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Metabolomics Society News

Conference Corner

Open Call to Society Members for Workshop Suggestions

We are busy planning the conference agenda and we are eager for your input on pre-conference workshops. The workshops will provide a terrific venue to discuss a wide range of important topics and practical aspects of metabolomics and may include hands-on learning opportunities. You can submit your workshop application online by clicking the link below and completing the simple form.

Also, please advise us if your workshop submission is affiliated with the Early Career Members Network of the Metabolomics Society (EMN).

Members Corner

Early-Career Members Network (EMN)

EMN Webinars

The EMN will host the seventh of its series of webinars for 2019. Dr. Camila Caldana will present "Metabolomics as a tool for elucidating plant growth regulation" on 20 November 2019 at 15:00 UTC. The link to register for the webinar is [here](#), and the past webinars are available [here](#). Please stay tuned for future EMN webinars.

International Affiliates Corner

- **Australian & New Zealand Metabolomics Network (ANZMN)**
Visit <http://www.anzmn.org>
- **Asia-Oceania Metabolomics Forum (AOMF)-Merlion Metabolomics Symposium, 2019 in Singapore**

The AOMF - Merlion Metabolomics Symposium 2019 is a two-day event (21-22 November, 2019) to be held at the National University of Singapore (NUS) that aims to promote metabolomics in the ASEAN and Pan-Pacific region. We are welcoming metabolomics enthusiasts and practitioners from Asian-Oceania Region to join in the Symposium, together with metabolomics community members from other parts of the world. This symposium is jointly organized by NUS Environmental Research Institute, Singapore Centre for Environmental Life Science Engineering (SCELSE), Singapore Phenome Centre (SPC) and NUS Synthetic Biology for Clinical and Technological Innovation (SynCTI) with support from our industry partners (Waters, Thermo Scientific and Agilent Technologies). We have received welcoming response from Asia-Oceania region and representatives from nine countries (Singapore, Malaysia, Indonesia, Thailand, China, Japan, New Zealand and Australia) who would join us at the Symposium.

For more details regarding speakers and program, visit our website [here](#).

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Réseau Français de Métabolomique et Fluxomique (RFMF)

Visit <http://www.rfmf.fr/>



<https://rfmf-mpf-2020.sciencesconf.org/>

The French-speaking Metabolomics and Fluxomics Network (RFMF), Metabolomics Profiling Forum (MPF, Metabomeeting) and European regional metabolomics networks (Scottish Metabolomics Network, Swiss Metabolomics Society, Nordic Metabolomics Society, Netherlands Metabolomics Centre, Italian Metabolomics Network, Spanish Metabolomics Society, German Society for Metabolomics Research) are pleased to announce a joint conference taking place from 22nd to 24th January 2020 in Toulouse (France).

The Metabolomics Society is an independent non-profit organisation dedicated to promoting the growth, use and understanding of metabolomics in the life sciences.

General Enquiries

info@metabolomicssociety.org

Membership Enquiries

membership@metabolomicssociety.org



20 travel grants are available for early-career scientists (see website for details).

This event will be the opportunity to strengthen scientific collaborations between European regional networks in the field of metabolomics and fluxomics.

Thematic sessions dedicated to:

- Analytical developments in Metabolomics & Fluxomics
- Computational and statistical developments in Metabolomics & Fluxomics
- Cutting edge applications of Metabolomics and Fluxomics in:
 - Human health
 - Agriculture & food
 - Environmental science
 - Microbiology & biotechnologies

Confirmed plenary and keynote speakers:

- Pr. Warwick (Rick) Dunn, University of Birmingham, UK.
- Dr. Maria Fedorova, Universität Leipzig, Germany.
- Pr. Zoran Nikoloski, Max Planck Institute, Germany.
- Dr. Emma Schymanski, University of Luxembourg, Luxembourg.
- Pr. Marcel Utz, University of Southampton, UK.

SpOtlight

Comprehensive Drug Surveillance in an Era of Polypharmacy by Multisegment-Injection-Capillary Electrophoresis-Mass Spectrometry



Feature article contributed by:

Meera Shanmuganathan, Zachary Kroezen, Sabrina Macklai and Philip Britz-McKibbin
Department of Chemistry and Chemical Biology, McMaster University, Canada

Synopsis

Increased exposure to a plethora of prescribed medications represents an emerging public health emergency in an era of polypharmacy. This alarming trend in drug prevalence, misuse, and abuse is notably problematic for older persons with chronic metabolic diseases (e.g., obesity, diabetes, cardiovascular disease), as well as high-risk populations suffering from chronic pain, anxiety and/or depression. Indeed, the opioid crisis in North America is only one stark manifestation of this issue, which has been exacerbated by the over-prescription of synthetic opioids at pain management clinics without adequate communication of the risks for dependence, and frequent treatment monitoring. However, conventional screening technologies for targeted analysis of major drug classes based on immunoassays, or limited drug panels by LC-MS/MS are not suitable for reliable and accurate determination of contemporary drug exposures in a cost-effective manner. This includes screening for emerging designer drugs that continue to evade detection, such as highly toxic analogs of fentanyl responsible for an unprecedented surge in overdose deaths. In this context, metabolomics based on high resolution mass spectrometry (HRMS) offers a new paradigm for comprehensive drug surveillance as required for screening of prescribed drug adherence, self-medication and/or illicit drug use. We recently introduced a new approach for non-targeted drug analysis that enables rapid screening of drugs of abuse and their metabolites in urine when based on multisegment injection-capillary electrophoresis-mass spectrometry (MSI-CE-MS) [1].

We have also further expanded sample throughput of MSI-CE-MS based on serial injection of up to 13 samples together with stringent quality control (QC), which is applicable to screening virtually an unlimited panel of drugs of abuse directly in human urine [2]. In this case, four criteria are used to confidently authenticate a putative drug and its metabolite(s) from isobaric interferences when using full-scan ion monitoring by HRMS in conjunction with high efficiency multiplexed separations based on CE, namely:

- 1:** Co-migration of a drug target with its matching deuterated internal standard (d-IS). This provides an orthogonal approach to filter out isobaric/isomeric interferences from background to reduce false-positives; there is no deuterium effect in CE separations unlike LC/GC methods.
- 2:** Detection of a target drug(s) with matching d-IS based on its known accurate mass with low mass error. Molecular formula match provides additional confidence in assignment.
- 3:** Detection of one or more corresponding drug metabolites excreted in urine based on their known accurate mass with low mass error. This provides higher confidence in drug identification with a longer detection window for slow metabolizing drugs.
- 4:** Measurement of drug and its metabolite(s) above screening cut-off limits when using an expanded drug panel mixture that are analyzed within the same run. This provides additional quality control, and quantitative information for assessing the pharmacokinetics of drug exposure without risk due to overdose or adverse drug interactions in individual patients.

We used MSI-CE-MS as a high throughput platform for comprehensive drug surveillance as required for monitoring high-risk populations, such as patients on methadone maintenance therapy for treatment of prescribed opioid (e.g., oxycodone) and/or illicit heroin addiction. All single-spot, random urine specimens were diluted with d-IS mixture following enzyme hydrolysis/deconjugation prior to MSI-CE-MS analysis. Figure 1 depicts a serial injection format used for analysis of 13 discrete samples within a single run (< 3 min/sample), which includes 11 urine samples from de-identified patients, as well as two samples that contain a 84 drug panel mixture injected as the first (1.5-fold above cut-off level) and last (5-fold above screen cut-off level) sample in series. The latter two samples function as internal references for confirming that screen-positive drug cases detected are above an accepted minimum threshold, while also serving as QC for assessing technical precision at two different concentrations levels. A robust QC-based batch correction algorithm can also be applied to adjust for long-term signal drift in large-scale drug screening applications by MSI-CE-MS. Also, all drug concentrations can also be reported normalized to creatinine to correct for hydration status.

For example, Figure 1 shows a definitive screen-positive result for methadone was evident in only 1 (#A41) out of 11 patients tested in this run. Also, its major urinary metabolite, EDDP was also clearly detected in the same sample position (#11; third last sample injection). In both cases, methadone and EDDP were found to co-migrate with their matching d-IS with low mass error (< 2 ppm) for their protonated molecular ions that also generated correct molecular formulae (refer to full-scan MS spectra). Acceptable technical precision was obtained for d-IS injected in every sample position when using MSI-CE-MS (CV < 15%, n=13), which is also useful for confirming the exact sample position, and correct for variations in injection volume on-capillary between-samples. Furthermore, since the normalized responses for both methadone and EDDP from patient#A41 was above the minimum cut-off level after correction for a 4-fold dilution in deionized water, a definitive true positive result was concluded, which was consistent with patient self-reporting.

Importantly, the same patient was also confirmed as screen-negative for the major heroin metabolite, 6-acetylmorphine, oxycodone and its metabolites (i.e., noroxycodone, oxymorphone), and other commonly prescribed opioids (e.g., codeine, hydrocodone etc.). As a result, this patient was confirmed as adherent to methadone maintenance therapy without evidence of opioid substitution/misuse or drug intoxication.

In summary, multiplexed separations based on MSI-CE-MS offer an innovative strategy for rapid yet accurate drug screening that is urgently needed in an era of polypharmacy as compared to targeted approaches based on immunoassays and LC-MS/MS. This method allows for large panels of drugs to be monitored simultaneously at incremental costs, which is also applicable to discovery-based unknown drug identification and retrospective analysis when combined with MS/MS. Current work is underway at validating MSI-CE-MS technology as part of an inter-laboratory method validation study for therapeutic drug monitoring of high-risk patient populations at pain management centres and psychiatric hospitals, including customized software tools needed for automated data processing of multiplexed data sets.

References

- [1] A. DiBattista, D. Rampersaud, H. Lee, N. Kim, and P. Britz-McKibbin. High Throughput Screening Method for Systematic Surveillance of Drugs of Abuse by Multisegment Injection-Capillary Electrophoresis-Mass Spectrometry. *Anal Chem.* 2017, 89, 11853-11861.
- [2] M. Shanmuganathan, S. Macklai, C. Barrenas Cárdenas, Z. Kroezen, M. Kim, W. Zizek, H. Lee, and P. Britz-McKibbin. High-throughput and Comprehensive Drug Surveillance Using Multisegment Injection-Capillary Electrophoresis Mass Spectrometry. *J. Vis. Exp.* 2019 (146), e58986. doi: 10.3791/58986.

Spotlight | Comprehensive Drug Surveillance

Methadone Maintenance Treatment for Opioid Addiction: Rapid Monitoring of Patient Adherence by MSI-CE-MS

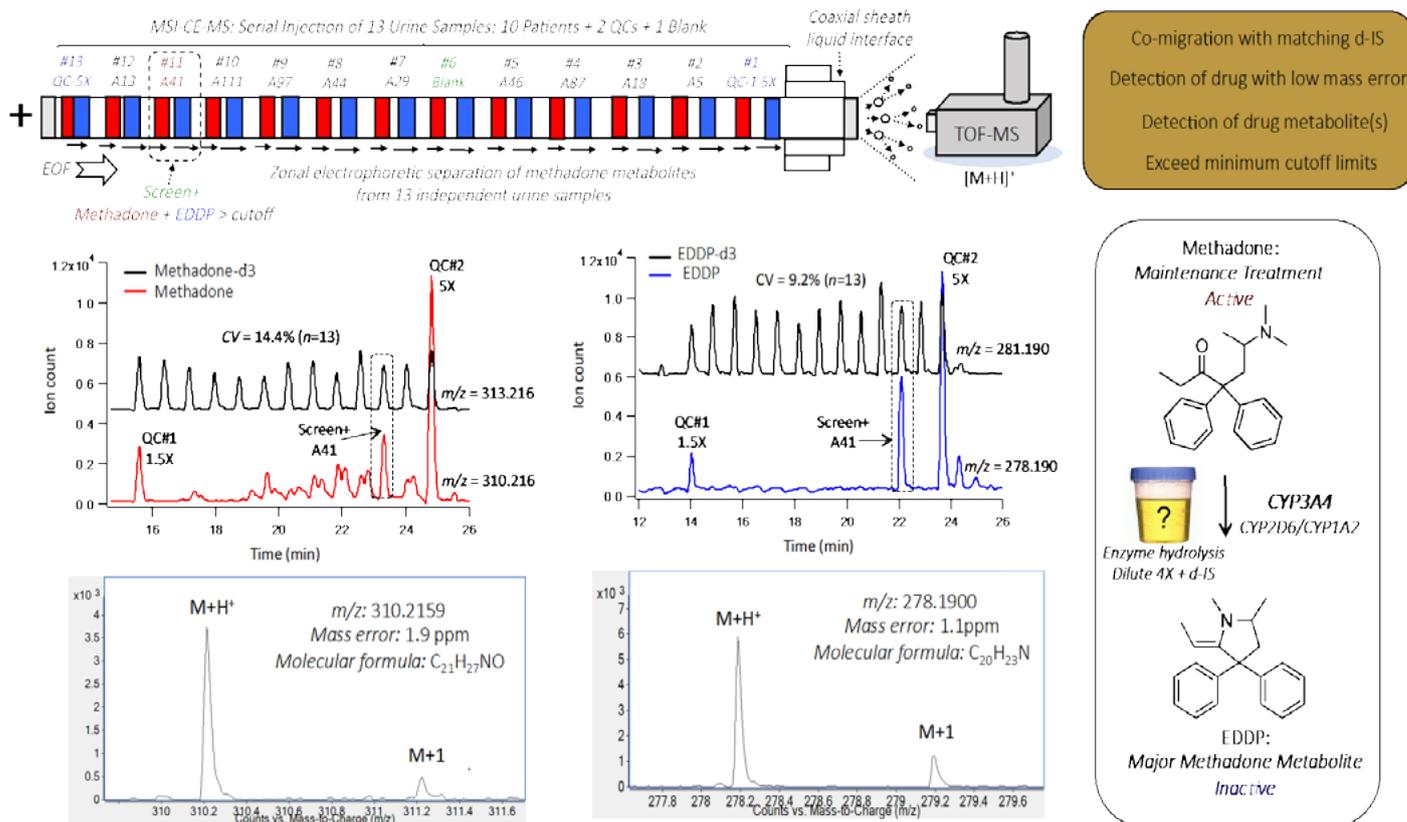


Figure 1. Comprehensive surveillance of drugs of abuse in urine when using MSI-CE-MS that takes advantage of a serial injection format comprising 13 discrete samples within a single run, including quality controls (QC). Unambiguous identification of methadone in a patient’s (#A44) urine sample (position 11) was realized based on co-migration with its matching d-IS, detection of a protonated molecular ion based on its accurate mass with low mass error, detection of its major urinary metabolite, EDDP, and measured concentrations for both pro-drug and its metabolite exceeding recommended cut-off limits of QC. These four criteria allow for unambiguous identification and retrospective analysis of complex drug exposures that is accurate, reliable, inexpensive and broad in coverage as compared to conventional screens for targeted drug classes based on immunoassays and/or LC-MS/MS.

Recent Publications

Recent Publications

Recently published papers in metabolomics

- [Metabolomics for improved treatment monitoring of phenylketonuria: urinary biomarkers for non-invasive assessment of dietary adherence and nutritional deficiencies.](#)
- [Metabolic Trajectories Following Contrasting Prudent and Western Diets from Food Provisions: Identifying Robust Biomarkers of Short-Term Changes in Habitual Diet.](#)
- [International Ring Trial of a High Resolution Targeted Metabolomics and Lipidomics Platform for Serum and Plasma Analysis.](#)
- [PathBank: a comprehensive pathway database for model organisms.](#)
- [NMR-Based Metabolomics in Cardiac Research.](#)
- [Perspective: Dietary Biomarkers of Intake and Exposure—Exploration with Omics Approaches](#)
- [Normalizing Untargeted Periconceptual Urinary Metabolomics Data: A Comparison of Approaches.](#)
- [Metabolite Changes in an Estuarine Annelid Following Sublethal Exposure to a Mixture of Zinc and Boscalid.](#)
- [Allergic disease and low ASQ communication score in children.](#)
- [Accumulation of sugars and nucleosides in response to high salt and butanol stress in 1-butanol producing *Synechococcus elongatus*.](#)
- [A Unified Conceptual Framework for Metabolic Phenotyping in Diagnosis and Prognosis](#)



Metabolomics Events

**BIRMINGHAM
METABOLOMICS**
TRAINING CENTRE

21 Oct - 15 Nov 2019

Metabolomics Data Processing and Data Analysis

Venue:

The University of Florida Clinical & Translational Science Institute, Gainesville, Florida USA

Overview

This online course explores the tools and approaches that are used to process and analyse metabolomics data. You will investigate the challenges that are typically encountered in the analysis of metabolomics data, and provide solutions to overcome these problems. The course is delivered using a combination of short videos, articles, discussions, and online workshops with step-by-step instructions and test data sets. We provide quizzes, polls and peer review exercises each week, so that you can review your learning throughout the course.

The material is delivered over a four-week period, with an estimated learning time of four hours per week. We support your learning via social discussions where you will be able post questions and comments to the team of educators and the other learners on the course. In the final week of the course there is a live question and answer session with the entire team of educators. If you do not have time to complete the course during the 4-week period you will retain access to the course material to revisit, as you are able.

Topics Covered

- An introduction to metabolomics
- An overview of the untargeted metabolomics workflow
- The influence of experimental design and data acquisition on data analysis and data quality
- Processing of NMR data
- Processing direct infusion mass spectrometry data
- Processing liquid chromatography-mass spectrometry data
- Reporting standards and data repositories

Course link:

<https://www.birmingham.ac.uk/facilities/metabolomics-training-centre/courses/Metabolomics-Data-Processing-and-Data-Analysis.aspx>

Metabolomics Events

15-17 Nov 2019

MANA 2019 Conference

Venue:

Atlanta, Georgia, USA

Overview

Metabolomics researchers from across North America are invited to the first-ever meeting of the Metabolomics Association of North America (MANA) at the Georgia Tech campus in Atlanta, GA, on November 15-17.

The goal of MANA 2019 is to help catalyze more interactions, scientific exchange, and collaboration in the North American metabolomics community. Oral and poster presentation topics will include all sub-disciplines and applications of metabolomics. Additionally, a variety of offerings will focus on trainees and early-career scientists, including lightning talks, social and networking opportunities, and the MANA 2019 Young Investigator Award for excellence in metabolomics work by an early-career scientist.

MANA 2019 will be the premier “big tent” metabolomics meeting in North America this year, and we look forward to seeing you there! For more information, please visit <http://mana2019.org/>



20-21 November 2019

Metabolite identification with the Q Exactive and LTQ Orbitrap

Venue:

Birmingham Metabolomics Training Centre, School of Biosciences, University of Birmingham, Birmingham, UK

Overview

This two-day course will provide a hands-on approach to teach the attendees about the latest techniques and tools available to perform metabolite identification in non-targeted metabolomics studies. The course will be led by experts working within the fields of metabolomics and chemical analysis and will include a significant proportion of hands-on experience of using mass spectrometers, software tools and databases. A maximum of four people will be working on each mass spectrometer in a session. We will apply these tools on the Q Exactive and LTQ-Orbitrap family of mass spectrometers.

Topics Covered

- Importance of mass spectral interpretation
- Types of data which can be collected on the QE and LTQ-Orbitrap (m/z, retention time, MS/MS, MS_n)
- Conversion of raw data to molecular formula and putative metabolite annotations
- MS/MS experiments in metabolic phenotyping for on-line data acquisition using the QE (DDA, DIA, all-ion)
- MS/MS and MS_n experiments for sample fractions using the LTQ-Orbitrap
- Mass spectral libraries (using mzCloud)
- Searching mass spectral libraries
- Tools for mass spectral interpretation
- Reporting standards for metabolite identification
- Question and answer session with the experts

Course link: <https://www.birmingham.ac.uk/facilities/metabolomics-training-centre/courses/metabolite-identification.aspx>

Metabolomics Events

26-29 November 2019

Hands On Data Analysis for Metabolic Profiling

Venue:

Imperial International Phenome Training Centre, Imperial College London, London, UK

Overview

Cost

- Earlybird: £900
- Standard: £1100

This 4 day course provides a comprehensive overview of data analysis for metabolic profiling studies with data acquired from NMR spectroscopy and Liquid Chromatography-Mass Spectrometry. It combines lectures and tutorial sessions to ensure a thorough understanding of the theory and practical applications.

Day 1

Introductory lectures and tutorials regarding the pre-processing of data acquired via NMR and LC-MS.

Day 2

Lectures and tutorials introducing exploratory chemometrics approaches, including PCA.

Day 3

Lectures and tutorials covering advanced chemometrics techniques including PLS and Orthogonal PLS.

Day 4

The next step - computational tools to aid metabolite identification and pathway analysis.

This course has been approved by the Royal Society of Chemistry. This event has been awarded 20 CPD credits by the Royal Society of Medicine in accordance with its current guidelines.

More details and registration

<http://www.imperial.ac.uk/imperial-international-phenome-training-centre/courses/dates-and-registration/>



Metabolomics Events

2-7 Feb 2020

Workflow4Experimenters International Course (W4E2020)

Venue:

Brussels, Belgium

Overview

Cost

- Earlybird: £1750
- Standard: £1950

Overview

The French Institute of Bioinformatics (IFB, Elixir-FR) and the Infrastructure for Metabolomics and Fluxomics (MetaboHUB) organize in collaboration with the Université libre de Bruxelles the next Workflow4Experimenters International Course (W4E2020).

Analyze your own data with Galaxy and the Workflow4metabolomics e-infrastructure! The next Workflow4Experimenters international course (W4E2020) will take place in Brussels (February 3 to February 7, 2020). During this one-week course (entirely in English), you will learn how to use Galaxy and the W4M infrastructure to analyze your own LC-MS, GC-MS, or NMR data set. Morning sessions will be dedicated to methodology and tools. Afternoon sessions will be devoted to tutoring.

Invited speakers: Dr S. Marr (Leibniz Institute of Plant Biochemistry, Germany), Dr R. Weber (Phenome Centre Birmingham, United Kingdom), Dr N. Poupin (Unité Toxalim, INRA Toulouse, France)

Registrations: <https://workflow4metabolomics.org/w4e2020>

Contact: contact@workflow4metabolomics.org

Metabolomics Jobs

Metabolomics Jobs & Collaborations

If you have a job you would like posted, please email Ian Forsythe (metabolomics.innovation@gmail.com).

Jobs Offered

| Job Title | Employer | Location | Posted | Closes | Source |
|---|--|------------------------|-----------|--------------|--|
| Various positions | | | 25-Oct-19 | | Metabolomics Association of North America Jobs |
| Research Bioinformatician | The Australian Wine Research Institute | Glen Osmond, Australia | 24-Oct-19 | 29-Nov-19 | The Australian Wine Research Institute |
| Director Business Development - Home Based in the US | Biocrates Life Sciences | US based | 10-Oct-19 | Until filled | Metabolomics Society Jobs |
| Business Development Manager - Home Based in the USA | Biocrates Life Sciences | US based | 10-Oct-19 | Until filled | Metabolomics Society Jobs |
| Postdoctoral Researcher Position Microbial Metabolomics | Friedrich Schiller University Jena | Jena, Germany | 7-Oct-19 | | Friedrich Schiller University Jena |
| Postdoctoral Fellow, GC-MS Metabolomics | Wake Forest University Health Sciences | Winston-Salem, NC, USA | 7-Sep-19 | | Wake Forest University Health Sciences |

Metabolomics Jobs

Jobs Wanted

This section is intended for very highly qualified individuals (e.g., lab managers, professors, directors, executives with extensive experience) who are seeking employment in metabolomics.

We encourage these individuals to submit their position requests to Ian Forsythe (metabolomics.innovation@gmail.com). Upon review, a limited number of job submissions will be selected for publication in the Jobs Wanted section.

- [Seeking New Challenges in Metabolomics](#)
-