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EDITORIAL

Editorial

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The theme of this topical issue is the application of NMR spectroscopy in metabolomics. When the Journal of Biomolecular NMR was conceived more than 20 years ago, and the aims and scope of the journal revised occasionally over the years, metabolomics was not on the horizon. A search for metabolomics today yields thousands of 'hits'. Metabolites are the end products of all of the chemical or biochemical processes within the system, and by their integrative nature are diagnostic for the state of the system. Metabolomics is the observation, identification, and quantitation of these metabolites on a system wide basis. The major tools of metabolomics are arguably NMR and mass spectroscopy, so it seemed appropriate to the editors to have a special issue devoted to the role NMR takes in this emerging area. NMR is non-destructive, quantitative, and reproducible; and offers powerful approaches to metabolite identification and special features such as isotopomer identification which can be used to follow metabolite flux. It is, however, relatively insensitive. The manuscripts assembled in this issue cover a wide range of subjects ranging from the development and testing of new NMR methodologies for this field, to the application of NMR based metabolomics to very diverse subjects including animal models, biological tissues, biofluids such as urine and blood, and natural products such as German white wine. Of course, any single issue of a journal can not include all researchers in the field, and as a consequence the papers in this issue only partially reflect the diversity of applications as more and more researchers turn to NMR metabolomics in the effort to solve chemical, biological, and medical problems. The issues addressed in the field include the types of NMR experiments used to obtain the spectra, the different approaches to the extraction of metabolite data from the raw NMR spectra, and the statistical approaches used to extract conclusions about the usefulness of the data in addressing the questions addressed.

Several articles concern the application of metabolomics to tissues, cells, and biological fluids. Interestingly, they take quite different approaches to the extraction of data from the NMR spectra, and the statistical handling of this data. Vogel and coworkers examined a murine model of ascorbic acid deficiency, and are able to predict phenotypic parameters such as body mass using their model (Duggan et al. 2011). Griffin and coworkers used metabolic profiling combined with multivariate analysis to examine mouse models of neurodegenerative diseases (Salek et al. 2011). Weljie and coworkers (2011) examined the metabolomic profile of a breast cancer model system under hypoxia using both in vitro and in vivo approaches. Reily and coworkers measured metabolite indicators in the media to assess factors of protein production in a Chinese hamster ovary cell line and identified metabolites important for the viability of the liver tissue (Aranibar et al. 2011). They used a quantum mechanical total line shape analysis to quantify low concentration metabolites in regions of spectral overlap. Xu and coworkers (2011) examined a myotube model of mitochondrial dysfunction, investigated both intra and extracellular metabolite concentrations to understand the etiology of mitochondrial disease. Markley and coworkers examined the contributions of three different metabolic pathways for the de novo synthesis of glutamate in red blood cells by assessing the enzymatic activity of the three enzymes involved (Ellinger et al. 2011).

Sample preparation is a key step in applying metabolomics to urine and plasma/serum samples. Bertini and

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coworkers examined and optimized pre-analytical treatments of biofluids prior to their deposition in biobanks. This is critical for generating consistent and reproducible data in future studies, and recommended defined protocols for the processing and management of these biofluids (Bernini et al. 2011). Lemire and coworkers report a careful analysis of the variability in the targeted profiling for *Saccharomyces cerivisiae* and *C. elegans* (Szeto et al. 2011).

Verpoorte and coworkers took a very detailed approach to the profiling of German white wines to determine which compounds contribute to the taste profile of the respective wines and to provide a more scientific approach to the assessment of wines (Ali et al. 2011). They focused on the relevance and applicability of metabolomics as a comprehensive approach to the analysis of food products.

Several other papers present new techniques or novel combinations of existing methods for NMR spectroscopy for metabolomics. Fan and Lane (2011) used isotope labeled molecules as tracers in conjunction with a variety of NMR approaches to gain insight into the metabolic networks and flux that exist in vivo. Raftery and coworkers compared 1D TOCSY for the quantitation of metabolite concentrations in complex mixtures such as urine (Sandusky et al. 2011). Markley and coworkers described a clever combination of the HMQC and COSY experiments that allows in one 2D experiment the ability to identify the structure of unknown compounds and potentially to identify multiple compounds in mixtures (Hu et al. 2011). Grimes and O'Connel (2011) evaluated the application of micro-coil NMR probe technology in increasing the sensitivity and throughput of NMR-based metabolomics. Wishart and coworkers present the results of the automated extraction of metabolite concentrations from NMR spectra collected from samples derived from cerebrospinal fluid, urine, and blood serum (Mercier et al. 2011).

This topical issue of the journal provides examples of recent advances in applying NMR spectroscopy to investigate metabolomics. As sample collection, NMR software and hardware developments become more sophisticated, the data from metabolites analysis will become more reliable and more useful in characterizing a variety of systems. Many of us hear constantly from our administrators and governments about issues like practical applications and translation research—is this an area where NMR can make a real contribution? I hope the work described in this topical issue will highlight for the reader the developments and applications of NMR to this field.

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Brian D. Sykes

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References

Ali K, Maltese F, Toepfer R, Choi YH, Verpoorte R (2011) Metabolic characterization of palatinate german wines according to sensory attributes, varieties, and vintages using NMR spectroscopy and multivariate data analyses. J Biomol NMR. doi:10.1007/s10858-011-9487-3

Aranibar N, Borys M, Mackin N, Ly V, Abu-Absi N, Abu-Absi S, Niemitz M, Schilling B, Li ZJ, Brock B, Russell II RJ, Tymiak A, Reily MD (2011) NMR-based metabolomics of mammalian cell and tissue cultures. J Biomol NMR. doi:10.1007/s10858-011-9490-8

Bernini P, Bertini I, Luchinat C, Nincheri P, Staderini S, Turano P (2011) Standard operating procedures for pre-analytical handling of blood and urine for metabolomic studies and biobanks. J Biomol NMR. doi:10.1007/s10858-011-9489-1

Duggan GE, Miller JB, Jirik FR, Vogel HJ (2011) Metabolic profiling of vitamin C deficiency in Gulo -/- mice using proton NMR spectroscopy. J Biomol NMR. doi:10.1007/s10858-011-9485-5

Ellinger JJ, Lewis IA, Markley JL (2011) Role of aminotransferases in glutamate metabolism of human erythrocytes. J Biomol NMR. doi:10.1007/s10858-011-9481-9

Fan TW-M, Lane AN (2011) NMR-based stable isotope resolved metabolomics in systems biochemistry. J Biomol NMR. doi:10.1007/s10858-011-9493-5

Grimes JH, O'Connell TM (2011) The application of micro-coil NMR probe technology to metabolomics of urine and serum. J Biomol NMR. doi:10.1007/s10858-011-9488-2

Hu KF, Westler WM, Markley JL (2011) Two-dimensional concurrent HMQC-COSY as an approach for small molecule chemical shift assignment and compound identification. J Biomol NMR. doi:10.1007/s10858-011-9494-4

Mercier P, Lewis MJ, Chang D, Baker D, Wishart DS (2011) Towards automatic metabolomic profiling of high-resolution one-dimensional proton NMR spectra. J Biomol NMR. doi:10.1007/s10858-011-9480-x

Salek RM, Pears MR, Cooper JD, Mitchison HM, Pearce DA, Mortishire-Smith RJ, Griffin JL (2011) A metabolomic comparison of mouse models of the neuronal ceroid lipofuscinoses. J Biomol NMR. doi:10.1007/s10858-011-9491-7

Sandusky P, Appiah-Amponsah E, Raftery D (2011) Use of optimized 1D TOCSY NMR for improved quantitation and metabolomic analysis of biofluids. J Biomol NMR. doi:10.1007/s10858-011-9483-7

Szeto SSW, Reinke SN, Lemire BD (2011) ^{1}H NMR-based metabolic profiling reveals inherent biological variation in yeast and nematode model systems. J Biomol NMR. doi:10.1007/s10858-011-9492-6

Weljie AM, Bondareva A, Zang P, Jirik FR (2011) ^{1}H NMR metabolomics identification of markers of hypoxia-induced metabolic shifts in a breast cancer model system. J Biomol NMR. doi:10.1007/s10858-011-9486-4

Xu QW, Vu H, Liu L, Wang T-C, William H. Schaefer WH (2011) Metabolic profiles show specific mitochondrial toxicities in vitro in myotube cells. J Biomol NMR. doi:10.1007/s10858-011-9482-8