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MetaboNews

This month in metabolomics

November, 2026
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MetaboNews is a monthly newsletter published in a partnership between The Metabolomics Innovation Centre (TMIC) and The Metabolomics Society

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Dr. Sheri Schmidt
(University of Alberta)

Metabolomics Society News

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

General Enquiries

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Members Corner

Board of Directors

Dear Members,

Greetings from a very sunny and exceptionally warm South Africa, where November traditionally marks the beginning of the year-end wind-down as we start wrapping things up and preparing for the festive season. I am certainly looking forward to the upcoming summer break!

On a more personal note, I would like to share a special gesture that has made the beginning of my presidency particularly memorable. Some dear friends surprised me with a thoughtful gift to celebrate my appointment as President. I am truly touched by their kindness and generosity, a lovely reminder of the value of friendship and support during new beginnings.

While there is still plenty happening



behind the scenes, I thought this would be a good opportunity to bring you up to speed on the latest developments as we work towards **Metabolomics 2027,** taking place from **20–24 June 2027 in Daegu, South Korea!** Please mark your calendars!

Several invited speakers for Metabolomics 2027 have already confirmed their participation, and we are developing some exciting new conference elements that we believe will be very well received. More on these soon!

Since our last communication, Board members have selected the committees in which they wish to serve, and the Society website is being updated to reflect the new committee structure and portfolios. There has been considerable activity and collaboration across the Board as we work towards delivering an exciting and memorable conference.

We also have a little trip down memory lane in store! Roy will be sharing a short piece on the history of our Society, allowing us to reflect on our beginnings, celebrate our achievements and recognise the people and collective efforts that have shaped MetSoc over the years.

The Education and Training Committee, under the leadership of Nik Rattray, plan to share an important teaching resource. We believe this will be a valuable addition to our community and look forward to receiving your feedback and suggestions once it is released.

As we continue to grow and strengthen MetSoc, we encourage everyone to ensure that their membership is up to date. Beyond discounted registration fees for Metabolomics 2027, membership offers several valuable benefits, including but not limited to:

- Access to protocols.io resources, including a complimentary three-month subscription valued at approximately US$300
- Opportunities to share relevant information and announcements on the MetSoc website.
- Early Career Researcher (ECR) Mobility Grants.
- Travel awards.

We recently hosted a webinar highlighting protocols.io and its role in supporting the sharing, accessibility and reproducibility of research protocols. We encourage members to explore this resource and take full advantage of the complimentary subscription and other opportunities available - https://www.youtube.com/watch?v=ena7w-5dv7w.

If you have not yet joined MetSoc, we encourage you to sign up here and enjoy these benefits.

As we shape the future direction and activities of MetSoc, it is important that our initiatives reflect the needs and aspirations of our members. A membership survey has been circulated, and we encourage everyone who has not yet completed it to do so. We genuinely want your voices to be heard and reflected in the work we do. Please also share the survey with colleagues and peers to help us reach a wider audience and ensure that our activities remain relevant and responsive to the community we serve.

There is much more on the horizon! In the coming weeks, keep an eye out for:

- The launch of the 2027 conference website.
- The official Call for Sponsorships.
- The Call for Workshop Submissions.
- Abstract submission announcements.
- Further details of the exciting new conference elements and initiatives we have been hinting at!

In the meantime, prospective sponsors can start reviewing their sponsorship plans, potential workshop organisers can begin developing their submissions, and researchers can start putting those abstracts together.

Most importantly, **remember to sign up for MetSoc membership** before registering for the conference to benefit from the discounted registration fees and other membership opportunities.

We look forward to your active participation, ideas and contributions as we work together to make Metabolomics 2027 a truly memorable event.

Stay engaged and watch this space!

Regards
Aurelia Alvina Williams
North-West University, South Africa
President, Metabolomics Society

EMN & Affiliates Virtual Symposium – Thank you for joining us!

The EMN & Affiliates Virtual Symposium was successfully held on 3 November 2026, bringing together early-career researchers and members of the international metabolomics community for an exciting exchange of scientific knowledge and ideas across two regional sessions: Europe/Africa and Asia/Oceania.
We would like to congratulate the winners of the Best Oral Presentation Awards, both generously sponsored by protocols.io:

- Kimberly De Windt – "*Design of Experiments-Guided Optimization of an Automated Biphasic Fecal Extraction for Simultaneous High-Throughput UHPLC-HRMS-based Metabolomics and Lipidomics*"
- Sarah Walsh – "*Bacterial bodyguards: Characterising the virus-repressing effect of Wolbachia in Drosophila melanogaster*"

A special thank you to all speakers, presenters, organizers, and attendees who contributed to the success of this event. We look forward to more opportunities for scientific exchange, networking, and collaboration across our global metabolomics community!

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MetaboInterview



Dr. Sheri Schmidt earned her undergraduate degree in chemistry at the University of Alberta then proceeded to graduate school to obtain a PhD in analytical chemistry under the supervision of Dr. James Harynuk. Her PhD work focused on volatile organic compounds (VOCs) released by plants as secondary metabolites. She developed an *in vivo* active sampling system and coupled it with TD-GC×GC-MS to comprehensively separate and identify VOCs released by plants. With this system, several plants species have been characterized and questions related to pest-plants and pollinator-plant relationships have been investigated. A large portion of her PhD work focused on analyzing *Triticum aestivum* (common wheat) to understand how different cultivars change their volatilomes in response to biotic stressors, including the pest *Sitodiplosis mosellana* (orange wheat blossom midge), and abiotic stressors. She recently completed my PhD degree in September 2026 and is now a post-doctoral fellowship under Drs. Benjamin Bourrie and James Harynuk. Her current post-doctoral research focuses on applying multi-omics approaches to enhances the flavour and aroma of fermented beverages.

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1. How did you get involved in metabolomics?

I first got involved in metabolomics during my undergraduate working with human urine to help a graduate student work on different data normalization strategies from metabolomics. Unfortunately, my time on this project was cut short due to COVID. I was then re-introduced to metabolomics, specifically plant metabolomics, during my graduate studies as I began working on a project to measure the volatile compounds released by wheat.

2. What are some of the most exciting aspects of your work in metabolomics?

I think one of the most exciting aspects of my work in metabolomics is developing a sampling method that allows for the global characterization of a plants volatilome and pairing this sampling technique to the current most powerful untargeted analytical platforms, comprehensive two-dimensional gas chromatography coupled to time-of-flight mass spectrometry (GC×GC-TOFMS) (Figure 1). With this sampling technique, it can be customized to fit different plants, allowing for endless opportunities to broaden the current knowledge of plant metabolomics.

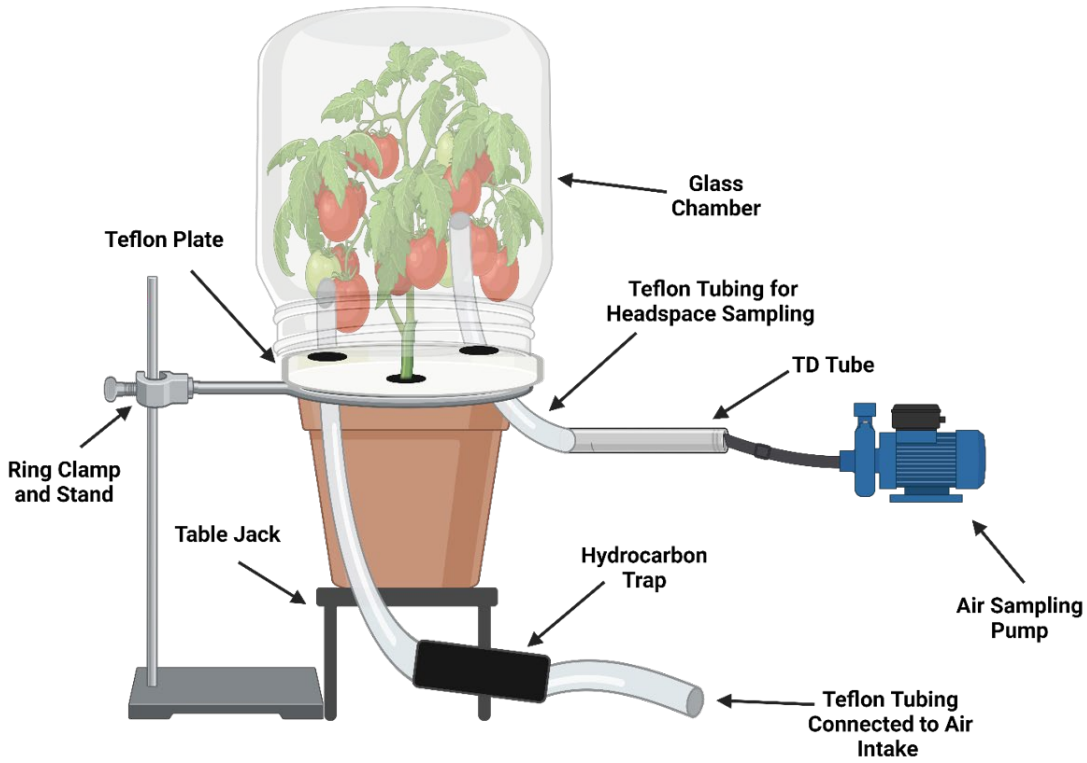


Figure 1. Schematic of the *in vivo* active sampling system.

3. Many of our readers work with blood, urine or tissue. How would you describe the volatilome, and what makes it different to study?

I would describe the volatilome as the gaseous portion, consisting of volatile organic compounds (VOCs), that is emitted by a sample. An example of this would be a plant inside a chamber and sampling the air around the plant (like I

did with my graduate work) or sampling the air above a sample inside a solid-phase microextraction (SPME) vial. The difference with studying the volatilome is that you are not working with the tissue or biofluid directly, but instead capturing any volatile organic compound (VOC) that is being released by the sample into the air. The volatilome typically consists of very to semi-volatile compounds. Typical sampling of the volatilome includes using SPME or collecting samples on a thermal desorption (TD) tube then thermally desorbing either a SPME fibre or a TD tube to inject the sample into a GC whereas with a biofluid, usually the sample is derivatized and injected as a liquid when working with GC.

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4. Wheat midge is a major pest across the Prairies. What led you to look at wheat volatiles to understand why the midge prefers some cultivars and growth stages over others?

Wheat midge is a major pest across the Prairies which is why researchers across Canada are trying to determine mitigation efforts against it. In my research, my collaborators and I were focusing on wheat volatiles to understand how wheat and wheat midge interact with each other as insects are known to interact with plant VOCs whether it is to attract pollinators or deter pests. Additionally, there have been some wheat cultivars that naturally deter wheat midge from laying their eggs on them, suggesting there may be a single VOC or a blend of VOCs that may be deterring wheat midge by these specific wheat cultivars.

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5. What were the most salient differences you found between the deterrent and susceptible cultivars, or between pre- and post-anthesis wheat?

The largest difference that I observed between a deterrent and susceptible wheat cultivar was the larger relative abundance of four green leaf volatiles (GLVs), plant metabolites known for the defense properties, in the deterrent wheat cultivar collected at night (between 5 pm-9 pm) (Figure 2). Interestingly, wheat midge attacks typically occur in the evening during this timeframe, demonstrating how the deterrent wheat cultivar may be altering its metabolism to produce defense compound in anticipation of a wheat midge attack. The largest difference that I observed between pre-anthesis (before flowering) and post-anthesis (after flowering) wheat was the larger relative abundances of

various methyl ketones in the post-anthesis wheat regardless of sample collection time or cultivar type. Methyl ketones, specifically 2-undecanone and 2-tridecanone (structures found in Figure 3), have known insect repellent properties, explaining why wheat midge prefers to attack wheat in pre-anthesis.

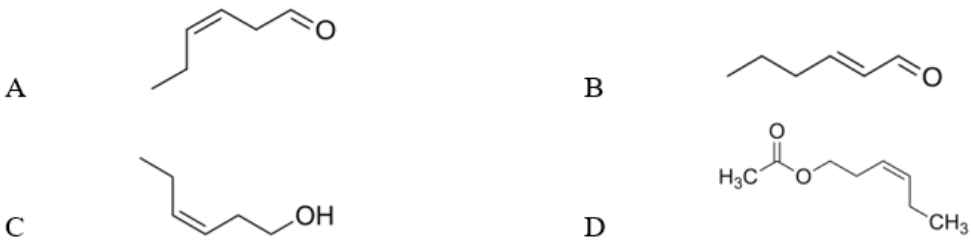


Figure 2. GLVs observed in higher relative abundances in deterrent nighttime wheat samples. A: (Z)-3-hexenal. B: (E)-2-hexenal. C. (Z)-3-hexen-1-ol. D: (Z)-3-hexenyl acetate.

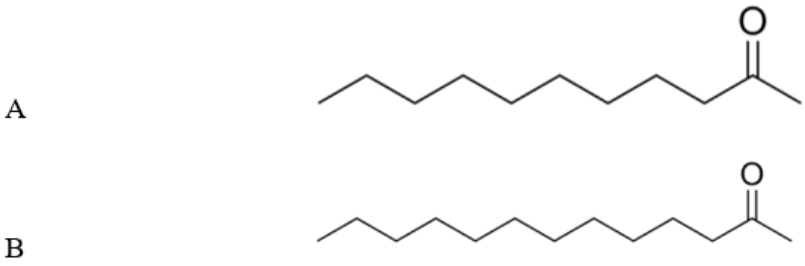


Figure 3. Methyl ketones seen in higher relative abundances in post-anthesis wheat samples. A: 2-undecanone. B: 2-tridecanone.

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6. Sampling a living plant is very different from analyzing an extract. What did it take to build your in vivo sampling system, and why pair it with GC×GC-TOFMS?

There were many challenges when designing the *in vivo* active sampling system. The main challenges were ensuring minimal carryover between samples by developing a cleaning protocol that involved testing different solvents and oven drying conditions. Another large challenge I faced when designing the *in vivo* active sampling system was ensuring the plant inside the chamber was not under any stress introduced by the system that may result in biases in data interpretation. To overcome this challenge, I had to determine appropriate air flows and chamber sizes to fit the plants needs. I paired the *in vivo* active sampling system with GC×GC-TOFMS because I wanted to provide the plant metabolomics community with a method that provides global coverage of volatile plant metabolites. Combining active sampling onto TD tubes from the

in vivo system enhances metabolite coverage and extraction while GC×GC-TOFMS provides a powerful platform to obtain higher resolution, peak capacity, and separation which then aids in metabolite identification as co-elutions commonly seen in one-dimensional GC are reduced and the quality of mass spectra is enhanced.

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7. What key metabolomics initiatives are you pursuing in your postdoctoral work on fermented beverages, and how does your experience with plant volatiles shape that work?

In my postdoctoral work, I am shifting gears to food metabolomics, specifically studying fermentation products. The broad, overall goal of this work is to understand how different styles of fermentation influence the flavour and aroma of fermented products, mainly beer. My experience working with plant volatiles will help me now study the volatilome of fermented products by establishing optimal extraction methods and applying my data analysis workflows to fermented products.

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8. How do you see your work in metabolomics being applied today or in the future?

I would love to see researchers across the globe incorporate my *in vivo* active sampling system into their labs to study the volatilome of different plant species. My system coupled to GC×GC-TOFMS is a powerful technique to understand plant metabolism and plant-plant and plant-insect relationships, opening an endless amount of opportunities for research related to plant metabolomics.

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9. How do you see metabolomics supporting other research disciplines in the future?

One of my favourite aspects of metabolomics is how interdisciplinary it is and it will only continue to expand in the following years. Metabolomics studies the end-products of biological systems and can be utilized to better understand diseases, metabolism, plants, food, exposures, environment, and much more. I believe researchers are beginning to understand the benefits of pairing their research with metabolomics to better understand the systems they are

studying.

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10. Many metabolomics users do not think of agricultural and food sciences when they first think of metabolomics. What could the wider field learn from these areas?

It is true agricultural and food sciences are not the typical fields people think of when thinking of metabolomics. However, working with these fields do provide critical information to the general public. We can improve agricultural practices, food quality, and quality control procedures. Furthermore, we can get a better understanding of how environmental stressors, such as climate change, is impacting crop growth and food quality by applying metabolomics to agricultural and food sciences.

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11. What do you see as the greatest barriers for metabolomics?

One of the greatest barriers for metabolomics is handling of the data, especially untargeted datasets where one sample has over 1000 compounds. It can be really tricky to handle these large datasets and pull out meaningful data. Additionally, between metabolomics groups, there are different data handling workflows which can be very intimidating to new users as there is not one simple solution to handle metabolomics data.

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12. What improvements, technological or otherwise, need to take place for metabolomics to really take off?

As I mentioned in Q11, I think for metabolomics to really take off would be to improved data analysis workflows and technology to readily interpret large, complex datasets. Additionally, I think once ‘multi-omics’ experiments are more established, metabolomics will become further integrated into research projects to enhance the understanding of biological systems.

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13. Where do you see metabolomics having its biggest impact over the next five to ten years?

I think metabolomics will have a large impact in disease screening protocols.

For example, metabolomics of breath is a large area of research in the GC×GC community to screen for respiratory infections and diseases. Additionally, I think metabolomics will be a big part of food quality control and testing in the next few years.

MetaboReads

Biofluid Signatures for Diagnosis and Stratification

The practical case for metabolomics in diagnosis rests on whether a sampled fluid carries enough information about a disease process happening somewhere else in the body. This month's three studies test that premise with very different matrices: exhaled breath in gout, plasma in a pediatric vasculitis, and paired serum and milk in dairy cattle. Each moves past a simple case-control list toward something more structured, whether a machine-learning classifier, an integrated proteomic layer, or a latent-component model that ties systemic chemistry to local immune cells. The results are encouraging but share a familiar limitation, since cohorts remain small and single-site, and near-perfect discrimination in a case-control design says little about performance in the ambiguous patients clinicians actually see. The more interesting shift is in interpretation, with each group trying to explain why a remote fluid should reflect local pathology rather than simply reporting that it does. That framing will matter as these signatures face the harder test of external validation.

Breath molecular feature profiling with machine learning for noninvasive diagnosis of gout: a single-center case-control study

Cai and colleagues in *Frontiers in Molecular Biosciences* reported that exhaled breath profiled by electrospray extraction ionization mass spectrometry separates patients with established gout from healthy controls with near-complete accuracy. Across 201 participants, random forest models built on 12 differential breath features reached a cross-validated AUC of 0.999, with a putative urate dimer elevated in patients and the remaining ions depleted. A trimodal model adding tongue-coating and clinical features did not raise discrimination further but proved more stable against short-term confounders. The authors frame the work as proof of concept, and the obvious next step is testing it against asymptomatic hyperuricemia and other inflammatory arthritides, where the diagnostic question becomes difficult.

Multi-Omics Analysis Uncovers a Link Between Dysregulated Steroid Hormone Biosynthesis and Pediatric IgA Vasculitis Nephritis

Wang and colleagues in *Frontiers in Bioscience-Landmark* found that children with IgA vasculitis nephritis carry a plasma metabolome distinct from both healthy controls and patients without renal involvement, dominated by depletion of steroid hormones. Of 65 differential metabolites, the steroid biosynthesis pathway was among the most altered, with tetrahydrocorticosterone, tetrahydrocortisone, cortisone, aldosterone, androsterone glucuronide and progesterone all lower in nephritis. Exploratory proteomics added enrichment of complement, coagulation and B cell receptor signaling, and the steroid deficits tracked alterations in immunoglobulins and clotting factors. The data point toward impaired steroid output as a feature of renal progression, a hypothesis that could be tested longitudinally given that several of these steroids are already measured in clinical laboratories.

Integrated serum metabolomics and milk immune cell profiling reveals systemic and local responses in Holstein cows with subclinical intramammary infection

Bisutti and colleagues in *Italian Journal of Animal Science* showed that serum 1H-NMR metabolomics correlates strongly with milk leukocyte profiles in cows with subclinical intramammary infection, supporting a blood-based route to mastitis detection. Using DIABLO to integrate serum metabolites, milk flow cytometry and udder health traits from 34 Holstein cows, they found a correlation of 0.73 between the metabolomic and leukocyte blocks. Infected animals had higher serum lactose, consistent with a leakier mammary barrier, alongside raised histidine and lower acetone, methanol, ethanol and 3-hydroxybutyrate, which the authors read as energy diverted from rumen-linked metabolism toward immune response. Lactose emerged as the best single marker and allantoin as the most sensitive, though the cohort is too small to settle diagnostic thresholds.

Metabolism as a Readout of Cell State

Core metabolic pathways are often treated as background housekeeping, yet the three papers here use them as direct readouts of what a cell is becoming. In fibrotic liver, a mitotic kinase controls how activated stellate cells feed glutamine into the TCA cycle. In virus-infected avian fibroblasts, a common saturated fatty acid acts through protein myristoylation to dampen interferon signaling and push lipid metabolism in a direction that favors viral spread. The third study turns the question around, using central carbon metabolites to judge whether stem cell-derived retinal organoids have matured into something resembling native tissue. Taken as a set, they argue that metabolite levels report activation and differentiation state with a resolution that transcript data often miss. This is where metabolomics earns its place in mechanism papers, as the layer connecting a signaling event to a measurable change in how the cell uses its fuel.

TTK Promotes Hepatic Fibrosis Through PKM2/H3T11-Mediated GLS1-Dependent Glutamine Catabolism

Lai and colleagues in *Liver International* demonstrated that threonine tyrosine kinase (TTK) drives hepatic stellate cell activation by switching on glutamine catabolism. TTK was elevated in fibrotic human liver and in CCl4 and thioacetamide models, and its silencing, stellate cell-specific knockout or pharmacological inhibition attenuated fibrosis. Metabolomics and Seahorse measurements showed that loss of TTK reduced entry of glutamate into the TCA cycle and limited the ATP supply that activation requires. Mechanistically, TTK phosphorylates PKM2, which moves to the nucleus and phosphorylates histone H3 at threonine 11 to support MIXL1-driven transcription of GLS1, placing a druggable kinase upstream of a metabolic dependency already of interest in fibrosis.

Myristic acid promotes cell-to-cell spread of Marek's disease virus by inhibiting STING-mediated IFN-β production and reprograming metabolic profiles

Nong and colleagues in *Veterinary Microbiology* reported that myristic acid suppresses STING-dependent type I interferon signaling in chicken embryo fibroblasts and promotes cell-to-cell spread of Marek's disease virus. Myristic acid lowered TBK1 and IRF7 transcripts after cGAMP stimulation and dampened IRF7 and IFN-β expression during infection, effects reversed by the N-myristoyltransferase inhibitor DDD85646. Treated cells showed higher glycoprotein gC expression and larger plaques, although total viral replication did not increase. Metabolomics showed that infection itself disturbed glycerophospholipid, amino acid and cofactor metabolism, and that myristic acid deepened the lipid disruption while selectively activating arachidonic and α-linolenic acid pathways.

Metabolic profiling of retinal organoids reveals conserved core metabolites and alterations in glycolytic and amino acid metabolism

Gupta and colleagues in *Metabolomics* found that mouse retinal organoids reproduce much of the metabolic composition of native retina but retain signs of incomplete maturation. Untargeted GC-MS of postnatal day 3 retina and day 28 organoids annotated 166 compounds, 148 of them shared between the two sample types. Differences concentrated in glycolytic and pentose phosphate intermediates such as glucose-6-phosphate and ribulose-5-phosphate, TCA-associated acids including citrate and fumarate, and alanine, aspartate and glutamate metabolism. Conditioned media tracked stage-dependent shifts in extracellular glutamate and glycine, offering a noninvasive way to follow organoid maturation and a benchmark for culture protocols that aim at metabolic fidelity.

Microbes as Mediators of Host Response

Microbiome research is moving from cataloguing community shifts toward isolating the organisms and metabolites that carry a host effect, and this month's papers sit at different points along that path. One maps how four breast cancer chemotherapies differ in their disruption of the gut, blood and brain in mice, information that bears

directly on which patients might benefit from gut-targeted supportive care. Another addresses a practical bottleneck in tumor microbiome work by describing how to recover live bacteria and fungi from cryopreserved, low-biomass pancreatic tissue. The third tests a probiotic strain against *Helicobacter pylori* infection, pairing gastric community data with an untargeted metabolome. Metabolomics plays a different role in each, from systemic phenotyping to characterization of a single isolate to pathway attribution, which says something about how flexibly the method now fits into microbial study designs. What still separates association from mechanism in most of these systems is access to cultured, clinically relevant strains, and that gap is starting to close.

A systematic assessment of the short- and long-term effects of commonly used breast cancer chemotherapeutics on the gut microbiome-blood-brain axis of female mice

Valentine and colleagues in *Gut Microbes* showed that paclitaxel and cisplatin disrupt the gut microbiome-blood-brain axis of female mice far more than cyclophosphamide or doxorubicin. Each drug was given at a translationally relevant regimen, and the team measured inflammatory, metabolomic and bacterial outcomes across gut tissue, gut contents, blood and brain, alongside fatigue and anxiety-like behavior. Paclitaxel produced prolonged circulating and central proinflammatory signals, while cisplatin caused sustained microbiome disruption. Because patients usually receive these agents in combination, a drug-by-drug map of this kind gives a practical basis for deciding where microbiome-directed interventions against gastrointestinal and neurological side effects are most likely to help.

Isolation of Bacteria and Fungi from Human Pancreatic Tumors and Duodenum

Awad and colleagues in *Gut Microbes* showed that an optimized workflow can recover live bacteria and fungi from cryopreserved, low-biomass pancreatic tumor and duodenal tissue. Applied to samples from pancreatic cancer patients and organ donors, and checked against 16S and ITS sequencing, the method recovered communities with clear similarity between pancreas and duodenum along with strains that persist inside the tumor. As proof of concept, the authors characterized a *Klebsiella oxytoca* isolate from a pancreatic tumor by whole-genome sequencing, metabolomics and ex vivo tumor culture. The contribution is chiefly methodological, but it addresses a real constraint in the field, since functional studies of the tumor microbiome have been limited by the scarcity of patient-derived isolates.

Integrated microbiome and metabolomics analysis reveals therapeutic efficacy and underlying mechanisms of Weizmannia coagulans on inflammation in Helicobacter pylori-infected mice

Wu and colleagues in *Journal of Future Foods* found that the probiotic *Weizmannia*

coagulans BC99 reduces gastric inflammation and restores barrier integrity in mice infected with *Helicobacter pylori*. BC99 recovered zonula occludens-1 and occludin expression, raised IL-10 and lowered IL-17A and IL-23, with effects routed through TLR4/NF-κB and JAK2/STAT3 signaling. The strain increased *Lactobacillus* and reduced *Enterobacter*, *Enterococcus* and several other genera in the gastric community. Untargeted metabolomics linked treatment to lower phosphatidylcholine, choline and acetylcholine through glycerophospholipid metabolism, and to reduced taurine, giving candidate metabolic routes for the anti-inflammatory effect.

Traditional Preparations Under Mechanistic Test

Traditional formulas and plant- or fermentation-derived preparations continue to account for a large share of the metabolomics literature, and the better studies in this area now pair chemical characterization with an explicit target hypothesis. The four papers here follow that template in different ways. Two address diabetic wound healing, one by using metabolomics to show what enzymatic hydrolysis releases from red yeast rice, the other by tracing *Panax notoginseng* saponins to a single eicosanoid-handling enzyme in macrophages. The remaining pair test classical formulas in stroke-related cognitive impairment and acute lung injury, combining network pharmacology with metabolomic and in vivo validation. The most persuasive evidence comes from rescue experiments, where overexpressing a target or antagonizing a metabolite abolishes the protective effect, something network pharmacology predictions cannot supply on their own. The weak point across the set remains the leap from multicomponent mixtures to single mechanisms, and the Feining Granules authors are candid that causality and safety still need work.

Tongmai Yizhi Decoction improves post-stroke cognitive impairment by inhibiting monoamine oxidase to reduce dopamine metabolism

Gao and colleagues in *Journal of Ethnopharmacology* showed that Tongmai Yizhi Decoction improves post-stroke cognitive impairment in rats by suppressing monoamine oxidase and preserving dopamine. Network pharmacology and metabolomics pointed to the dopamine pathway, with MAOA and MAOB emerging as core targets. In rats subjected to middle cerebral artery occlusion and reperfusion, the decoction improved cognition and synaptic ultrastructure, raised tyrosine hydroxylase and dopamine receptor D2, and lowered MAOA and MAOB. MAOB overexpression in HT22 cells under oxygen-glucose deprivation partly abolished the neuroprotective effect, supporting MAOB as a functional target of the formula.

Pretreatment with Feining Granules mitigates LPS-induced lung injury in mice: Pharmacological and serum metabolomics evidence

Tan and colleagues in *Journal of Ethnopharmacology* reported that pretreatment with Feining Granules, a cough remedy approved for chronic bronchitis, attenuates LPS-

induced acute lung injury in mice. UHPLC-Orbitrap profiling putatively annotated 66 constituents, mostly flavonoids, organic acids and alkaloids. The preparation lowered inflammatory cytokines and nitrite in RAW264.7 macrophages and reduced apoptosis in MLE-12 epithelial cells, and in mice given seven days of oral pretreatment it eased histological injury and lowered IL-1β, IL-6, TNF-α and IL-18 in lavage fluid. Serum metabolomics pointed to lipid- and energy-related changes, which the authors present as accompanying the protection rather than as an established mechanism.

Enzymatic Hydrolysate of Red Yeast Rice Accelerates Diabetic Wound Healing in Mice: Association with Modulation of Inflammatory, Matrix-Remodeling, and Angiogenesis-Related Markers

Du and colleagues in *International Journal of Molecular Sciences* demonstrated that an enzymatic hydrolysate of red yeast rice speeds closure of full-thickness wounds in type 2 diabetic mice. Widely targeted UPLC-MS/MS metabolomics detected 810 metabolites in the preparation, 199 of which changed with hydrolysis, mostly upward, consistent with release of free amino acids, small peptides and other low-molecular-weight constituents. Applied topically at 5%, the hydrolysate approached the effect of recombinant human EGF. By day 14, treated wounds showed better re-epithelialization, lower TNF-α, IL-6 and IL-1β, reduced MMP-2 and MMP-9, more collagen I/III and stronger VEGF and CD31 staining, a pattern the authors attribute to action on several stages of repair at once.

Panax notoginseng Saponins Accelerate Diabetic Wound Repair by Minimizing Mitochondrial Dysfunction and Inhibiting Pyroptosis of Macrophage via Regulating Ephx2/11,12-EET Axis

Chen and colleagues in *Food Science & Nutrition* found that *Panax notoginseng* saponins accelerate diabetic wound repair by suppressing macrophage Ephx2 and raising 11,12-EET. In streptozotocin-diabetic mice, the saponins improved closure, collagen deposition, glucose tolerance and insulin sensitivity, and untargeted metabolomics was combined with in vitro and in vivo validation to locate the mechanism. Lower Ephx2 expression preserved 11,12-EET, which limited NLRP3-mediated pyroptosis and mitochondrial dysfunction in macrophages. The protective effect was abolished by the EET antagonist 14,15-EEZE but not enhanced by the Ephx2 inhibitor TPPU, and five major saponins (R1, Rg1, Re, Rb1 and Rd) each reproduced the pro-healing effect in vivo.

Ploidy, Genomes and Stress in Crop Metabolism

Crop improvement increasingly treats the metabolome as the trait itself rather than a downstream curiosity, and the three papers in this section approach that idea from the chromosome set, the genome and the field. Chromosome doubling in rice turns out to shift grain nutrition broadly, with amino acid biosynthesis as the metabolic signature of the change. A haplotype-resolved genome for a pigmented ginger

relative connects genome expansion with the anthocyanins that give its flower buds commercial value. A biostimulant sprayed on drought-stressed potato redirects carbon toward starch whose processing properties matter to manufacturers more than to consumers. In each case metabolomics converts a genetic or agronomic intervention into a compositional outcome that breeders and processors can act on. The shared limitation is that pathway enrichment still carries most of the mechanistic weight, and targeted validation of the proposed links will be needed before these findings feed into breeding decisions.

Integrated nutrient profiling and metabolomic analysis reveal nutritional enhancement in autotetraploid brown rice

Wang and colleagues in *Frontiers in Plant Science* found that autotetraploid brown rice outperforms its diploid counterparts on several nutritional measures, with amino acid biosynthesis as the dominant metabolic change. Three matched diploid and autotetraploid japonica pairs were compared across 77 nutritional traits, and the tetraploids produced larger grains with more resistant starch, crude fat, crude protein, storage protein and essential amino acids. Vitamin A rose while vitamin D fell, and B vitamins varied by genotype. UPLC-MS/MS metabolomics identified 1,211 metabolites, with upregulated amino acids and derivatives, downregulated flavonoids, and enrichment in amino acid biosynthesis pathways that fits the higher protein content.

A haplotype-resolved triploid genome assembly of Zingiber striolatum sheds light on genome expansion and trait evolution in Zingiberaceae

Chen and colleagues in *Horticulture Research* reported that the first haplotype-resolved, chromosome-scale genome of *Zingiber striolatum*, a medicinal and edible ginger relative valued for the red pigment of its flower buds, owes much of its size to an ancient family-wide duplication and recent retrotransposon activity. The triploid 'Ziyanghe' cultivar resolved into three haplotypes of 2.64 to 2.80 Gb, and comparison across five Zingiberaceae genomes placed a family-specific whole-genome duplication at roughly 52.5 million years ago, with bursts of LTR retrotransposons between 0.15 and 0.66 million years ago. Metabolomic profiling identified cyanidin-3-O-glucoside, peonidin-3-O-glucoside, delphinidin-3-O-glucoside and delphinidin-3-O-rutinoside as the main pigment components, with quercetin-3-O-glucoside acting as a co-pigment. The integrated data give an initial framework for pigment biosynthesis and a resource for engineering anthocyanin production in the species.

Exogenous fulvic acid improves the structure and industrial functional properties of potato starch under drought stress

Yao and colleagues in *Industrial Crops and Products* showed that a foliar application of fulvic acid at tuber expansion protects both drought tolerance and starch quality in

potato. The optimal treatment, 0.05 mM, reduced reactive oxygen accumulation and lipid peroxidation and raised antioxidant enzyme activity in drought-stressed plants. It also restored soluble starch synthase and starch branching enzyme activity, improved granule morphology and size distribution, and stabilized peak viscosity, breakdown and setback. Joint transcriptome and metabolome profiling linked these effects to hormone-mediated transcriptional changes in leaves and to activation of MAPK signaling, phenylpropanoid and flavonoid metabolism and central carbon pathways in tubers, consistent with more photosynthate being directed toward starch synthesis.

Quality, Provenance and Material Identity

Some of the most consequential applications of metabolomics have little to do with disease, asking instead what a material is, where it came from, and how its chemistry maps onto the qualities people pay for. Two papers here tie composition to sensory and commercial value, defining an objective oxidation index for oolong tea and linking a feed additive in Tibetan sheep to meat traits through the gut-muscle axis. A third shows that moving a desert medicinal plant onto saline-alkali land changes its marker constituents, a question with direct consequences for quality control as cultivation expands. The fourth carries the same logic into the museum, using molecular networking on embalming residues and historical *Mumia vera* samples to recover what ancient and early modern practitioners actually used. Read together, they show untargeted profiling working as a forensic and authentication tool, where the discriminating features matter more than any single pathway. The Egyptian study also shows that, with careful sampling, the method can answer questions that textual evidence alone has left open for centuries.

Evaluation of aroma profile of oolong tea through GC-MS-based metabolic profiling of volatile compounds and the oxidation index

Xing and colleagues in *LWT* showed that the ratio of theaflavins and thearubigins to total catechins works as an objective index of oxidation degree in oolong tea and tracks systematic shifts in aroma. Across 28 samples, the ratio showed the strongest correlation with infusion color parameters such as b*, C* and browning index. GC-MS profiling detected 203 volatiles, from which multivariate analysis and odor activity values selected 24 potential key aroma compounds. Higher oxidation tracked lower levels of orchid-type compounds such as indole and α-farnesene and higher levels of sweet-floral, ripe-fruit and honey-like contributors such as linalool and methyl salicylate, while roasted and fruity notes showed no significant relationship.

Guanidinoacetic acid enhances Tibetan sheep-meat quality through the gut-muscle axis: insights from metabolome-microbiome integration

Sa and colleagues in *Food Chemistry: Molecular Sciences* reported that dietary

guanidinoacetic acid at 0.12% is associated with improved meat quality in Tibetan sheep, with changes in jejunal microbiota and muscle lipid metabolism as candidate links. In a 90-day trial with 120 weaned males across four dose groups, the highest dose raised the abundance of several jejunal taxa including *Bacillus*, along with acetate and propionate. Untargeted muscle metabolomics identified altered glycerophospholipids such as PC 37:5, PC 38:4 and LPA 14:0. The same group showed higher antioxidant capacity, redder meat and lower shear force, and correlation analysis connected these traits to the microbial and metabolite shifts, although the design supports association rather than causation.

Systematic identification of characteristic chemical constituents in Cistanches Herba from saline-alkali land based on hierarchical filtering of mass spectrometry data and spatial metabolomics technology

Li and colleagues in *Chinese Medicine* demonstrated that a layered mass spectrometry workflow can identify chemical markers distinguishing Cistanches Herba grown on saline-alkali land from material harvested in its traditional desert habitat. UPLC-QTOF-MS annotated 74 constituents, dominated by phenylethanoid glycosides, iridoid glycosides and lignans, and OPLS-DA and WGCNA together narrowed these to 12 candidates. PCA loadings and targeted UPLC-TQ-MS quantification then settled on verbascoside, echinacoside, isoacteoside and pinoresinol, all higher in saline-alkali samples. DESI imaging in mouse tissues added a distribution layer, with echinacoside concentrated in brain and verbascoside or isoacteoside strongest in lung, which may help connect habitat-driven chemistry to pharmacological use.

New molecular and historical evidence on ancient Egyptian embalming

Berger and colleagues in *Proceedings of the National Academy of Sciences* found that ancient Egyptian embalming materials and the early modern drug *Mumia vera aegyptiaca* carry recurring molecular signatures of conifer resin and *Aloe*, combining LC-MS/MS metabolomics, molecular networking and machine-learning-assisted annotation with analysis of 41 historical texts. The 24 museum objects, including commercial *Mumia* products, embalming residues, bandages and mummified skulls, proved chemically heterogeneous but repeatedly carried aged conifer resin markers, among them oxidized abietane diterpenoids. Several samples contained aloeresin- and aloin-related compounds, and the convergence of this molecular evidence with the textual record suggests that an unresolved Egyptian term from the second millennium BC may refer to *Aloe*. Comparative profiling also matched an undocumented powder to a specific mummified head, and one historical extract gave modest protection against influenza-induced cytopathic effects in MDCK cells, although its major compound, 7-oxodehydroabietic acid, was inactive alone.

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Metabolomics Events

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Patient-Centric Sampling and Quantitative Multiomics – Overcoming the Challenges for Routine Implementation

December 1 - 3, 2026

Venue: Hilton University of Florida Conference Center, Gainesville, FL, USA

Pairing multiomics with patient-centric home sampling has the potential to add convenience and accessibility to health monitoring and diagnostics. PCSIG is convening leaders for a workshop to explore challenges and solutions for moving this approach from experimental to mainstream, covering new sample types, biomarkers, assays, and home sampling. Closing keynote from Dr. David Wishart on home plasma sampling and quantitative metabolomics.

Host: Patient Centric Sampling Interest Group (PCSIG); organizers include Tim Garrett (University of Florida), Neil Spooner, Jeremiah Tipton, and others

Registration and event details

|MC:SUBJECT|

Imperial College London Metabolomics training course: Hands-on Data Analysis for Metabolomics

December 7 - 11, 2026

Venue: Online

This 5 day course provides a comprehensive overview of data analysis for metabolomics studies focusing on data from NMR spectroscopy and Liquid Chromatography-Mass Spectrometry. It combines lectures and tutorial sessions using open source software to ensure a thorough understanding of the theory and practical applications.

Visit website for more details

MANA SODAMeet

December 8, 2026

Venue: Online

The goal of SODA is to provide a community-driven resource of actively-maintained software, test datasets used for software benchmarking, and results produced by software. SODAMeets is a platform where data generators and computational scientists can share their use of software/data. During SODAMeets (every 2 months), two speakers will present on software or data they would like to share with the community, emphasizing how these software/data are used. Speakers will be requested to fill out a form on our SODA website so that we collect relevant information on these software/data presented.

Join the web seminar

MetaboTalks

December 14, 2026

Venue: Online

MetaboTalks is TMIC's new webinar series spotlighting the researchers and ideas shaping metabolomics today. Each session features an in-depth presentation from a leading voice in the field — covering their work, their methods, and what's next for the discipline.

Join the web seminar

Introduction to Applying GC-MS in Untargeted Metabolomics

February 2 - 4, 2027

Venue: Liverpool, England, United Kingdom

The course provides an introduction to metabolomics, experimental design and the application of GC-MS in untargeted metabolomics, sample preparation, hands-on data acquisition using the LECO Pegasus BT 4D GC x GC-ToF MS, data processing and analysis. The course is delivered using a combination of lectures, laboratory sessions and computer workshops to develop your knowledge, skills and confidence to apply GC-MS in your own research. The course is aimed at individuals with minimal knowledge of GC-MS based metabolomics, and only a small number of attendees are accepted on each course to maximise opportunities for laboratory experience and interaction with instructors.

Registration and event details

2027 Metabolomics and Human Health Gordon Research Conference and Gordon Research Seminar

February 27 - March 5, 2027

Venue: Liverpool, United Kingdom

The 2027 Metabolomics and Human Health Gordon Research Conference and affiliated Gordon Research Seminar will bring together scientists across metabolomics, exposomics, One Health, nutrition, environmental health, and human disease. The GRS is organized by and for early-career researchers, including students and postdoctoral fellows, while the GRC provides opportunities to engage with world leaders in metabolic research and build collaborations across disciplines. The 2027 GRC theme is “One Health, the Exposome, and Lifecourse Health and Disease,” and the GRS theme is “Decoding Metabolism at the Health-Disease-Environment Interface Through Emerging Technologies.”

|MC:SUBJECT|

Gordon Research Conference

Gordon Research Seminar

14th International Singapore Lipid Symposium (iSLS 14)

April 20 - 23, 2027

Venue: National University of Singapore, Singapore

The Singapore Lipid Symposium has expanded from lipidomics to include metabolomics and the exposome. Workshops on Data Analysis and Ensuring Quality in Omics precede the main symposium. Three travel awards of SGD 1,500, each accompanied by an oral presentation, will be selected from submitted abstracts.

Abstract submission by **November 30, 2026** for travel-award eligibility.

Click here for more details

8th Annual Canadian Metabolomics Conference CanMetCon 2027

May 6 - 7, 2027

Venue: Canmore, Alberta, Canada

Join us for the 8th Annual Canadian Metabolomics Conference 2027 in Canmore, Canada, from May 6 - 7, 2027. The conference brings together researchers, professionals, and students from across the metabolomics community for an engaging program of scientific presentations, networking, and knowledge exchange. For more details about the program, speakers, and registration, please check our website regularly for updates.

Early-Bird registration is **open.**

Registration and event details

Metabolomics Jobs

Metabolomics Jobs

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Job Title	Employer	Location	Source
Senior Research Scientist - Metabolomics	UMass Chan Medical School	Worcester, MA, US	UMass Chan Medical School
Bioinformatic Research Position — Statistical Analysis and Cancer Lipidome Atlas Development	University of Pardubice	Czech Republic	University of Pardubice
Bioinformatic Research Position — Multiomics Data Integration and Biological Interpretation	University of Pardubice	Czech Republic	University of Pardubice
PhD Studentship — Ancient Metabolomes and Past Climate Change: Lessons for Health (2027-L04)	University of Leicester	Leicester, United Kingdom	Metabolomics Society
Senior Post-doctoral Research Fellowship – Biomedical and Molecular Metabolism (BioMMet)	North-West University	Potchefstroom Campus, South Africa	Metabolomics Society

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