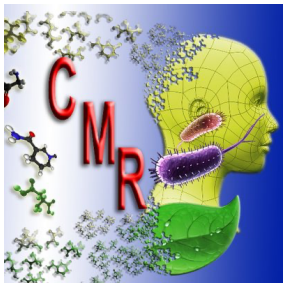
Centre for Metabolomics Research

part of the

NERC Environmental 'Omics Facility



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NERC ENVIRONMENTAL OMICS FACILITY

We are a specialist mass spectrometry-based facility where our aim is to study the metabolome. We combine this with vibrational spectroscopies for spatial analyses. We have experience in analysing an extensive range of sample types.

What we do:

- With you, we optimise the whole metabolomics pipeline – from experimental design, through to sample processing, mass spectrometry and data processing. This helps you get the most out of your samples.
- Develop and apply a combination of liquid chromatography-mass spectrometry (LC-MS) and gas chromatography-mass spectrometry (LC-MS) for untargeted metabolomics.
- Analyse metabolites from different sample matrices: solids, liquids as well as volatiles.
- Develop and apply robust data analysis incorporating statistical validation.
- Perform targeted analysis of key metabolites where absolute quantification is needed.
- Use stable isotopes of metabolites for exploration of important pathways.
- Develop and apply Raman and related methods (*viz*. SRS and CARS), as well as optical photothermal infrared spectroscopy, for single cell spatial analyses (resolution = 0.5 µm).

What we can't do:

- Provide metabolite identification on every peak detected with GC-MS or LC-MS.
- Quantify global metabolite levels.
- Interpret the data in terms of biochemistry or physiology. We will of course help with mapping metabolites onto metabolic pathways and networks. But, we are expecting that you know something about the organism or system that you are studying

FAQ:

How much material do we need?
This is sample dependent. For serum, plasma, urine, sweat and semen we need typically need 200 µL; for cells we need 2-20x10^6 eukaryotic cells and 20-30 mg bacteria (dry weight). For solid materials we need 200 mg mammalian tissue (wet weight), or 30 mg plant leaves (dry weight) are typical. For samples not covered here we welcome a conversation.

Is this a destructive technique?
Yes. For MS-based analysis we need to break open the cells/tissues to extract the metabolites, then LC-MS or GC-MS we employ are also destructive. For spectroscopy, while this is non-invasive, it is hard to recover your sample without contamination.

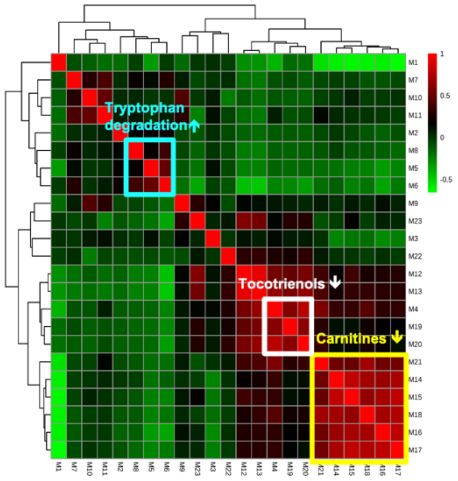
Do we need a genome sequence?
No. Once we learn how to identify a metabolite say from a plant, we can apply the same MS-based identification process to samples from mammalian or bacterial systems.

How do you identify metabolites?
We follow the Metabolomics Standards Initiative (MSI) for metabolite identification, and we were involved in its establishment. For definitive identification (MSI Level 1) we run authentic metabolite standards (if they exist) on the same instrument and match the standard and 'unknown' peak to retention time, accurate mass of the metabolite, as well as fragmentation patterns.

How do you quantify metabolites?
We analyse authentic metabolite standards with known concentrations to calibrate the GC-MS or LC-MS. This can be done externally or internally. The latter is better and is achieved by the standard addition method, or through the use of isotopologues.

How many replicates?
This depends on several factors that are linked to variability that exists at the biological, sample processing, and instrument levels. Experience tells us that most of the variation is at the biological level and sample extraction levels. When we analyse samples, we conduct preliminary analyses in order to establish reproducibility of sample extraction and sample analysis. We then use this information to suggest the number of biological replicates that are needed for robust metabolomics.

Is my sample suitable for mass spectrometry analysis?
There are many ways to make samples suitable for analysis by MS. We have a variety of validated strategies in-house for preparing difficult samples to remove unwanted material for optimal metabolome analysis.



Case Studies:

These along with more information on the CMR can be found here:

- https://www.liverpool.ac.uk/liverpool-shared-research-facilities/facilities/multi-omics/cmr/

Further reading:

An excellent review on Environmental Metabolomics can be found here:

- https://doi.org/10.1007/s11306-008-0152-0

Read our *Nature Protocols* paper where we established our robust metabolomics pipeline for long-term metabolomics, which we use for the analysis of all sample types with GC-MS and LC-MS:

- https://doi.org/10.1038/nprot.2011.335

We have several SOPs here for the preparation of different sample types:

- http://www.biospec.net/resources/sops/

A review on the use of system suitability and quality control samples in MS metabolomics:

- https://doi.org/10.1007/s11306-018-1367-3

A review highlighting the role of Raman spectroscopy within quantitative metabolomics, which also contains an introduction to image analysis with Raman microspectroscopy:

- https://doi.org/10.1146/annurev-anchem-091420-092323