Introduction to the MU Metabolomics Center

Non-targeted profiling of the fecal metabolome in rats using GC-MS

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Phytohormone Analysis by LC-MS

Quantitative Analysis of Kynurenine and Indoxy Sulfate by LC-MS MRM

Sphingolipid Profiling by LCMS

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Quantitative analysis of ethanol in Kombucha beverages using 1H-NMR

Quantitative Analysis of Amino Acids by LC-MS MRM

Comparison of the effects of Bisphenol A and Bisphenol S on the mouse placental metabolome using GC-MS analysis
Providing cutting-edge targeted and untargeted metabolomics services

The mission of the University of Missouri Metabolomics Center (MUMC) is to provide advanced, cutting-edge metabolomics capabilities and expertise to both the MU community and outside entities. MUMC has multiple platforms for targeted and non-targeted small molecules or metabolites analyses. We also assist users in their grant proposals (letters of support, budgeting, Co-PI contributions to specific aims involving metabolomics) and manuscript publications (methods and MS figures). MUMC also hosts annual metabolomics workshops or one-on-one training to train researchers who would like to learn and use metabolomics in their research.

MUMC is equipped with state-of-the-art mass spectrometry instrumentation:

- Agilent 6890N Gas chromatography coupled to a 5973N mass selective detector (GC-MSD)
- Agilent 7890 GC interfaced with 7200B quadrupole time of flight mass spectrometer (GC-QTOF MS)
- Bruker Impact II quadrupole time of flight mass spectrometer coupled to Waters Acquity ultrahigh performance liquid chromatography (UPLC-QTOF MS)
- Waters Xevo triple quadrupole MS coupled to UPLC (UPLC-QQQ MS)
- Bruker Autoflex Speed MALDI MS
- Bruker Compact QTOF MS
Our Services

**Large-Scale Targeted and Untargeted Metabolic Profiling**
Metabolites are profiled using GC-MS and/or LC-MS to provide a large-scale view of metabolites in a sample. The sample can be tissues, culture media, cells, urine, and serum. GC-MS profiling is performed using Agilent 6890N Gas chromatography coupled to a 5973N mass selective detector (GC-MSD) or Agilent 7890 GC interfaced with 7200B quadrupole time of flight mass spectrometer (GC-QTOF MS). For LC-MS profiling, Bruker Ultra-high resolution quadrupole time of flight mass spectrometer (Impact II) coupled to Waters Acquity ultrahigh performance liquid chromatography (UPLC) is used to profile metabolites in complex samples.

**Lignin Composition and Content Determination**
Plant tissues are first subject to thiolysis and then GC-MSD analysis for determination of lignin composition.

**Volatile Organic Compound Analysis**
Volatile analysis can be performed on solid and liquid samples using a headspace sampling technique. GC-QTOF MS is used to analyze the volatiles. This technique can be used to determine volatiles emitted by plant leaves, fruits, animal urines or other samples.

**Accurate Mass Determination**
Accurate mass of small molecules is measured using the Bruker Ultra-high resolution QTOF MS with mass accuracy of less than 5 ppm. The accurate mass is useful for confirmation of synthesized compounds and annotation of unknowns.

**Plant Hormone Analysis**
Plant hormones are measured using Waters Xevo triple quadrupole MS coupled to UPLC. Plant hormones are first extracted and enriched from plant materials, and then subject to detection and quantitation on UPLC-QQQ MS via an MRM (Multiple Reactions Monitoring) experiment.

**Other Services**
In addition to the routine services listed above,
The following application notes provide summaries for specific applications of mass spectrometry to metabolomics research that are available at the MU Metabolomics Center. Any of these applications can be tailored specifically to your needs and other applications may be possible through custom method development.
Non-targeted profiling of the fecal metabolome in rats using GC-MS

Method developed by: Saurav J. Sarma, MU Metabolomics Center
Samples provided by: Cheryl S. Rosenfeld, Biomedical Sciences, University of Missouri

The gut microbiome has recently gained much attention as a strong influence in a range of physiological conditions including digestive and cardiovascular diseases, various types of cancers and even susceptibility to mental disorders. Analysis of the host fecal metabolome is a simple and non-invasive way of accessing how the host metabolic parameters are influenced by their gut microbiota. The correlation of the fecal metabolome to the gut microbiome of the host can provide meaningful insights into biomarker discovery towards early detection or predictions of health conditions that can be induced by the host gut flora.

GC-MS analysis of the fecal metabolome in soy fed ovariectomized female rats was used to identify the metabolites differentially accumulated in fecal samples of soy fed rats (SOY) as opposed to that of rats on a controlled diet (CON). S-equol, which is not indigenous to soy but a bacterial metabolite of soy-flavonoids, was found to be the most differentially accumulated metabolite between these two groups (Figure 1), and directly correlated to several positive health outcomes in the host.¹

Experimental Details

Sample Preparation: To 10 ± 0.06 mg of each fecal sample, 10µL of H2O containing 1µg/µl ribitol (internal standard) and 500 µl of 80% methanol were added. The samples were vortexed for 5 seconds, sonicated for 15 min, shaken for 2hr on an orbital shaker at 140 rpms, and then centrifuged at 13000 g for 15min. 400 µl of the supernatant was collected into a autosampler glass vial, dried under a gaseous nitrogen stream, methoximated in pyridine with 40 µL of 15mg/mL methoxyamine hydrochloride, and then trimethylsilylated with 40 µL MSTFA (N-methyl-N-(trimethyl-silyl)trifluoroacetamide) + 1% TMCS (chlorotrimethylsilane) reagent.

Data Analysis: The data were deconvoluted using AMDIS and annotated using an in-house constructed spectral library and commercial NIST17 mass spectral library. The abundances of the ions was extracted using custom MET-IDEA software and normalized to the internal standard, ribitol. Statistical analyses such ANOVA, box plots were performed, after data pre-treatment, using MetaboAnalyst3.0 program (http://www.metaboanalyst.ca/).

GC Conditions

GC System: Agilent 6890
Column: DB-5MS, 60 m, 0.25 mm ID, 0.25 µm film thickness, J&W Scientific
Injection vol: 1 µL
Gas type: Helium
Flow Rate: 1.0 ml/min
Temperature: 80°C for 2 min, then 5°C/min to 315°C and held at 315°C for 12 min
Front inlet mode: 1:5 Split

MS Conditions

MS System: Agilent 5973 MSD
Ionization mode: EI
Scan range: m/z 50 to m/z 650

¹ Vieira-Potter et. al. Scientific Reports, volume 8, Article number: 16896 (2018)
Lignin Composition Analysis of Arabidopsis Leaves by GC-MS

Method developed by: Saurav J. Sarma, MU Metabolomics Center
Samples provided by: Antje Hesse, Department of Biochemistry, University of Missouri

Lignin is a component of the cell walls in plants, and the most abundant non-carbohydrate biopolymer on earth with a highly heterogeneous structure. Lignin results from the oxidative coupling of aryl propane units called monolignols; the most common ones being p-coumaryl (H), coniferyl (G) and sinapyl (S) alcohol. The relative abundance of these monolignols may significantly differ in lignin based on the sources. The S/G ratio in lignin signifies the degree of polymerization and thus the structural strength of the polymer as well as it’s susceptibility to degradation for biofuel production.

GC-MS analysis of chemically degraded lignin is an efficient method to determine the S/G ratio in lignin samples. Figure 2 shows the peaks of G and S lignin in leaves from Arabidopsis Thaliana, observed in GC-MS analysis using an Agilent GC coupled to a single quad MSD mass spectrometer.

**Experimental Details**

Sample Preparation: Leaves were lyophilized and extracted with MeOH, MeOH/CHCl3 and water to remove polar and non-polar metabolites. Remaining lignin component was chemically degraded by thioacidolysis, using 4h incubation at 100°C. Derivatization was performed using 1:1 pyridine/BSTFA.

Thioacidolysis Reagent:
- 2.5% Boron trifluoride-diethyl etherate (BF3-Et2O)
- 10% Ethane thiol (EtSH)
- 87.5% Dioxane by volume.
- Tetracosane as internal standard

GC Conditions
- GC System: Agilent 6890
- Column: DB-5MS, 60 m, 0.25 mm ID, 0.25 µm film thickness, J&W Scientific
- Injection vol: 1 µL
- Gas type: Helium
- Flow Rate: 1.0 ml/min
- Temperature: 80°C for 2 min, then 5°C/min to 315°C and held at 315°C for 12 min
- Front inlet mode: 1:1 Split mode

MS Conditions
- MS System: Agilent 5973 MSD
- Ionization mode: EI
- Scan range: m/z 50 to m/z 650
- Solvent delay: 9 min
- EM voltage: 1259 V
- MS Source Temp: 230°C
- MS Quad Temp: 150°C

**Figure 1** Three most important monomer units present in lignin, that determines the degree of polymerization or structural strength.

**Figure 2** Chromatogram showing the G-Lignin at 46.05 min and G-lignin at 47.30 min. Both signals appear as a duplet and the total area of the two peaks in a duplet reflects the abundance of the monomer.
Phytohormone Analysis by LCMS  
Method developed by: Barbara Sumner, Zhentian Lei, University of Missouri Metabolomics Center

Phytohormones play an essential role in the proper growth, development and function of plants. These hormones are separated into classes which differ in their structure and function: abscisic acid, auxins, cytokinins, gibberellins, jasmonates, and phenolics. Quantitative profiling of plant hormones from different classes provides a way to monitor hormone activities and identify hormone networks regulating plant functions. The quantification of plant hormones has been achieved with reverse phase UHPLC coupled with ESI/TQ MSMS using MRM (Multiple Reaction Monitoring). Table 1 lists 12 phytohormones that have been successfully detected in a single sample injection of an extract of Medicago truncatula at the MU Metabolomics Center. An example of quantification of a phytohormone (salicylic acid) is shown if Figure 1. Absolute quantification can be obtained with the use of a stable label internal standard for the hormone of interest.

### Table 1  MRM optimization conditions for the detection of 12 Phytohormones detected by LC/MSMS.

<table>
<thead>
<tr>
<th>Hormone</th>
<th>FW</th>
<th>Parent (m/z)</th>
<th>RT (min)</th>
<th>Product(s)</th>
<th>Cone (V)</th>
<th>CID (eV)</th>
<th>Mode</th>
</tr>
</thead>
<tbody>
<tr>
<td>Me-JA</td>
<td>224.3</td>
<td>224.05</td>
<td>16.15-18.65</td>
<td>151.05, 207.01</td>
<td>24, 25</td>
<td>13, 10</td>
<td>ES+</td>
</tr>
<tr>
<td>t-ZR</td>
<td>351.14</td>
<td>352.20</td>
<td>3.4-3.6</td>
<td>136.05, 220.13</td>
<td>30, 30</td>
<td>34, 20</td>
<td>ES+</td>
</tr>
<tr>
<td>BA</td>
<td>122.12</td>
<td>121.02</td>
<td>7.85-8.25</td>
<td>76.97</td>
<td>30</td>
<td>10</td>
<td>ES-</td>
</tr>
<tr>
<td>SA</td>
<td>138.12</td>
<td>136.97</td>
<td>8.24-8.64</td>
<td>93.00</td>
<td>25</td>
<td>15</td>
<td>ES-</td>
</tr>
<tr>
<td>AAA</td>
<td>175.18</td>
<td>174.00</td>
<td>8.59-8.98</td>
<td>130.00</td>
<td>25</td>
<td>5</td>
<td>ES-</td>
</tr>
<tr>
<td>IPA</td>
<td>189.21</td>
<td>188.11</td>
<td>11.05-11.45</td>
<td>59.04, 144.09</td>
<td>24, 24</td>
<td>12, 10</td>
<td>ES-</td>
</tr>
<tr>
<td>tBA</td>
<td>203.24</td>
<td>202.08</td>
<td>12.85-13.25</td>
<td>116.01, 158.08</td>
<td>30, 30</td>
<td>18, 14</td>
<td>ES-</td>
</tr>
<tr>
<td>JA</td>
<td>210.27</td>
<td>209.17</td>
<td>12.80-13.20</td>
<td>58.98</td>
<td>22</td>
<td>12</td>
<td>ES-</td>
</tr>
<tr>
<td>AA-LA</td>
<td>246.27</td>
<td>245.04</td>
<td>7.70-8.10</td>
<td>87.09, 155.09</td>
<td>30, 30</td>
<td>17, 15</td>
<td>ES-</td>
</tr>
<tr>
<td>ABA</td>
<td>264.32</td>
<td>263.09</td>
<td>10.70-11.10</td>
<td>152.09, 219.15</td>
<td>22, 22</td>
<td>10, 12</td>
<td>ES-</td>
</tr>
<tr>
<td>IAA-Asp</td>
<td>288.26</td>
<td>287.17</td>
<td>5.80-6.20</td>
<td>132.02, 173.75</td>
<td>28, 28</td>
<td>14, 14</td>
<td>ES-</td>
</tr>
<tr>
<td>GM4</td>
<td>322.39</td>
<td>321.23</td>
<td>15.64-16.04</td>
<td>213.18, 257.23</td>
<td>42, 42</td>
<td>30, 22</td>
<td>ES-</td>
</tr>
<tr>
<td>GA3</td>
<td>346.37</td>
<td>345.11</td>
<td>6.90-7.30</td>
<td>143.04, 239.17</td>
<td>32, 32</td>
<td>30, 15</td>
<td>ES-</td>
</tr>
</tbody>
</table>

**Figure 1**  Quantification of salicylic acid (SA) in a M. truncatula leaf sample and root sample using a dilution series of salicylic acid standard.

**Experimental Details**

**Sample Preparation:** A stock solution of the 12 standard plant hormones was prepared (77ug/mL in methanol), and a dilution series ranging from 100x to 64000x was prepared. A 2 uL volume of each standard solution was injected. M. truncatula plants were frozen immediately after harvesting with liquid nitrogen, and quickly ground and weighed while frozen. Samples of 50 mg were extracted:

- 1 mL Isopropanol:H2O:HCl(2:1:0.002) and shake vigorously for one hour at 4°C
- Add 0.5 mL Dichloromethane and shake vigorously for 30 min at 4°C
- Spin at 3500xg at 4°C and remove bottom layer using glass syringe
- Dry samples under nitrogen and re-dissolve in 0.10 mL of MeOH and 1 mL of 1% Acetic Acid
- Run sample over Oasis HLB Column, wash with 1% Acetic Acid, elute with 80% MeOH, 1% Acetic Acid
- Dry eluted fraction under nitrogen
- Re-dissolve dried sample in 25 μL MeOH and 25 μL 1% Acetic Acid
- A 10 uL volume of each sample was injected

**LC Conditions**

**LC System:** Waters Acquity UPLC

**Column:** Acquity UPLC BEH C18, 2.1 x 150 mm, 1.7 μm

**Column Temp:** 60°C

**Flow Rate:** 400 μL/min

**Mobile Phase A:** Water, 0.1% Formic Acid 2 mM Ammonium Formate

**Mobile Phase B:** Methanol, 0.1% Formic Acid 2 mM Ammonium Formate

**Gradient:** 50% B/1.1 min, 50% to 80% B/1.2 min, 80% to 100% B/8 min, 100% B/5 min, 100% to 50% B/0.1 min, 50% B/2.9 min

**MS Conditions**

**MS System:** Waters Xevo TQ

**Ionization mode:** ESI

**Capillary voltage:** 4500 V

**Desolvation Temp:** 250°C
Kynurenine (1) and indoxyl sulfate (2) are two important metabolites derived from the amino acid tryptophan (3). While the former is metabolized from tryptophan in the liver, the latter is produced by gut microorganism from tryptophan. Both compounds have been associated with various conditions, including psychiatric disorders, neurological diseases, chronic kidney disease, and the early onset of cardiovascular disease. Accurate quantification of them is critical in understanding their implications in health.

Quantification of kynurenine and indoxyl sulfate is performed on a Waters Acquity UPLC coupled to Xevo triple quadrupole mass spectrometer. Stable labeled standards, kynurenine-d4 and indoxyl sulfate-d4, as internal standards are used for accurate quantification. Samples (plasma and urine) are cleaned up with C18 SPE (solid phase extraction, HLB 30 mg SPE cartridge) and then subject to MRM (Multiple reaction monitoring) analysis.

**Experimental Details**

**Sample Preparation:** 200 µL of the plasma is mixed with 500 µL of 0.1% formic acid solution containing Kyn-d4 and IS-d4 as internal standards. The mixture is then applied to a HLB 30 mg SPE cartridge. The compounds are recovered by eluting with 50% MeOH containing 0.1% formic acid (1 mL). The solution is then dried under nitrogen stream and then resuspended in 50 µL of MeOH. 2 µl was injected.

**LC Conditions**

- **LC System:** Waters Acquity UPLC
- **Column:** Acquity UPLC BEH C18, 2.1 x 150 mm, 1.7 μm
- **Column Temp:** 60°C
- **Flow Rate:** 560 μL/min
- **Mobile Phase A:** Water 0.1% Formic Acid
- **Mobile Phase B:** Acetonitrile
- **Gradient:** 2% B/1 min, 15% B/5 min, 98% B/8 min, 98% B/9 min, 2% B/10 min, 2% B/12 min

**MS Conditions**

- **MS System:** Waters Xevo TQ
- **Ionization mode:** ESI positive
- **Capillary voltage:** 3500 V
- **Desolvation Temp:** 250°C
- **Desolvation Gas Flow:** 10 L/min
- **Acquisition range:** 50-500 m/z

**MRM Transitions**

- **Kynurenine-d4:** 216.1>136.1, MS (+)
- **Kynurenine:** 212.1>132.1, MS (+)
- **Cone voltage:** 10 eV
- **Collision energy:** 10 eV
- **Indoxyl sulfate:** 209.2>192.2, MS (-)
- **Indoxyl Sulfate-d4:** 213.1>196.2, MS (-)
- **Cone voltage:** 26 eV
- **Collision energy:** 18 eV
Sphingolipids are important components of mammalian cell membrane structure and are involved in recognition and signaling pathways. Changes in sphingolipid metabolism can be an indicator in many neurological, skin, and lung diseases, as well as diabetes and cancer. Non-targeted and targeted profiling of sphingolipids is possible with LCMS. Separation, detection and identification of a broad range of sphingolipid classes has been achieved with a reverse-phase UHPLC coupled with ESI/QTOF MS/MS. Table 1 lists 14 sphingolipid and ceramide standards that have been successfully detected in a single sample injection at the MU Metabolomics Center. The chromatogram for 10 of these standards is shown in Figure 1.

<table>
<thead>
<tr>
<th>RT [min]</th>
<th>Compound Name</th>
<th>(M+H)+</th>
<th>Fragment for MRM</th>
</tr>
</thead>
<tbody>
<tr>
<td>3.7</td>
<td>Sphingosine (D17:1)</td>
<td>286.28</td>
<td>268.3</td>
</tr>
<tr>
<td>3.8</td>
<td>Sphinganine (D17:0)</td>
<td>289.29</td>
<td>270.3</td>
</tr>
<tr>
<td>4.2</td>
<td>Sphingosine-1-P (D17:1)</td>
<td>366.25</td>
<td>250.3</td>
</tr>
<tr>
<td>4.5</td>
<td>Sphinganine-1-P (D17:0)</td>
<td>368.26</td>
<td>252.3</td>
</tr>
<tr>
<td>4.7</td>
<td>Sphingosine-1-P (D18:1)</td>
<td>380.26</td>
<td>264.3</td>
</tr>
<tr>
<td>7.4</td>
<td>C8 Ceramide (D18:1)</td>
<td>426.39</td>
<td>264.3</td>
</tr>
<tr>
<td>8.5</td>
<td>Lactosyl(beta) C12 Ceramide (D18:1/12:0)</td>
<td>806.57</td>
<td>264.3</td>
</tr>
<tr>
<td>8.6</td>
<td>Glucosyl (beta) C12 Ceramide (D18:1/12:0)</td>
<td>644.51</td>
<td>264.3</td>
</tr>
<tr>
<td>8.8</td>
<td>Sphingomyelin (D18:3/12:0)</td>
<td>647.52</td>
<td>184.1</td>
</tr>
<tr>
<td>9.0</td>
<td>C12 Ceramide-1-P (D18:1)</td>
<td>562.42</td>
<td>264.3</td>
</tr>
<tr>
<td>9.1</td>
<td>C12 Ceramide (D18:1/12:0)</td>
<td>482.46</td>
<td>264.3</td>
</tr>
<tr>
<td>10.6</td>
<td>C16 Ceramide (D18:1/16:0)</td>
<td>538.52</td>
<td>264.3</td>
</tr>
<tr>
<td>11.8</td>
<td>C20 Ceramide (D18:1/20:0)</td>
<td>594.58</td>
<td>264.3</td>
</tr>
<tr>
<td>13.4</td>
<td>C25 Ceramide (D18:1/25:0)</td>
<td>664.64</td>
<td>264.3</td>
</tr>
</tbody>
</table>

Table 1 Sphingolipid and ceramide standards detected by LC/MSMS, with the fragment masses required for MRM measurement.

**Figure 1** Chromatogram showing the 10 sphingolipid standards from a 2 μL injection of a 2.5 μM solution of the AVANTI Sph/Cer mix.

**Experimental Details**

**Sample Preparation:** Standard sphingolipids and ceramides were obtained from Avanti Polar Lipids (Alabaster, Alabama) in a 25 μM methanol solution. The standards were diluted to a 2.5 μM concentration and a 2 μL volume was injected.

**LC Conditions**

- **LC System:** Waters Acquity UPLC
- **Column:** Acquity UPLC BEH C18, 2.1 x 150 mm, 1.7 μm
- **Column Temp:** 60°C
- **Flow Rate:** 400 μL/min
- **Mobile Phase A:** Water, 0.1% Formic Acid
  2 mM Ammonium Formate
- **Mobile Phase B:** Methanol, 0.1% Formic Acid
  2 mM Ammonium Formate
- **Gradient:** 50% B/1.1 min, 50% to 80% B/1.2 min, 80% to 100% B/8 min, 100% B/5 min, 100% to 50% B/0.1 min, 50% B/2.9 min

**MS Conditions**

- **MS System:** Bruker impact II QTOF
- **Ionization mode:** ESI positive
- **Capillary voltage:** 4500 V
- **Desolvation Temp:** 250°C
- **Desolvation Gas Flow:** 10 L/min
- **Acquisition range:** 100-1500 m/z
Cuticular wax is an important component of plant cuticle with crucial physiological functions. Although its primary function is to work as a protective barrier to prevent evaporation of water from areal parts of plants, cuticular wax also reduces permeability of plant tissues by dust, ultraviolet light and pathogenic microbes and thereby contribute towards plant health. It is mostly consisted of long chain fatty acids, alkanes, alcohols, esters, aldehydes, ketones and sometimes sterols and triterpenes. While composition of the cuticular wax varies among different species of plants, even within a species it may vary according to the spatial and geographical distribution. GC-MS analysis of the fecal metabolome in soy fed ovariectomized female rats was used to identify the metabolites differentially accumulated in fecal samples of soy fed rats (SOY) as opposed to that of rats on a controlled diet (CON). S-equol, which is not indigenous to soy but a bacterial metabolite of soy-flavonoids, was found to be the most differentially accumulated metabolite between these two groups (Figure 1), and directly correlated to several positive health outcomes in the host.¹

### Experimental Details

**Sample Preparation:** Cuticular wax of leaf was collected from the top four fully expanded trifoliates from the major stem and that of stem was collected from the top four internodes. Each sample was placed in a 20 mL glass vial and added 10 or 5 mL of hexanes for leaves or stem respectively. Samples were agitated on a rotator at 50 rpm for 2 mins, then the solvent was decanted into another vial. Ringed the vial and tissue with 10 (or 5) ml of hexanes and dried the combined fractions of hexanes under nitrogen flow. Reconstituted in 15 µL of pyridine (70%)/MSTFA+TMCS(30%) solution containing 0.01 µg/µL of cholesterol as internal standard, for each 1 cm² surface area of tissue and heated at 50°C for 1h, then vortexed for 5 seconds before GCMS analysis.

**Data Analysis:** The data are average of two injections for each sample with six replicate samples for each tissue type. Agilent Chemstation software was used to extract peak areas by integration of total ion chromatogram. Quantification of metabolites were done by using peak area after normalization to the internal standard cholesterol.

### GC Conditions

- **GC System:** Agilent 6890
- **Column:** DB-5MS, 60 m, 0.25 mm ID, 0.25 µm film thickness, J&W Scientific
- **Injection vol:** 1 µL
- **Gas type:** Helium
- **Flow Rate:** 1.0 ml/min
- **Oven Temp:** 120°C for 2 min, then 5°C/min to 315°C and held at 315°C for 8 min
- **Front inlet mode:** Splitless
- **Inlet Temp:** 280°C

### MS Conditions

- **MS System:** Agilent 5973 MSD
- **Ionization mode:** EI
- **Scan range:** m/z 50 to m/z 650
- **Solvent delay:** 9 min
- **MS Source Temp:** 250°C

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¹ Zhang et.al, The Plant Journal (2005) 42, 689-707
Quantitative analysis of ethanol in Kombucha beverages using 1H-NMR
Method developed by: Saurav J. Sarma, MU Metabolomics Center
Samples provided by: Julie Kapp, School of Medicine, University of Missouri

Kombucha tea is an ancient traditional drink especially in the Asian countries that has recently gained popularity in the USA due to its presumed health benefits through probiotic contents. It is prepared by using symbiotic cultures of yeast and bacteria to ferment sugared black tea over a period of 4-5 days which results in the formation of small amount of ethanol along with many other compounds. There are numerous claims about the drink being beneficial to a wide range of adverse health conditions including diabetes and heart diseases but no clinical studies have confirmed this. To pursue clinical studies of the proclaimed health effects and also for quality control purposes to categorizes kombucha beverages as non-alcoholic, there is a need of simple yet reliable and accurate methods for ethanol quantification in such products. Here a fast and reproducible method of determining ethanol contents in kombucha beverages is presented, which can also be extended to other beverages such as cider and beers.

Experimental Details

Sample Preparation: Kombucha tea samples was allowed to come to room temperature and vortexed rigorously for few minutes. 100 µM solution of maleic acid in deuterated water was prepared. 20 µL of kombucha sample was added to 60 µL of the maleic acid solution and vortexed for 20 s. Transferred 35 µL of this solution to a 1.7 mm NMR tube for data acquisition.

Data Analysis: The data are average of two injections for each sample with six replicate samples for each tissue type. Agilent Chemstation software was used to extract peak areas by integration of total ion chromatogram. Quantification of metabolites were done by using peak area after normalization to the internal standard cholesterol.

Data Acquisition

- 600 MHz Bruker NMR spectrometer equipped with a 1.7 mm micro-cryoprobe (part Z108160) was used.
- 1H NMR spectra were obtained using solvent suppression pulse program ‘wetdc’ with 64 scans each.
- NMR field was locked on D2O signal
- Magnetic field shim was achieved by ‘topshim’ program of Bruker.
- DS= 24, D=16384, D1=3 sec, P1=10.75 µsec, SWH=12019.23 Hz

Data Processing and Calculations

- Topspin 3.5.7 plot editor was used as the data processing software.
- Signals were calibrated by setting the singlet peak for TMS to 0.000 ppm.
- HC=CH peak of maleic acid appears as a singlet at 6.41 ppm and its integration is set to 2.
- CH3 peak of ethanol appear as a triplet at 1.18-1.15 ppm and the integration of this peak is used to calculate the µM concentration of ethanol in Kombucha samples
- Density of ethanol was used as 789 Kg/L at 20°C for v/v % calculations.

![Figure 1](image)

**Figure 1** 1H NMR peak of Maleic acid (internal standard) at 6.41 ppm and ethanol at 1.17 ppm, in a representative sample of kombucha tea.

<table>
<thead>
<tr>
<th>Sample name</th>
<th>Maleic C=CH integration</th>
<th>Ethanol CH₃ integration</th>
<th>Ethanol Conc. µM</th>
<th>Ethanol Conc. g/L</th>
<th>Ethanol v/v %</th>
</tr>
</thead>
<tbody>
<tr>
<td>H</td>
<td>2</td>
<td>0.668</td>
<td>66.8</td>
<td>3.077</td>
<td>0.390</td>
</tr>
<tr>
<td>K-2</td>
<td>2</td>
<td>0.487</td>
<td>48.7</td>
<td>2.243</td>
<td>0.284</td>
</tr>
<tr>
<td>K-3</td>
<td>2</td>
<td>0.561</td>
<td>56.1</td>
<td>2.584</td>
<td>0.327</td>
</tr>
<tr>
<td>K-4</td>
<td>2</td>
<td>1.057</td>
<td>105.7</td>
<td>4.869</td>
<td>0.617</td>
</tr>
<tr>
<td>K-6</td>
<td>2</td>
<td>0.545</td>
<td>54.5</td>
<td>2.510</td>
<td>0.318</td>
</tr>
</tbody>
</table>

Table 1 Concentration of ethanol in different samples of Kombucha tea as determined by integration of the 1H NMR of methyl group of ethanol using maleic acid as an internal standard.
Amino acids are a group of organic compounds that contain amine (-NH2) and carboxyl (-COOH) groups. There are about 500 naturally occurring amino acids, but only 20 are the essential building blocks of life and genetically encoded. They are used to make proteins and enzymes, and participate in many biochemical processes such as neurotransmitter biosynthesis and plant secondary metabolism.

Quantification of amino acids is performed using LC-MS MRM (Monitor Reaction Monitoring). There are two transitions (i.e., qualitative and quantitative transitions) for each of the amino acids except valine. Quantification is based on the quantitative transition which is shown below in Table 1.

### Experimental Details

#### Sample Preparation:
For free amino acids, plant or seed samples (50 mg) are first extracted with 1.4 mL of aqueous solution containing internal standard methionine-d3. After centrifugation at 13,000g for 15 min, supernatant is recovered and filtered through a 20 µm membrane filter. 2 µL is injected.

For bound amino acids (amino acids in proteins), samples (500 mg) are first hydrolyzed in 6 M HCl Methanol (10 mL) containing methionine-d3 at 110 oC for 24 hours at the presence of phenol (20 mg). 400 µl of hydrolysate is mixed with 380 µl of 6 M NaOH and then 20 µl of water, then filtered through a 20 µm membrane filter. 2 µl is injected.

#### LC Conditions
- **LC System:** Waters Acquity UPLC
- **Column:** Acquity UPLC HSS C18, 2.1 x 150 mm, 1.7 μm
- **Column Temp:** 40°C
- **Flow Rate:** 400 μL/min
- **Mobile Phase A:** Water
- **Mobile Phase B:** Methanol
- **Ionization mode:** ESI positive
- **Capillary voltage:** 3500 V
- **Desolation Temp:** 250oC
- **Desolation Gas Flow:** 10 L/min
- **Acquisition range:** 50-500 m/z

### MRM Qualitative Transition of Amino Acids

<table>
<thead>
<tr>
<th>Name</th>
<th>t_R (min)</th>
<th>Exact Mass</th>
<th>Quantitative Transition</th>
<th>Cone, CE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alanine</td>
<td>0.94</td>
<td>89.05</td>
<td>90.08 -&gt; 44.05</td>
<td>14, 8</td>
</tr>
<tr>
<td>Arginine</td>
<td>0.87</td>
<td>174.11</td>
<td>175.14 -&gt; 70.09</td>
<td>16, 20</td>
</tr>
<tr>
<td>Asparagine</td>
<td>0.92</td>
<td>132.05</td>
<td>133.02 -&gt; 87.07</td>
<td>14, 10</td>
</tr>
<tr>
<td>Aspartic Acid</td>
<td>0.94</td>
<td>133.04</td>
<td>134.07 -&gt; 88.03</td>
<td>14, 10</td>
</tr>
<tr>
<td>Cysteine</td>
<td>1.02</td>
<td>121.02</td>
<td>121.93 -&gt; 75.91</td>
<td>14, 10</td>
</tr>
<tr>
<td>Glutamic Acid</td>
<td>0.97</td>
<td>147.05</td>
<td>148.08 -&gt; 84.08</td>
<td>16, 16</td>
</tr>
<tr>
<td>Glutamine</td>
<td>0.94</td>
<td>146.07</td>
<td>147.10 -&gt; 84.08</td>
<td>16, 16</td>
</tr>
<tr>
<td>Glycine</td>
<td>0.89</td>
<td>75.03</td>
<td>76.06 -&gt; 30.07</td>
<td>14, 6</td>
</tr>
<tr>
<td>Histidine</td>
<td>0.85</td>
<td>155.07</td>
<td>156.10 -&gt; 110.08</td>
<td>18, 14</td>
</tr>
<tr>
<td>Isoleucine</td>
<td>2.19</td>
<td>131.1</td>
<td>132.13 -&gt; 86.09</td>
<td>14, 10</td>
</tr>
<tr>
<td>Leucine</td>
<td>2.31</td>
<td>131.1</td>
<td>132.07 -&gt; 89.09</td>
<td>14, 10</td>
</tr>
<tr>
<td>Lysine</td>
<td>0.82</td>
<td>146.11</td>
<td>147.08 -&gt; 84.06</td>
<td>18, 18</td>
</tr>
<tr>
<td>Methionine</td>
<td>1.68</td>
<td>149.05</td>
<td>150.08 -&gt; 133.06</td>
<td>16, 10</td>
</tr>
<tr>
<td>Phenylalanine</td>
<td>2.03</td>
<td>165.08</td>
<td>166.11 -&gt; 120.11</td>
<td>12, 16</td>
</tr>
<tr>
<td>Proline</td>
<td>1.12</td>
<td>115.06</td>
<td>116.03 -&gt; 70.05</td>
<td>18, 12</td>
</tr>
<tr>
<td>Serine</td>
<td>1.15</td>
<td>105.04</td>
<td>106.14 -&gt; 74.02</td>
<td>4, 2</td>
</tr>
<tr>
<td>Threonine</td>
<td>0.97</td>
<td>119.06</td>
<td>120.09 -&gt; 73.98</td>
<td>16, 8</td>
</tr>
<tr>
<td>Tryptophan</td>
<td>2.35</td>
<td>204.09</td>
<td>205.06 -&gt; 187.9</td>
<td>14, 4</td>
</tr>
<tr>
<td>Tyrosine</td>
<td>1.96</td>
<td>181.07</td>
<td>182.17 -&gt; 136.15</td>
<td>16, 12</td>
</tr>
<tr>
<td>Valine</td>
<td>1.47</td>
<td>117.08</td>
<td>118.05 -&gt; 72.02</td>
<td>10, 6</td>
</tr>
<tr>
<td>Methionine-d3</td>
<td>1.38</td>
<td>152.07</td>
<td>153.04 -&gt; 136.08</td>
<td>14, 10</td>
</tr>
</tbody>
</table>

Table 1: Quantitative MRM transitions for 20 amino acids. Each amino acid has two transitions, i.e., qualitative and quantitative transitions. Cone: Cone voltage (V), CE: Collision energy (eV), t_R: Retention time.
Bisphenol A (BPA) is an industrial chemical which is commonly found in polycarbonate plastics that are widely used in food and beverage packaging and storage. BPA is known to mimic estrogen and thus it has raised significant concerns as an endocrine disruptor, leading to investigations into its role in several health issues. Due to the increased awareness about the adverse health effects of BPA, plastic manufacturers have looked into using alternatives of BPA, resulting in development of plastic products labelled as 'BPA free' to capture consumer interest. Bispolynenol S (BPS) has emerged as one of the most common alternative of BPA, but the health effects of BPS on consumers have been poorly studied. Even less information is available about the impact on a developing fetus with a dietary exposure of the mother to BPA analogues such as BPS. Since placenta is the connecting link between mother and fetus, to map the fetal impact of BPA and BPS exposure on a molecular level, we looked into the variations in the placental metabolome using untargeted GC-MS analysis.1

Experimental Details

Sample Preparation: Added 1.5 ml of H2O containing 25 μg/ml ribitol (internal standard) to 6.0 mg of lyophilized placental tissue. Samples were vortexed for 20 seconds, sonicated for 15 min then incubated at 50°C for 1 h. Sample tubes were centrifuged at 13000g for 15 min. 1mL supernatant from each sample tube were collected into an auto-sampler glass vial and dried under a gaseous nitrogen stream. Dry samples were methoximated in pyridine with 25μl of 15mg/ml methoxyamine hydrochloride andy incubated at 50°C for 1 h, and then derivatized with 25μL MSTFA (N-methyl-N-(trimethyl-silyl)trifluoroacetamide) + 1%TMCS (chlorotrimethylsilanle) reagent at 50°C for another hour before GC-MS analysis.

Data Analysis: The data were deconvoluted using AMDIS and annotated using an in-house constructed spectral library as well as commercial GOLM and NIST17 mass spectral libraries. Abundances of the ions were extracted using custom MET-IDEA software and then normalized to ribitol, used as the internal standard. Statistical analyses including volcano plot and box plots were done using MetaboAnalyst 3.0 after data pre-treatment (http://www.metaboanalyst.ca).

GC Conditions

- **GC System:** Agilent 6890
- **Column:** DB-5MS, 60 m, 0.25 mm ID, 0.25 µm film thickness, J&W Scientific
- **Injection vol:** 1 µL
- **Gas type:** Helium
- **Flow Rate:** 1.0 ml/min
- **Temperature:** 80°C for 2 min, then 5°C/min to 315°C and held at 315°C for 12 min
- **Front inlet mode:** 1:5 Split mode
- **Pressure:** 9.16 psi

MS Conditions

- **MS System:** Agilent 5973 MSD
- **Ionization mode:** EI
- **Scan range:** m/z 50 to m/z 650
- **Solvent delay:** 9 min
- **EM voltage:** 1259 V
- **MS Source Temp:** 230°C
- **MS Quad Temp:** 150°C

Figure 1 Volcano plot of BPA exposed vs control and BSA exposed vs control placental tissues showing significant metabolites as red dots.

Figure 2 Example of metabolites with significant fold changes between BPA or BSA exposed placental tissues from control. Relative fold changes are demonstrated by box plots generated using Metaboanalyst 3.0.

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1 Mao et al. PNAS March 2020, 117 (9) 4642-4652
The MU Metabolomics Center staff make significant contributions to research which are recognized by inclusion in publications. The following is a list of publications from 2016 - 2020. The MU Metabolomics Center staff members are highlighted by bold text.
2020


2019


2018


2017

Nikolic, D., Martin, J., Sumner, L.W. and Warwick, D. CASMI 2014: Challenges, Solutions and Results. Current Metabolomics, April 2017, Volume 5, Number 1, pp. 5-17

2016


Edison, A.S., Hall, R.D., Junot, C., Karp, P.D., Kurland, I. J., Mistrik, R., Reed, L.K., Saito, K. Salek, R.M., Steinbeck,