagues (Baker IDI Heart and Diabetes Institute, Melbourne) describe the complementary analysis of lipids, a rapidly growing sub-discipline of metabolomics termed lipidomics. Plant physiologists were one of the driving forces in the development of metabolomics, and Ute Roessner and Tony Bacic (University of Melbourne) describe the particular challenges of doing metabolomics in plant systems. Finally, Jens Kroemer and Lars Neilson (University of Queensland) provide a primer on one of the most challenging sub-specialisations of metabolomics, namely the measurement of metabolic fluxes (fluxomics).

The focus of the reviews in this Special Technical Feature is on the methodology that underpins metabolomics, including the limitations and challenges of various approaches. However, it should be clear that information obtained from these analyses can be used in a variety of applications, including biomarker identification, drug discovery and development, clinical toxicology, nutritional studies, and quantitative phenotyping and bioengineering of plants or microbes.

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Cover Illustration

Image of a new generation gas chromatography-triple quadrupole mass spectrometry instrument. GC-MS instruments are one of several major mass spectrometry platforms used in metabolomic analyses.

Image courtesy of Christian Krill, Murdoch University.

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Australian Biochemist – Editor Rebecca Lew, Editorial Officer Liana Friedman

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Metabolomics Australia – an Integrated Metabolomics Service for the Australian Research Community

Metabolomics Australia (MA; <http://www.metabolomics.net.au>) is a government-funded national metabolomics service consortium funded under NCRIS (National Collaborative Research Infrastructure Strategy) as part of Bioplatforms Australia Pty Ltd, which also incorporates Genomics Australia, Proteomics Australia and the Australian Bioinformatics Facility. MA was founded in 2007 and is the first high-throughput metabolomics facility in Australia. MA services are focussed on all areas of technology for small molecule analysis, with the aim of providing access to world-leading advances and technology for researchers in academia, government research organisations and industry. MA acts as both a service provider and a research hotel. The five MA nodes possess synergistic technologies and expertise, enabling the consortium to offer a far broader range of services to our clients and collaborators. The nodes include:

- The University of Melbourne School of Botany (Australian Centre for Plant Functional Genomics and Victorian Centre for Plant Functional Genomics) and Bio21 Institute, Melbourne, Victoria;
- The Australian Wine Research Institute Ltd, Adelaide, South Australia;
- The University of Western Australia, ARC Centre of Excellence in Plant Energy Biology and Centre of Excellence for Plant Metabolomics, Perth, Western Australia;
- Murdoch University, Perth, Western Australia; and
- The University of Queensland (Australian Institute for Bioengineering and Nanotechnology), Brisbane, Queensland.

Through Bioplatforms Australia, an integrated ‘-omics’ pipeline enabling the design and execution of a systems biology approach can be developed.