Sample preparations in metabolomics

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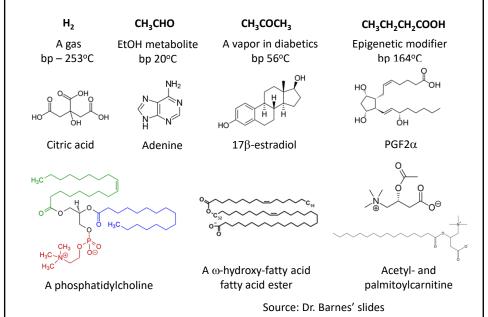
1

Backgrounds

- Metabolite coverage (>8000 endogenous and 40,000 exogenous metabolites human metabolomes) with wide dynamic concentration range
- Retaining of analytes and removal of undesirable matrix components- pre-concentration step
- It affects qualitative and quantitative analysis of metabolites and hence biological interpretation
- Avoiding loss/degradation (quenching and rapid extraction)
- Non-selective (global or untargeted) and selective (targeted) extraction of metabolites
- Simple, rapid, reproducible and quantitative recovery of metabolites

Vuckovic et al. Anal Bioanal Chem 2012

Metabolites/metabolome are structurally diverse



3

A typical metabolomics workflow

- 1. Sample collection
- 2. Extraction
- 3. Analysis of the extracted compounds
- 4. Data Processing
- 5. Metabolite annotation
- 6. Biological interpretation

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Biological samples

- Bio-fluids- urine, plasma, bile, saliva etc.
- Fecal samples
- Muscles/epithelial tissues
- Plant- roots, leaves
- In vitro microscopic cell cultureculture medium, cell lysates

5

Sample preparations

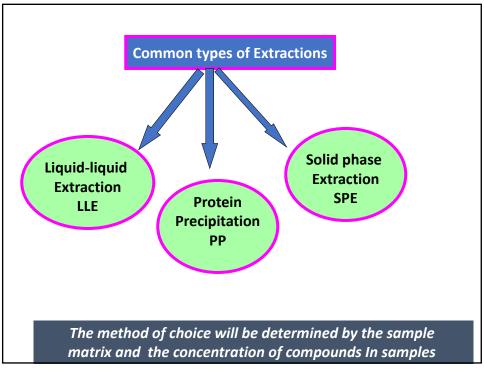
- Collection (filtration, centrifugation/addition of bacteriostatics) and quenching
- Storage
- Homogenization
- Extraction

Mushtaq et al. Phytochem. Anal. 2014 Smith et al. Metabolites, 2020

Prevalent challenges with extraction and analysis

- · Metabolite concentration range (pM-mM), high turnover rate
- Structural diversity (105), chemical stability and ionizability
- · Quantitation of endogenous metabolites- lack of analyte free matrix
- · Endogenous substances
 - From matrix, i.e., organic or inorganic molecules present in the sample and that are retained in the final extract.
 - Examples: EDTA, phospholipids, drugs administered to the patient and proteins/peptides
- · Exogenous substances,
 - molecules not present in the sample but coming from various external sources during the sample preparation.
 - Detergents, plasticizers, solvent residues, column siloxanes

7



Extraction of Metabolites from Cellsintra-cellular metabolites

- · Adherent cells in petri dish/flask
 - · Prepare ice-cold physiologic saline (0.9% NaCl w/v)
 - Tilt plate/flask and remove cell culture medium with vacuum pipet from cellular monolaver
 - Immediately add 10 ml ice-cold physiologic saline, swirl and remove medium with vacuum pipet
 - Spike with IS and add cold MeOH (-20°C) and ice cold H20 (400 ul each 1:1 v/v)quenching
 - Scrape the well with a cell scraper, and transfer the extract into an eppendorf tube containing 400 uL of CHCI3 (-20°C)
 - Agitate the cell extract for 20min at 1400 rpm, followed by 5min of centrifugation at a minimum of 16,100 x g and transfer the phases into a new tube, concentrate (evaporation under nitrogen, lyophilization etc) if necessary and store -20 °C until analysis
- · Suspended or non-adherent cells
 - Centrifuge cells in medium at 250 x g for 5 min to separate the medium and cell pellets.
 - Wash cells with ice cold saline and follow the similar procedure as above. (quenching, extraction and separation of phases)

Adopted from Dr. Barnes slides and Sapcariu et al. MethodsX 2014

9

Tissue -metabolite extraction

- Tissue MUST BE snap-frozen (liq N₂) to prevent further metabolism
- Grind the tissue in a pestle and mortar
 - Pre-cool in liq N₂
 - Pour powder as a slurry into extraction tube
 - Allow N₂ to evaporate



- Extract at 0-4°C for 30 min
- Centrifuge collect supernatant
- Re-extract and centrifuge
- Combine supernatants



Source: Dr. Barnes' slides

Urine

- Urines can be spot (collected at the time) or 24hour collections
 - The 24-hour collection is an integral of urinary output
 - For rat studies, best collected using a metabolic cage where the urine drips into a beaker set in a container filled with dry ice
 - For mice, roll them on their back they will pee for you
- It's worth noting that urine resides in the bladder at ~37°C for several hours before it is collected
 - Once it's out of the bladder, it will be exposed to microbes that may alter its composition
 - For clinical studies, the urine can be collected and then placed in a refrigerator – some add ascorbic acid (1%) or 1% sodium azide (NaN3).

11

Urine storage and extraction

- Urines must be centrifuged to remove particulate matter
 - Cleared human urine could be used directly (need to divert the initial eluate since it is predominantly electrolytes and very hydrophilic metabolites such as urea, glucose, etc.)
 - Rodent urines contain MUP proteins these must be precipitated by adding 4 volumes of ice-cold MeOH
 - · Precipitated protein removed by centrifugation
 - Supernatant is evaporated to dryness under N₂ and redissolved in water

Blood, plasma and serum

- Blood consists of cells (reticulocytes, white cells/monocytes and plasma or serum)
- Plasma requires the use of heparin or EDTA
 - Heparin is preferred for NMR analysis
 - EDTA is preferred for LC-MS analysis
- Serum has no required additions, but be careful not to lyse the reticulocytes since the released heme is highly oxidative
 - add 50 mM nitriloacetic acid to complex Fe^{2+/3+}
- Store in 1 ml aliquots at -80°C
- Small animals mice, zebrafish yield only μl volumes

13

Fecal collection

- Note: feces have been in the presence of a trillion bacteria at 37°C for several days during colonic passage
 - · Some metabolism can occur after collection
 - Slowed by cooling can be frozen as for tissue
- Sometimes feces are collected for microbiome analysis
 - Placed in Cary Blair (NaCl, Na thioglycollate, Na₂HPO₄, pH 8.4) minimal medium
 - Glycerol added to prevent freezing when stored at -20°C

Fecal extraction

- Treat frozen feces like tissue
 - Powder in liq N₂
 - Extract with 4 volumes of cooled (-20°C) MeOH
- Fresh feces
 - Extract with 4 volumes of cooled (-20°C) MeOH
- Feces in Cary-Blair medium
 - Extract with 4 volumes of cooled (-20°C) MeOH
- Feces in Cary-Blair medium plus glycerol
 - Disperse in aqueous medium and extract with ethyl acetate

15

Extraction of lipids

Auto-oxidation and pH are two important issues

Bligh/Dyer extraction

Homogenized Cell suspension/ biological fluids (1 mL) + IS

> 2.5 mL MeOH + 1.25 mL CHCl3 Agitation/sonication (10 sec)

1.0 mL H2O + 1.25 mL CHCl3 Vigorous shaking, centrifugation

Aqueous phase

Lipid soluble CHCl3 layer

Concentration, reconstitution and analysis

Using isotopes to monitor recovery

- Isotopically labeled compounds, particularly ¹³C (a stable isotope), behave the same as their unlabeled counterparts
 - They have different masses 1.003 Da for every ¹³C
 - Can be measured independently from the real metabolite
 - Not available for every metabolite
 - "All" metabolites would be very expensive
 - Alternative is to use the IROA Technologies reagent
 - An exhaustively ¹³C-labeled yeast product

17

Choice of Good Internal Standards

- A stable isotopically labeled IS is preferable
 - If ¹³C, then there must be at least three ¹³C atoms to avoid contributions of natural abundance ¹³C
- A compound not found in the samples
 - In the absence of stable isotopically labeled internal standard, the unlabeled internal standard needs to be structurally similar to the analyte
- Should not react chemically with the analyte

Quality control

- A pool of all or a batch of study samples- average metabolites (matrix and analytes) of all samples
- Assess the analytical variable of data- drift in Rt and ion signals
- Analyzed in a fixed interval of sample run

19

Controls

- Positive controls- where changes are expected
- Negative controls- where no change is expected
- Sham controls- incidental effects induced by the procedure or operation as a control

Vanisevic J and Want EJ., Metabolites 2019

Quantification

Relative quantification

• normalizes the metabolite signal that of an internal standard signal intensity in large scale un-targeted profiling (e.g., non-naturally occurring lipid standards - Cer C_{17} or stable isotope labeling through metabolism-AA-d₄.

Absolute quantification

• based on external standards or internal isotopically labeled standards - targeted metabolomics.

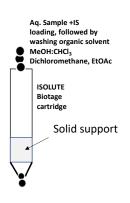
Matrix effects

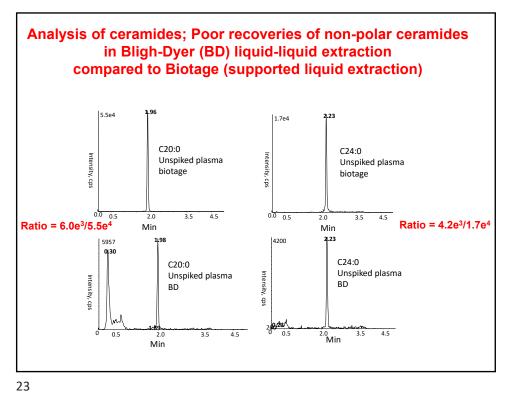
- · Affect selectivity, accuracy and reproducibility.
- Signal suppression or enhancement are major issues. Stable isotope labeled standards are needed.

21

Supported Liquid Extraction (SLE)

- Aq. sample is adsorbed on a porous highly polar solid support -Diatomaceous earth
- Sufficiently adsorbs the entire volume of sample
- Non-polar compounds at the surface of solid support
- Target analytes should be in nonionized form
- Eluted by non-polar solvent
- Simple, high throughput and extraction efficiency





Supercritical Fluid Extraction (SFE) Extraction of bioactive natural products

- Extraction method involving the use of supercritical solvent CO2 in extracting non-polar to moderately polar analytes from solid matrices
- Use of solvents above the critical conditions for temperature and pressure super critical carbon dioxide
- Able to penetrate solid matrix (botanical products) and solubilize compounds
- By controlling the levels of pressure/temperature, supercritical CO2 can extract a wide range of compounds
- Inexpensive, faster and environmental-friendly Green chemistry, renewable solvent
- · Extraction of thermally-labile compounds

Super Critical fluid

Critical point

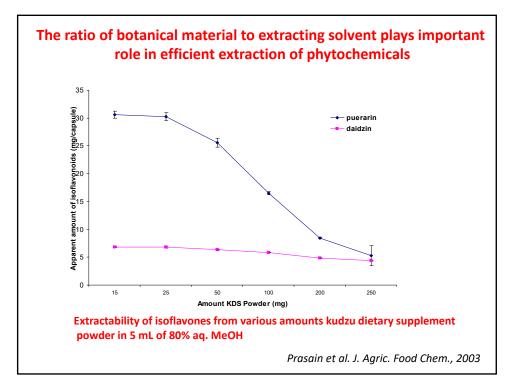
Gas

Temp

Microwave-assisted solvent extraction (MAE)

- Use of microwave energy to heat liquid organic solvent in contact with sample
 - Watch out for thermal degradation
- Non-ionizing, fast and effective extraction with limited volume of solvent
- Moisture or water serves as target for microwave heating
- Special approved microwave equipment should be used, not domestic microwave oven

25



Conclusions

- Development of optimal extraction method for a biological sample remains a significant challenge.
- Although conventional extraction methods SPE, PPT, and LLE are widely used, newer methods such as supported liquid extraction may be used for extracting many nonpolar compounds in biological samples efficiently.