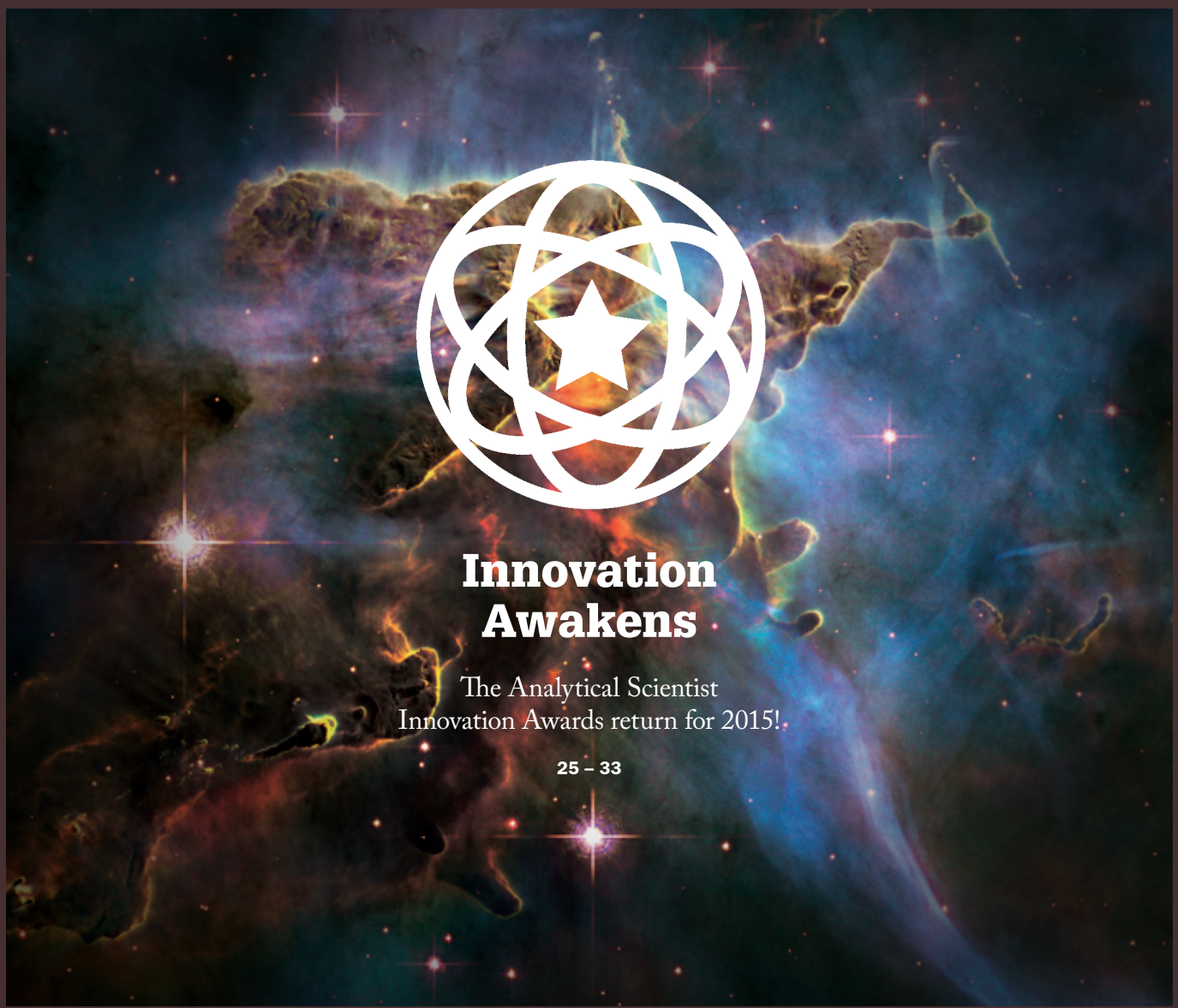
DECEMBER 2015 # 35

the Analytical Scientist



Innovation Awakens

The Analytical Scientist Innovation Awards return for 2015!

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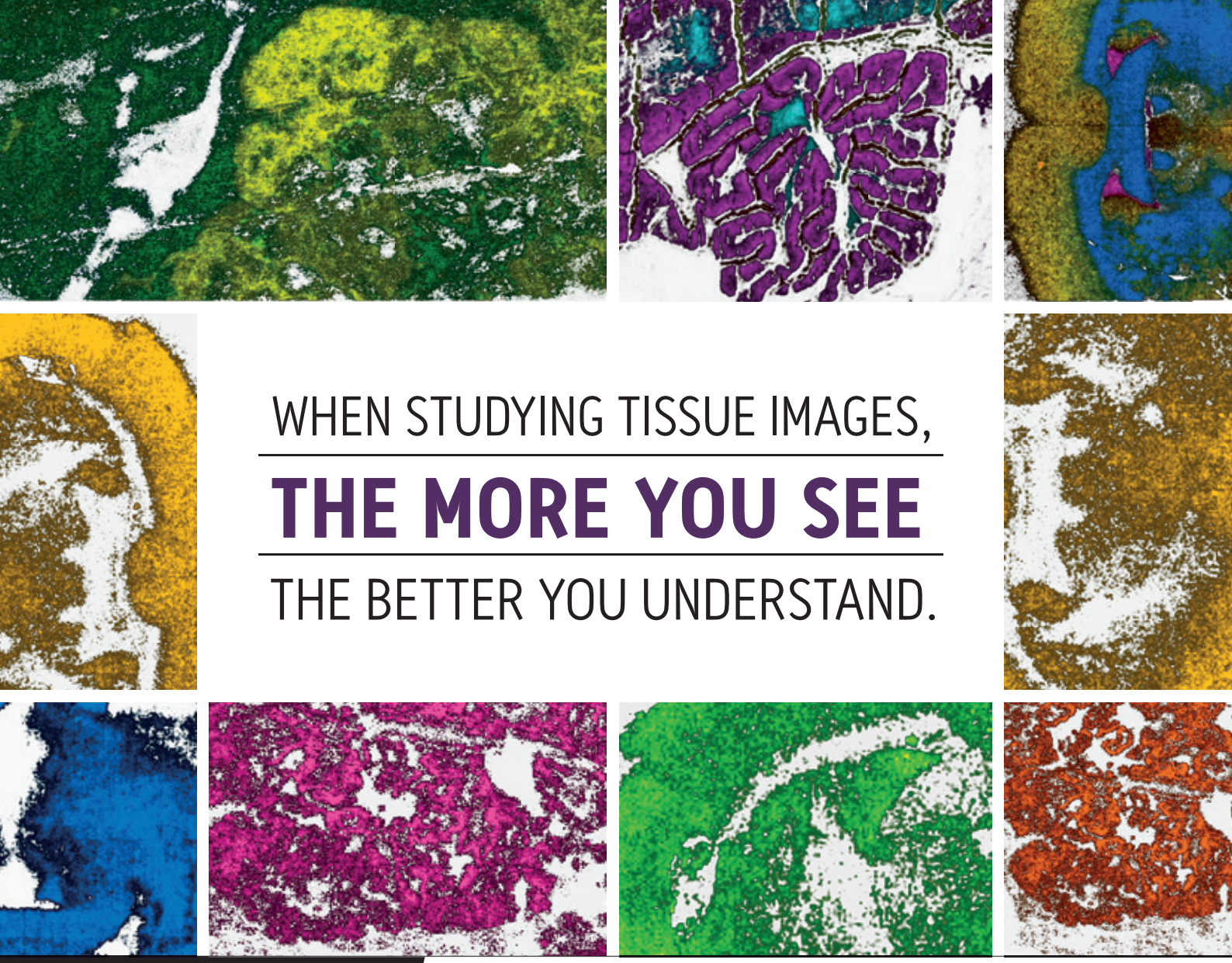

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Online this Month

Tea With Monika

The delightful Monika Dittman joins Rich Whitworth for tea in Geneva and once again "surfs" the limits of liquid chromatography. Monika considers a future where multidimensional separations are a necessity – after all, she says, instrument companies have already offered the ability to perform routine 2D-LC analyses. Looking further ahead, Monika believes Peter Schoenmakers' work on the potential of three-dimensional LC offers a glimpse of the future: seriously powerful separations.

Watch the video now:
tas.txp.to/1215/teawithmonika

Tea With Michal

Michal Holčapek sits in the midday sun in Geneva and enjoys (hot) Tea With Rich. Michal discusses the differences between theory and the application and gives his own work in advanced lipidomics and the different demands of clinical analysis as an example. Michal also looks forward to HPLC 2017 in Prague - especially as he will be the conference chair.

Watch the video now:
tas.txp.to/1215/teawithmichal

Have your say...

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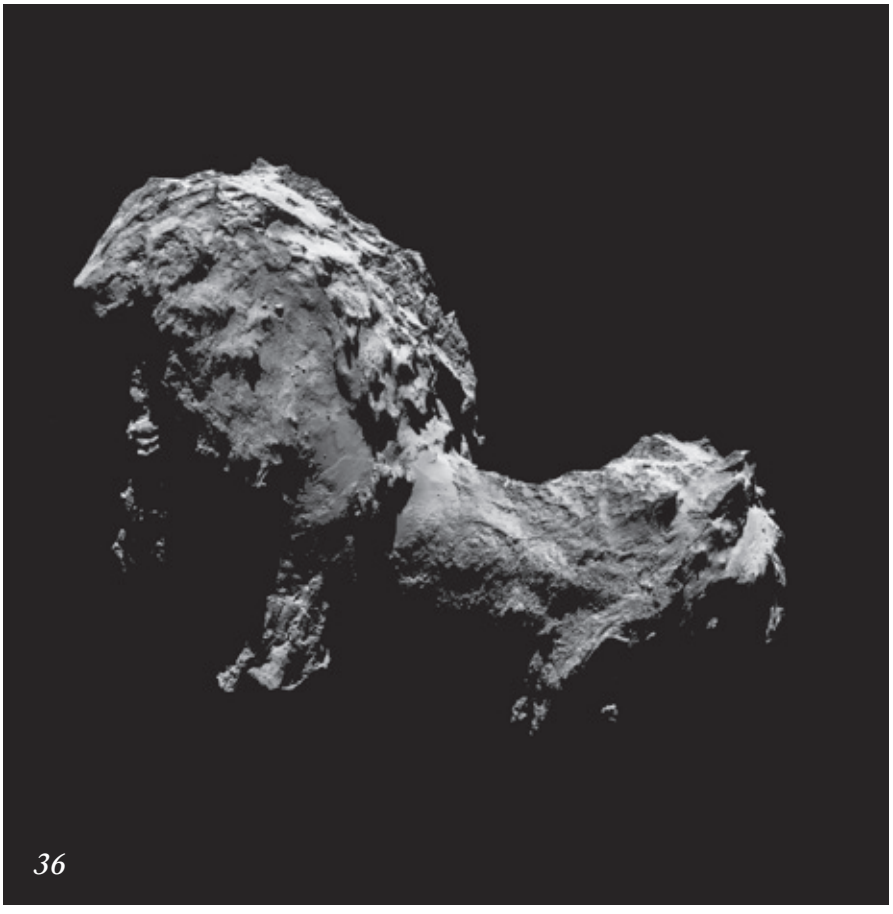

Upfront

In My View

On The Cover

Are The Analytical Scientist Innovation Awards "out of this world"?
Background image: NASA

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Sitting Down With

the **Analytical Scientist**
ISSUE 35 - DECEMBER 2015

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We've Only Just Begun...

Three years on, and our mission to record, celebrate and scrutinize analytical science is as strong as ever.

As 2015 comes to a close – and as we prepare to celebrate The Analytical Scientist's third birthday – it seems fitting to consider how far we've come (and where we're going). I've never known three years go by so fast, but when I look at the 34 copies of The Analytical Scientist in my archive (read: box file), I realize where the time has gone...

What have we recorded? Personal highlights for me are the life stories that we have captured along the way. From Alexander Makarov's walk along the tightrope of innovation, to Rick Russo's battle to gain recognition for laser induced breakdown spectroscopy, to John Yates' pioneering work in proteomics – preserving such personal stories means a great deal to me. Do not expect our strong focus on the people and personalities in analytical science to stop.

What have we scrutinized? Perhaps our coverage of anti-doping was the most controversial. In 2013, we asked four experts to jump atop the soapbox and shout out their opposition to WADA's approach (1). The anti-doping war rages on with no end in sight – and, on page 12, we share an analytical method designed to identify non-banned substances that mask the presence of banned compounds. But we've covered a good many other subjects that demanded discussion from sampling errors (2) and antiquated sample preparation (3) to sustainability (4) and the role of chromatographers (5). Are there any topics that we are afraid to cover? No. Just get in touch with me if you want to borrow our soapbox.

What have we celebrated? Our 2013 and 2015 Power Lists directed the spotlight firmly onto the Top 100 most influential analytical scientists – and we applauded the next generation in our Top 40 Under 40 in 2014 (one of whom is on page 50). In our final issue of the year, we present our third iteration of The Analytical Scientist Innovation Awards – turn to page 25 to discover the Top 15 advances of 2015.

Our field is something to be proud of; for us, every issue is a celebration of the people and processes that make up the wonderful world of analytical science.

Expect the party to continue in 2016.

Best wishes for the New Year,

Rich Whitworth
Editor

Steven Lehotay

Steve is a lead scientist with the USDA Agricultural Research Service, Eastern Regional Research Center in Wyndmoor, Pennsylvania, USA. Since 1992, his scientific investigations and method development research have focused on the analysis of pesticides, veterinary drugs, and other contaminants in food and environmental samples. Steve's research has addressed all aspects of the analytical process, including sample processing, preparation, separations, detection, screening, quantification, identification/confirmation, and data processing. Steve has used many types of analytical techniques applied in novel and useful ways and is also a co-developer of the QuEChERS method.

Steve offers tips to make you a manuscript master on page 46.

Vincenzo Palleschi

"Sometimes I ask myself if the choice of my university studies was the right one, in view of my current interests. Maybe I chose the wrong faculty, when (too many years ago) I decided that I would like to become a physicist," says Vincenzo Palleschi, a senior researcher for Italy's National Research Council and head of the Laboratory of Applied and Laser Spectroscopy in Pisa, Italy. "I love art, history and archaeology, I work in an institute of chemistry, and I teach archaeologists and art restorers. Should I have been a historian, philosopher, archeologist, or maybe even a chemist, instead of a physicist? But then I realize that if I can do what I love, I'm happy to be what I am!"

Vincenzo teaches plasma physics to computers on page 18.

Torsten Schmidt

"My fascination with water and analytical chemistry began in school and continued throughout my undergraduate studies, PhD, and beyond. In my work, I combine both interests perfectly," says Torsten, who has, since 2006, been Chair of the University of Duisburg-Essen's department of instrumental analytical chemistry, with a strong focus on development and applications of new analytical methods, mainly environmental. "I am deeply involved in water chemistry and water technology as a teacher and researcher, and for the past three years, I've been the President of the German Water Chemistry Society. My concurrent position as scientific director at the IWW Water Centre, a not-for-profit water-research institute active in applied research and consulting, helps me to keep involved in real world problems and their solutions."

On page 21, Torsten considers the pros and cons of direct injection.

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Upfront

Reporting on research, personalities, policies and partnerships that are shaping analytical science.

We welcome information on interesting collaborations or research that has really caught your eye, in a good or bad way. Email:
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Laptop Lab

Could NASA's "chemical laptop" breathe new life into the search for extraterrestrials?

Carrying around a full-sized mass spectrometer could well hinder the quest for alien life – even in lower gravity. And so, with the aim of downscaling off-planet chemical analyses, NASA has developed a portable lab that could be taken onboard a spacecraft or mounted on a Mars rover. We spoke with Peter Willis (picture, right), co-developer and NASA scientist, to find out more about the chemical laptop.

What inspired the "chemical laptop"?

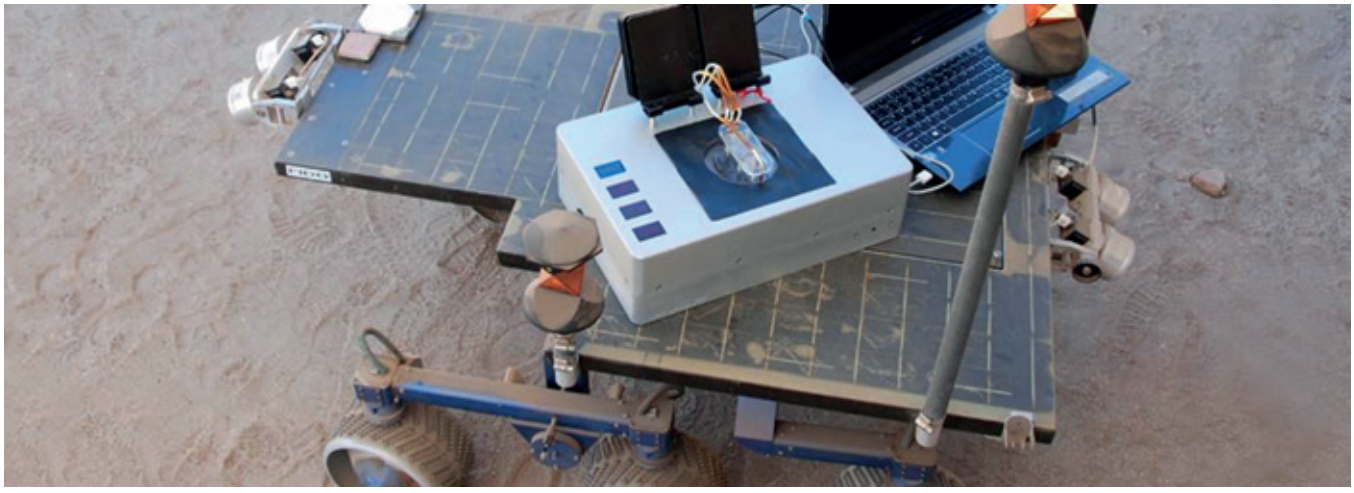
Essentially, I was motivated by the search for life on other worlds. The regular approach used on NASA missions usually involves taking solids and performing gas phase mass spectrometry to look for biological molecules. My approach is to use liquids for all stages of the analysis rather than gases, because it is drastically more efficient at extraction and also analysis. I wanted to develop a small portable instrument that could be used on spacecraft, and that would be reprogrammable by NASA mission operations personnel. And I realized that by solving this problem for NASA applications, we would also provide something that would be generally useful to society. I named it "the chemical laptop" so that people would be able to quickly understand that it was a portable instrument that looks like a laptop, that can be "reprogrammed" to perform different chemistry experiments.

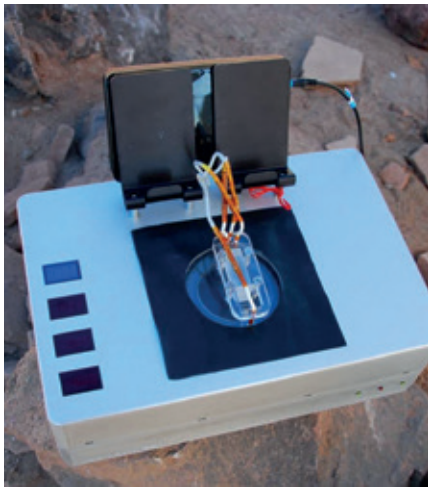
How does it work?

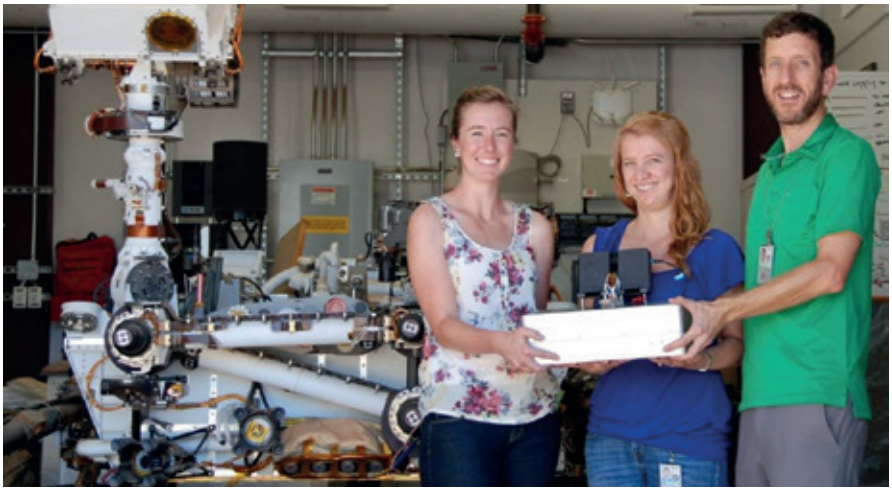
The base unit contains all the electronics, optics, and software just like a regular laptop. But there are two other important replaceable components. One is a microfluidic chip where the liquid analysis takes place. The other is a replaceable reagent cartridge that holds wet and dry chemicals needed for analysis. The user adds an unknown sample to the input port on the chip and selects an "application" from the laptop that is designed to look for a certain class of molecule. Then the unit performs all the steps needed for a chemical analysis: mixing, pumping, labeling, separation, and detection. Mixing, pumping and labeling is done using microfluidic valves on the surface of the chip that are opened and closed using gas pressure. Separation is performed using electric fields, and detection is achieved by measuring the fluorescence produced by labeled target molecules after they are hit by a laser beam. Measuring the fluorescence of molecules as they travel through a microchannel allows us to determine the identities and quantities of the molecules present. In our search for life, we are typically looking for quantities of biological molecules, such as amino acids or fatty acids in a sample, and their geometric distributions.

What was the biggest hurdle during development?

We've been tackling two big hurdles – and they are intimately related to one another. The first is the design and development of a fully integrated system for the pneumatics, electronics, and optics. We are basically squeezing all the components of a chemistry laboratory into an entirely new packaging format, where only solid blocks of material are used as the starting materials (just like in computer chip development). So there are no "tubes" inside the chemical laptop, but it still has to distribute both gases and liquids throughout complex networks. The second hurdle is in complete automation. The sample has to be introduced and data has to come out, without any tweaking by the user. This is a tremendously difficult and underappreciated problem. I think it is fair to say that these problems are universal in







Photos courtesy of NASA/JPL-Caltech

the field of microfludics, which has been slow to deliver useful technology.

Where do you see this kind technology heading?

I see a future where this type of technology is integrated into smart phones and tablets. The phones won't actually look any different but there will be an additional input like a headphone jack where samples can be introduced, and a slot the size of an SD card for reagents to be added. You will download an app with the software for an analysis and, if necessary, you would receive a tiny vacuum-sealed reagent cartridge in the mail. I see progress being driven by open source development rather than one big company. And I believe that for this to really take off and benefit society, we would need to decide upon a single set of standards that everyone can use and go from there. That would leave people to focus on developing the applications.

What next?

We need to get this technology ready for a field test in the Atacama Desert in Chile (a location that is similar to Mars) by January 2017. As part of a collaboration with Brian Glass at NASA Ames, we will be mounting our instrument on a test rover that will drill and deliver powdered samples to the instrument. We needed to develop a new front end for the instrument that takes powdered dirt and extracts molecules from the dirt using heated liquids. Basically, it's like a mini espresso maker for dirt. And we need to automate this entire process so that it can be performed by the operators of the test rover. In addition, we are developing new methods that could be used to analyze material collected from moons like Europa and Enceladus. In those cases, the sample would be ice collected in a vacuum. Here, we need to develop a system that could work inside a vacuum chamber that simulates these conditions.

For more analysis in space, see page 36.

Keeping Up with the Dopers

A new LC-MS/MS screening method simultaneously detects a wide range of non-banned potentially performance enhancing drugs and masking agents in urine

The cat and mouse game of anti-doping is in constant flux as new connections between drugs and performance are identified and exploited. A number of non-prohibited drugs have been linked to performance – but unless detection procedures are up to speed, the cheaters will always stay one pace ahead.

Francesco Botrè and his colleagues at the "Sapienza" University and at the Anti-Doping Laboratory of Rome have developed a screening procedure that can simultaneously detect a number of potential performance enhancing drugs (1). Botrè, co-author of the study, suggests that the method would allow for the prompt identification of the drugs, should they be included in the World Anti-Doping Agency's list of prohibited substances and methods.

"Some other non-banned substances have been shown to alter the metabolic pathways of specific banned substances 'in vitro', with the consequence of potentially masking banned substances and confounding standard analysis." says Botrè. "The method we have developed could help us to better understand whether these kinds of effects are real or just hypothetical."

The work harnessed liquid chromatography coupled to electrospray ionization tandem mass spectrometry (LC-ESI-MS/MS) because, says Botré, "This combination of chromatographic retention time and mass spectrometric fragmentation pattern gives a very high level of certainty of identifying each compound. LC-ESI-MS/MS can also be used to monitor a huge number of different substances in the same chromatographic run." The LC-MS/MS methods currently in use in Botrè's laboratory (using a triple quadrupole MS with selected reaction monitoring), allows 100-200 different substances to be screened from 1-2 ml of urine.

Botrè believes the secret to beating doping is to anticipate new challenges, pre-empt new illicit practices, and to be analytically-ready should they arise. "In other words, we have to forget for a moment that we are the 'good guys', and instead think like our 'colleagues' working on the other side," says Botrè. "It is sometimes an unbalanced competition, since our work and results are public, and theirs are secret – as far as I know, there is no Journal of Doping Science and Methods in which they publish their results!" At least, not yet... *JS*

Reference

1. *M. Mazzarino et al., "A multi-targeted liquid chromatography-mass spectrometry screening procedure for the detection in human urine of drugs non-prohibited in sport commonly used by the athletes", J. Pharm. Biomed. Anal. 117 47-60. PMID: 26342446*

The Forensic Acid Test

Criminals "sweating it out" beware: a new amino acid test can tell male from female fingerprints

Authorities have been using fingerprint analysis to catch criminals for more than 100 years. And technological advances have made it faster than ever to match fingerprints – nevertheless, a simple smudge or distortion can still render a print unusable.

"It's nearly 2016 and fingerprint analysis is still focused only on pictures," said Jan Halámek, Professor of Chemistry at State University of New York. Halámek and his team wanted to figure out what they could use within fingerprints to obtain forensically relevant information, without the need for an image. The researchers knew that women had approximately double the concentration of amino acids in their sweat compared to men – information they could use. But how do you extract amino acids from finger sweat?

The team's novel protocol combines heat and acidic conditions to extract water-soluble amino acids from the lipid-based content of the fingerprint. Adding hydrochloric acid and applying 40 °C heat to fingerprints – deposited onto a portable polyethylene surface – causes the amino acid content in the fingerprint to migrate from the lipid-based content into the aqueous acidic solution, which the team can then use as an analytical sample (1).

Halámek and his team were then able to determine the levels of amino acids in the sample using a dual-enzyme cascade assay. (The cascade is initiated when L-amino acid oxidase reacts with the amino acids, resulting in the conversion of O_2 to H_2O_2. Horseradish peroxidase then consumes the H_2O_2, causing the oxidation of the dye, odianisidine. The concentration of oxidized odianisidine was measured through spectrophotometry at 436 nm, using a Molecular Devices SpectraMax Plus384).

The researchers tested the method on 25 male and 25 female "mimicked fingerprint samples" which were correctly identified in 99 percent of samples. The team moved onto fingerprints from females taken from multiple surfaces, including a doorknob and a computer screen. And though the second part of the study only included three (female) participants, the researchers were able to identify the sex correct; from the fingerprints left on each of the five surfaces tested. "The results of this study proved that we could successfully extract amino acids from multiple surfaces and still be able to identify a female fingerprint," said Halámek.

Halámek recognizes that the method has limitations, and notes "our method is destructive and therefore the fingerprint cannot be used for other tests. It also cannot be used if other methods (fluorescent powder, graphite, etc.) were already used to develop the fingerprint image." But despite the constraints, the team isn't dissuaded from further work on the topic and is currently in the process of developing methods for differentiating between other forensically-relevant attributes, such as age, ethnicity, or health status, as well as improving on the current fingerprint concept.

Reference

1. *C. Huynh et al., "Forensic identification of gender from fingerprints", Anal. Chem. (2015) 22 11531–6. PMID: 26460203*

Exporting Analytics

GSK and the RSC embark on a five-year partnership to bring GC-MS skills to Africa

The UK's Royal Society of Chemistry (RSC) has trained more than 100 African scientists in gas chromatography-mass spectrometry (GC-MS) over the past five years through its Pan Africa Chemistry Network (PACN). Now – with the support of GSK – they aim to treble that number.

"Analytical Chemistry is a key area of expertise for both the RSC and GSK," says Hannah Spry, Strategic Partnerships Executive at the Royal Society of Chemistry. "GSK will bring a high level of technical and leadership skills, as well as providing numerous staff engagement opportunities, bringing industry expertise to the academic community."

In 2008, the PACN's "Africa's Water Quality" report highlighted the importance of analytical skills to chemical monitoring and water management activities in Africa. This prompted the RSC to launch its own training program in GC-MS, delivered by three analytical chemists based in the UK, Switzerland and Kenya.

"GC-MS is the most important equipment I used during my studies to identify and quantify pesticide residues in environmental samples from the Mwea region, the main rice growing area of Kenya," said Preston Akenga, who attended the course. "Monitoring residue levels in the environment and foodstuffs is very important to protect and maintain good standards, whether for domestic consumption or export. This work enables farmers to make informed decisions about pesticide application."

Fredrick Munga, another program participant, used GC-MS to develop mass spectral libraries of volatile compounds in Kenyan coffee. "My knowledge and experience of GC-MS has been crucial in my career at the Coffee Research Foundation and now at Bio Sciences East and Central Africa," he said. "I have also been fortunate to be able to share my knowledge by facilitating two hands-on training seminars for the upstream and downstream oil industry in Kenya and Uganda."

The RSC hopes to provide a sustainable legacy to the program by equipping more people like Munga with the skills to train others. "With the support of GSK we can move from working with volunteers for delivery, to a local training capability based in our PACN hubs," says Spry. "This will enable us to treble the number of scientists who receive training across a much wider region and will allow us to focus our efforts on introducing other types of analysis in the future." *JS*

Spot the Rot

Could carbon nanotubes hold the key to real-time, portable testing for meat freshness?

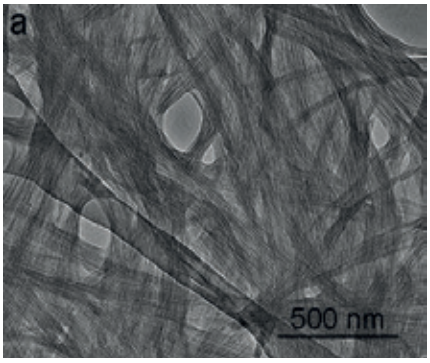
Detecting meat spoilage can be a headache for manufacturers and restaurateurs. Microbial enzymes decarboxylate the amino acids in rotting meat to form biogenic amines (BAs), partly responsible for the offensive odor. But for those working with large batches, a simple sniff won't suffice.

Laboratory tests to detect the presence of BAs, such as chromatography and capillary electrophoresis, typically require specialized instrumentation, operated by highly-trained personnel. The researchers from the Key Laboratory of Photochemistry at the Chinese Academy of Sciences, saw the need for a simple, rapid and portable way to detect the BAs produced by spoiled meat (1).

Previous studies have showed that electronic sensors employing functionalized carbon nanotubes met that criteria, but

could only produce a fluorescence quantum yield of less than 25 percent – too low for practical use. To overcome this problem, the researchers assembled nanotubes from chiral asymmetric perylene diimide molecules (PDIs). "PDIs are a typical and critical class of n-type organic semiconductor that have never been controllably constructed into nanotubes – despite the occasional formation of tubular structures in some kinetic systems," said Yanke Che, co-author of the study. "We set out to address this challenge."

The researchers found that the nanotubes produced from chiral PDI molecules had a highly emissive fluorescence yield – greater than 46 percent. The authors next envisioned that the combination of high emission efficiency and the nanotubes' intrinsic hollow structures – which favor the diffusion of analytes into sensory



materials – would greatly enhance the sensitivity of the nanotubes to amines compared to other PDI nanostructures.

When the researchers noticed that electronic sensors used in previous studies couldn't respond to meat spoilage within one day, they decided to put their nanotubes to the test. The team sealed samples of beef, chicken, pork, fish and shrimp in containers for up to four days. When they exposed the nanotubes to the vapor emitted by the samples, it reacted in under an hour, fast enough to be used as real-time test of meat freshness.

The researchers have now developed new achiral nanotubes, which are much easier and cheaper to synthesize, but still have similar molecular organization, optical properties, and sensitivity to the biogenic amines. The team is now looking to commercialize the new achiral nanotube technology for restaurateurs, food manufactures and for use in customs. *JS*

Reference

1. *Y. Hu et al., "Detection of amines with fluorescent nanotubes: applications in the assessment of meat spoilage", ACS Sensors (2015). DOI: 10.1021/acssensors.5b00040*

In My View

In this opinion section, experts from across the world share a single strongly-held view or key idea.

Submissions are welcome. Articles should be short, focused, personal and passionate, and may deal with any aspect of analytical science. They can be up to 600 words in length and written in the first person.

Contact the editors at
edit@texerepublishing.com

Celebrating Innovation – and 25 Years of SPME and GC×GC

Two important innovations in analytical science have reached their 25th anniversaries: solid phase micro-extraction (SPME) and comprehensive two-dimensional gas chromatography (GC×GC). Here's why I think they are worth applauding.

By Abhijit Ghosh, Postdoctoral Research Associate, Department of Chemistry & Biochemistry, Brigham Young University, Provo, USA.

Solid phase micro-extraction (SPME) was a revolutionary sampling technique invented by Janusz Pawliszyn in 1990, followed by the introduction of comprehensive two-dimensional gas chromatography (GC×GC) by the late John Phillips in 1991. And there is a link between them; these two prolific analytical scientists crossed paths in the early 1980s when Pawliszyn obtained his PhD under the guidance of Phillips at Southern Illinois University. A lesser-known link is that I have been fortunate enough to get hands-on experience of both techniques – and I'd like to share my opinions by comparing apples with oranges!

SPME is an extremely simple method for collecting and concentrating compounds prior to chromatographic analysis. You expose a small fiber to your sample for a specified period of time then directly desorb the fiber in a carrier stream leading to the separation column. The brilliance of the design is that it matches the size scale of the sampling material (the fiber) to the small radial scale of a modern chromatography column. I find myself looking at the tiny fiber hanging out of the assembly and appreciating the ingenuity of the inventors. The development of such a simple yet effective device deserves a standing ovation – especially when the route to needless complexity seems to be more than common these days. Indeed, it is the very simplicity of the technique that allows a user to become proficient in the implementation of SPME sampling in a single afternoon. I know I did. But...

The small size of the fiber does lead to one major drawback that I experienced with SPME. Essentially, compounds with low partition coefficients can quickly reach an equilibrium state with the fiber sorbent material, which means that sample collection could be biased. For example, in the case of a complex VOC mixture, the larger molecular weight VOCs with bigger partition coefficients are collected more efficiently than the smaller molecular weight VOCs with smaller partition coefficients. Why? Because highly volatile, smaller compounds saturate quickly on the small SPME fibers, whereas less volatile and bigger compounds keep accumulating for a longer time. The result is a chromatogram where peak size is heavily influenced by both the concentration of the components but also by their partition coefficients. Fortunately, new sorbent materials have been (and

"Right after Seeley's talk, a prominent person in the organization told him, 'GC×GC is just a solution in search of a problem.'"

continue to be) introduced to address this issue. For instance, SPME fibers based on ionic liquids, carbon nanotubes (Guibin Jiang), polymeric ionic liquids (Jared Anderson) and so on, are being tested for their efficiency.

From an "ease of adoption" point of view, GC×GC is the polar opposite of SPME. GC×GC adds a second stage of gas chromatographic separation to an otherwise conventional GC analysis. And when done correctly, GC×GC generates beautiful two-dimensional chromatograms that greatly increase the information content and peak capacity of the analysis. The early days of GC×GC research were largely devoted to developing the modulation hardware and data analysis strategies for generating high-resolution separations. The second (and current stage) of GC×GC research has focused on demonstrating the utility of this analytical technique for tackling a wide range of analytical applications. And though both phases of development have been highly successful, GC×GC has not benefitted from the broad adoption that we have seen for SPME.

Perhaps one reason for the delay is relatively lukewarm support from major instrument manufacturers. A few years back, my former PhD advisor (John Seeley, Oakland University), was invited to give a talk to a major analytical instrumentation company in USA. Right after Seeley's talk, a prominent person in the organization told him, "GC×GC is just a solution in search of a problem". Clearly, pictures of beautiful separations by themselves are not enough to sway the skeptics. And though the criticism may have been semi-valid 15 years ago, the literature is now full of examples of tough problems being solved by GC×GC.

So what is really holding GC×GC back? In my opinion, there is a level of complexity that is inherent and unavoidable in GC×GC. Unlike SPME, where the process can be separated into discrete steps, GC×GC involves multiple simultaneously occurring processes (separation in the primary column, modulation, separation in the secondary column, detection). It results in a highly complex system where small changes to individual experimental parameters can significantly alter the appearance of the resulting 2-D chromatogram. Indeed, becoming proficient at optimizing a GC×GC separation involves understanding the confounding influence of multiple experimental settings. The high sensitivity to multiple conditions has been nicely outlined by Tadeusz Gorecki (University of Waterloo) in a series of articles appearing in academic journal and trade publications. Certainly, GC×GC involves a "steep learning curve", but many of us have found it to be well worth the effort. To make GC×GC more acceptable, experts and commercial vendors should continue to search for more user friendly designs. I also believe we should also develop "cookbook" methods that allow new adopters to experience success in a shorter period of time. Finally, we need to continue to develop theoretical methods that allow users to "pre-optimize" experimental conditions. I remember being horrified when I heard at a GC×GC workshop that the best column selection strategy was "trial and error". Clearly, we can do better than that.

Experienced users of GC×GC also have to guard against over-selling or over-mystifying the technique. The enhanced peak capacity of GC×GC is not always a complete solution. There remain critical pairs that are still hard to resolve. For example, even with its extremely high peak capacity, GC×GC can barely separate m and p-xylenes (I hope Jack Cochran, who had done such analysis, would agree). "Orthogonality" is a nebulous concept that I feel has been given too much importance in the early development of GC×GC. Orthogonality in GC×GC means different things to different people, but it was most often used to describe the difference in the retention mechanisms between the primary and secondary stationary phases. The old rule of thumb was that the primary column should be non-polar and the secondary column should be as polar as possible, the belief being that it maximized "orthogonality". We now know that unique and highly effective column combinations that go beyond the maximum orthogonality dogma can be found with the aid of simple GC×GC retention models. For example, we found that siloxanes can be best separated from complex hydrocarbon mixtures by using two non-polar columns, DB-1 and SPB-Octyl.

In my view, both SPME and GC×GC have consolidated their positions as effective analytical techniques. But they are obviously (and fortunately) very different. SPME is constantly in search of new, selective and more efficient sorbents, whereas GC×GC is striving to become more user friendly and cost effective.

Teaching Computers Plasma Physics

The analytical performance of laser-induced breakdown spectroscopy (LIBS) can be improved dramatically by using an artificial neural network approach, opening up new opportunities for its application.

By Vincenzo Palleschi, Head of the Applied and Laser Spectroscopy Laboratory at the Institute of Chemistry of Organometallic Compounds, Pisa, Italy.

With LIBS, a pulsed laser ionizes matter and the instrument collects and analyzes the spectrum emitted during electron recombination. I've used the technique for more than 30 years, beginning with environmental analysis of pollutants in atmosphere, water and soil, and latterly industrial diagnostics, forensic and bio-medical applications, as well as cultural heritage studies and conservation. It is an interesting technique suitable for a range of applications, particularly when robustness, reliability, speed of analysis and operational availability are important.

To get accurate, reproducible results from LIBS you need to plan your measurements thoroughly – and have access to a good instrument. But the procedure for extracting relevant information from the LIBS spectrum is just as important as the quality of the instrument being used to acquire it.

The classical approach to quantitative analysis of materials with LIBS uses calibration curves obtained from several reference samples. Unfortunately, LIBS signals are extremely sensitive to any change in laser-sample coupling produced by laser irradiance fluctuations or by matrix effects. Consequently, LIBS is placed at the lower end of the analytical figures of merit, behind more established techniques, such as X-ray fluorescence (XRF) or inductive coupled plasma-optical emission spectroscopy (ICP-OES), for example.

Several years ago – to address the above lower ranking of LIBS – my group developed a calibration-free (CF) approach using our knowledge of the chemical/physical processes in the laser-induced plasma. And it proved very effective for correcting all the effects that would prevent its use. For example, CF-LIBS analysis overcomes the matrix effect enabling in principle very accurate measurements. However, the CF-LIBS algorithm must be applied to a single spectrum, eventually averaging the elemental concentrations when taking several measurements from the same sample. Many people do the reverse and (for practical reasons) apply the CF-LIBS method to the average spectrum instead, which is conceptually incorrect.

An alternative approach to LIBS quantitative analysis uses artificial neural networks (ANN), which is much quicker than the CF method. In the ANN method, the inputs (LIBS spectra intensities) are combined (non-linearly) to produce outputs (the corresponding elemental concentrations). During the training stage, you optimize the coefficients of the non-linear combination from the inputs to find the best correspondence between inputs and outputs using a set of test samples. Then you validate the reliability of the results using a different set of (known) samples. Training the ANN is similar to constructing a (multidimensional and nonlinear) calibration curve, which eventually becomes a surface in a multidimensional parameter space.

"To get accurate, reproducible results from LIBS you need to plan your measurements thoroughly – and have access to a good instrument."

ANNs are extremely fast and flexible, they operate on single spectra but suffer similar problems to other methods using calibration curves. In particular, the experimental conditions for acquiring calibration spectra must be consistent throughout the entire calibration process and must be constant during acquisition of LIBS spectra from unknown samples. In addition, the ANN approach is very sensitive to laser-sample coupling variations and matrix effects.

Most recently, I've demonstrated how to embed the basic equations used in CF-LIBS within an ANN algorithm, thus combining the advantages of the two methods: the speed of an ANN and the precision of CF analysis. Therefore, I have finally succeeded in teaching plasma physics to a computer – and it passed its final examinations with good grades!

When No Standard is the Gold Standard

Can multi-angle light scattering aid in the characterization of proteins and antibody drug conjugates?

By Thomas Jocks, Wyatt Technology Europe GmbH, Dernbach, Germany.

Some time ago, we isolated the protein GrpE – a member of the hsp70 protein family. This family of proteins acts as molecular chaperones to support the folding and transport of newly synthesized proteins. To determine molar mass, we applied size-exclusion chromatography (SEC) with conventional calibration, using globulin and albumin standards. The resulting elution volume corresponded with a molecular weight (M_w) of 147 kg/mol.

Were we able to simply sit back and relax? Not a chance! We had in mind a theoretical value of 42 kg/mol and we had nagging doubts about whether there might be something wrong. Did we measure monomers of GrpE? Oligomers? Impurities? Did our standard really behave like the sample and vice versa? Was there an interaction between sample and column? We simply could not get a definite answer with the method we had chosen. So what next? It became clear that an orthogonal method was needed to move forward with our investigation.

After some consideration, we decided that multi-angle light scattering (MALS) might help solve our problem; after all, light scattering has several interesting features for macromolecular analyses of this type. The main advantage in our case was that MALS has the ability to determine molecular weight without standards – and results are derived only from first principles. In other words, there is a strict correlation used to determine molecular weight:

- M_w: M_w = light scattering signal x [analyte].

"Were we able to simply sit back and relax? Not a chance! [...] We had nagging doubts about whether there might be something wrong."

If the latter term is known – and if it can be measured easily using a UV or RI detector – calculating M_w is relatively straightforward. Consequently, the use of a standard is expendable; data are a result of the calculation instead of conditional comparison.

With MALS, we found a surprisingly different M_w value compared with the data from conventional calibration. Light scattering yielded 41 kg/mol, which is almost exactly what we expected. So, we could claim a successful spot landing!

MALS is even more advantageous when looking at antibodies coupled to conjugates, such as toxins or other effector molecules, for example antibody drug conjugates (ADC). In such cases, ultra-high performance liquid chromatography (UHPLC) SEC columns can improve the separation between closely related compounds significantly. The approach needs less sample, reduces mobile phase consumption and allows shorter run times by using smaller particles in the stationary phase. However, for determining molar mass with a three-detector method (UV, MALS and dRI [differential refractive index]), secondary instrumental band broadening is important, so the narrow peaks obtained from UHPLC require detectors with reduced secondary band broadening.

When it comes to characterization of ADCs, we've shown that our three-detector approach allows discrimination between two different preparations and also determination of the drug-antibody ratio (DAR). In other words, for different experimental coupling conditions, it makes it possible to check whether the desired number of drug molecules have bound to the antibody.

In summary, light-scattering technology is able to determine molecular weights of macromolecules without the use of any weight standards because it is an absolute method. Whereas classic calibration failed to generate correct results for various reasons (molecular interaction, adhesion phenomena, shear force distortion), MALS solved our analytical dilemma – and in combination with UV and RI detection, helped give a better insight into molecular composition and the stoichiometry of molecular interactions.

Therefore, in my view, MALS really can serve as a gold standard – using no standards – when it comes to highly complex macromolecular characterization challenges.

What is pH?

This short and seemingly simple question belies the complexity of measuring – and interpreting – pH.

By William Tindall, Analytical Science Solutions, Church Hill, Tennessee, USA.

When teaching and consulting about pH and buffers, I often get asked if the pH can be measured in some solvent (other than water) and if it can, what does it mean? In fact, it is a good bet that the commonly employed glass electrode will work (I'll address the definition of "work" later) to measure pH in most situations and that the values displayed on the meter can be used to make quantitative comparison of the acidity of most places a pH probe can be stuck. Samples as diverse as concrete, LC solvents (1), chicken breasts, armpits, blood and dirt are measured routinely for practical purposes.

There are practical issues with measuring pH. A curious chemist will stick a pH probe into a sample; he or she will observe what appears to be an unusual reading on the meter, conclude the measurement is not working and give up. A lack of understanding of pH leads to this false conclusion. In school, we are taught that pH is the negative log of the hydrogen ion concentration. Indeed, this was the first definition proposed by Sørensen when the concept of pH was conceived in 1909. Though this definition makes solving test problems in the academic environment easy, the definition is of no practical utility. And no pH-measuring device is capable of measuring hydrogen ion concentration.

A more sophisticated definition is that pH is the negative log of hydrogen ion activity. But this gives us another problem: how do we prepare calibration standards of known hydrogen ion activity in the sample matrix of interest? It took nearly 100 years to solve this problem for dilute aqueous solutions in the midrange of pH (2). Standards of estimated hydrogen ion activity for a few partially aqueous solutions have also been developed (3).

But commerce demanded the world's standardization organizations establish a consistent definition for pH that could support manufacturing, trade, research, and so on, in all sorts of samples. The result was a definition for pH unlike most we encounter in science – it has a value resulting from a series of distinct operations; so, it's an "operation definition". The pH-measuring device is calibrated by some disclosed procedure, the sample is measured, and pH is the resulting measurement. We would be hard pressed to figure out hydrogen ion activity from these pH measurement, but this limitation does not diminish in the slightest our ability to put the measurement to practical use.

There is one case where the pH measurement does yield a value for negative log of hydrogen ion activity. Primary Standard aqueous pH standards are dilute, aqueous and cover the midrange of pH values. The hydrogen ion activity of these standards has been measured/calculated to three significant figures (2). If a pH electrode is calibrated with these standards and then used to measure sample that is dilute (low ionic strength), aqueous and in the midrange of pH, the value measured is the hydrogen ion activity in the solution. This value can be reliably used to calculate species activities in equilibrium, if the equilibrium constant is known.

Interpretation problems arise when pH electrodes are stuck in places other than dilute aqueous solutions. How can we interpret the reading in a solvent other than water or a mixture of solvent and water, for example an LC mobile phase? The glass electrode responds in a predictable way to changes in hydrogen ion activity in many solvents and solvent mixtures – alcohols, glycols, acetic acid, acetonitrile, to name a few. A successful approach is to calibrate the electrode with aqueous standards and take the measurement in the solvent or solvent mixture. It may take minutes for the electrode to equilibrate in this new environment so be patient. If the measurement is stable and the value seems to correlate with the solution's acidity, it is likely that it can be used to quantitatively compare the acidities among samples of this solvent composition.

The pH measured will be proportional to the solutions hydrogen ion activity but the measurement will offer no clue as to the absolute acidity or basicity. Do not make the mistake of interpreting the number based on a pH scale in water. For some thermodynamic reasons involving standard state and some electrochemical details (such as a change in junction potential), pH 7 will not be the neutral pH of some solvent other than water. A measured pH of 7 in this or that solvent could even be strongly acidic or basic. There is no way to know from the measurement. But that does not make the measurement meaningless or useless.

In summary, only in rare cases does a pH measurement yield an absolute measure of a solution's hydrogen ion activity. However, in most cases the pH measurement will provide a quantitative comparison of solution acidity/basicity – providing the solutions being compared have essentially the same solvent composition.

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The Pros and Cons of Direct Injection

In water analysis, direct injection of samples into your LC-MS/MS system (without sample preparation beyond filtration) is possible because of advances in instrumentation. However, matrix effects must be monitored carefully – and sometimes may even prove useful.

By Torsten Schmidt, University Duisburg-Essen, Centre for Water and Environmental Research and Instrumental Analytical Chemistry, Essen, Germany; IWW Water Centre, Muelheim a. d. Ruhr, Germany.

I'm a big advocate of proper sample preparation – after all, it's an essential step in the analytical process. Typically, this important process enriches target analytes and enables sample clean-up, which eliminates matrix effects. You cannot correct errors that occur in this step even with the most sophisticated analysis. However, over the last few years there has been tremendous progress in mass spectrometry (MS) instrumentation combined with liquid chromatography (LC) that has, to some extent, rendered sample enrichment obsolete, when no significant signal suppression by matrix components occurs. In fact, this is often the case with very clean matrices, such as aqueous samples.

Successful determination of organic compounds down to the low ng/L range has been described, often in combination with injecting large water volumes (above 10 percent of the void volume of the analytical column), which focuses the target analytes on the stationary phase, allowing them to elute only after initiating the elution gradient. The approach clearly requires some retardation of target analytes under the initial eluent conditions, otherwise, we face two problems:

i. Insufficient focusing will lead to broad peaks. For instance, in the past decade, the focus of water analysis beyond regular monitoring of priority pollutants has shifted to more polar contaminants and transformation products, so achieving sufficient retardation may be critical.
ii. Co-elution of most of the interfering polar matrix may suppress or unpredictably enhance the signal. Even in clean water samples, organic and inorganic matrix components are present in concentrations typically orders of magnitude higher than the target analytes.

So, what are the possible solutions? Stationary phases that enable purely aqueous initial conditions with an immediate solvent gradient can, in many cases, lead to satisfactory peak width and symmetry, as is seen for multiple pesticide metabolites. If on-column focusing is insufficient, consider using a very small pre-column filled with highly retentive material, such as porous graphitic carbon. And adding isotopically labeled internal standards before injection is another well-established approach that makes it possible to correct matrix effects on signal intensity (provided they are identical for both target and internal standard). For more complex matrices containing a lot of organic matter, it is best to check the sample by recording matrix effect profiles using constant post-column infusion of the target and the IS.

There are some drawbacks to the above approach, however. For example, for analyzing emerging contaminants and in particular transformation products, the corresponding isotopically-labeled standards may not be available commercially. Also, for multicomponent methods, many standards are cost prohibitive. Finally, low sensitivity caused by matrix suppression may hamper detection in the required concentration range – though it is possible to overcome this problem with a post-column additive, which is a well-established approach in other application areas of LC-MS/MS but rarely used in water analysis. Post-column addition of ammonia solution in the µmol range may, for example, enhance signal intensity for many compounds bearing an amide or amino group and at the same time compensate for differences in response due to the natural matrix.

If, however, the use of internal standards isn't possible, standard addition is the most appropriate choice. Unfortunately, scientists often avoid this approach because it requires time-consuming multiple analyses of each sample. However, in water analysis, where in many samples target analytes are not detected above the requested reporting limit, it could be less problematic if you use short columns to reduce analysis time and if you automate the entire process. Also, chromatographic software can decide after an initial run of the sample whether quantification using standard addition is necessary at all. I'd like to ask vendors to continue software development with this in mind.

To Attograms and Beyond

Every year sees new chemicals added to the list of analytes that may need to be measured in a given sample. At the same time, environmental levels of many older pollutants may be in decline – but still must be measured. How can analytical technology adapt to these evolving challenges of capacity and sensitivity?

By Donald G. Patterson Jr.

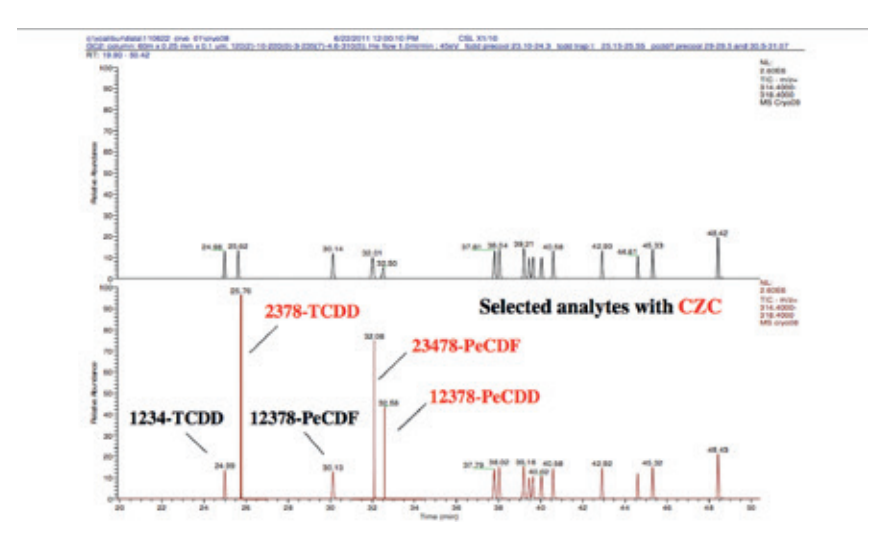

Figure 1. Time-controlled CZC: targeted cryofocusing allows selected peaks (in red) to be refocused. (DFS high-resolution GC-MS analysis of dioxins and furans on 60m column).

Since the advent of the industrial age, we've been in contact with synthetic chemicals – in our food, in the water, the dust, and the air. Analytical science has had to respond to the evolving challenges in assessing the routes and magnitudes of exposure to persistent organic pollutants (POPs) in different population segments, and I believe it is now on the verge of exquisite sensitivity.

Prediction or precision?

You can assess human POP exposure in two ways – prediction or measurement. Prediction relies on measuring POPs in the various media we come into contact with and on questionnaire data, which indicate an individual's exposure to those media. Mathematical models are needed to derive a predicted internal dose in this conventional human health risk assessment approach. By contrast, biomonitoring involves direct measurement of POPs in tissue samples taken from an individual, directly quantifying the internal dose, and thus removing the need for assumptions.

Operation Ranch Hand (the codename given to the defoliation program sprayers during the Vietnam War) resulted in dioxin-exposure to these veterans (specifically, 2,3,7,8-tetrachlorodibenzo-p-dioxin). The measurement of dioxin in these veterans nicely proves the point; predicted dioxin exposure level per veteran had no significant correlation with the actual serum dioxin measurements provided by biomonitoring. The moral of the story: don't predict – measure!

Many POPs, including dioxins, are lipophilic, and some dioxins can have half-lives in human tissues of ten years or more, enabling a direct measurement of exposure years after the event, using biopsy analysis. For lipophilic POPs, adipose tissue seems the obvious sample choice. But it may not be the best one. Back in the seventies, the US Centers for Disease Control (CDC) investigated the Times Beach incident, where a town in Missouri had become contaminated with dioxins after contaminated oil had been sprayed for dust control. I was one of the lead investigators at CDC.

To measure exposure, we asked residents to submit to a surgical procedure that removed a fairly large 20 gram sample of subcutaneous fat from the abdominal area (such was the sensitivity of the technology available). The procedure was invasive – leaving what you might call a fairly large dimple – and, unsurprisingly, the participation rate was low. Soon afterwards, we looked into using serum instead and demonstrated a very tight correlation with the adipose measurements (1). Thankfully, dioxin biomonitoring no longer demands a pound of flesh...

However, although serum sampling is more tolerable for study participants, it presents analytical scientists with a sensitivity problem. Adipose tissue is ~95 percent lipid, and accumulates lipophilic POPs in the parts per trillion to the parts per billion range. But serum averages only about 0.6 percent lipid, which requires detection sensitivities of parts per quadrillion (ppq). Rigorous quality assurance is needed to eliminate background contamination at these levels, and we did everything we could to get reliably low backgrounds, banning smoking (before no-smoking policies were common) and stopping janitors cleaning the floors (phenolic products were disrupting analyses).

Attaining the required sensitivity, though difficult, enabled us to establish

the 'normal levels' of POP exposure in the population; you must understand what is normal before you can know what is abnormal – and in industrialized societies, exposure to POPs is ubiquitous – we all have dioxins in our tissues. One ongoing initiative at the CDC assesses the exposure of the US population to >300 environmental chemicals; survey data get collated into the National Report on Human Exposure to Environmental Chemicals, which offers very valuable data about POP exposure, by sex, age and race/ethnicity, over time. Indeed, they've picked up some very interesting epidemiological points. For example; older people (over 60) typically have an internal dioxin dose three times that of people aged 20–39. And there are large differences in p,p-DDE (dichlorodiphenyldichloroethylene) levels between males and females in some ethnicities, but not in others. This information helps us to define 'normal' exposure for the US population.

Tools for the task

None of our work would be possible without the right equipment. Notably, automation is absolutely essential for large scale, epidemiological exposure studies. At the CDC, we used Fluid Management Systems (FMS) sample preparation and Thermo Scientific DFS™ Magnetic Sector gas chromatography-high resolution mass spectrometry (GC-HRMS) systems.

But... I'm an analytical scientist, so I always want more! In particular, I want lower detection limits. The levels of many POPs have been declining in the environment and in people and unless this can be matched by a parallel increase in detection sensitivity, increased false positives and negatives will reduce our ability to properly monitor the effects of these pollutants. Increased sensitivity also provides better 'statistical power' in epidemiological studies. Achieving equivalent power with fewer study participants saves time and money. Better sensitivity can also pick up completely unexpected information; for example, the large number of non-smokers in the US population with elevated serum cotinine – due to passive exposure – only became evident once analytical sensitivity allowed cotinine measurements at <5 ng/mL.

Down to the attogram level

Clearly, enhanced sensitivity is an ongoing need that demands continuing innovation – especially, to gain the robustness we need. CDC has been working on cryogenic zone compression (CZC) of GC analyte peaks, which when coupled to Magnetic Sector HRMS gives exquisite sensitivity, with very clearly defined peaks at very low sample quantities; for example, ~300 ag for TCDD. And by using GC×GC, we can also benefit from increased peak capacity. We used a GC×GC-TOF MS approach to resolve and quantify 59 analytes found in the human body from one injection, with obvious implications for efficiency and speed in all kinds of applications that demand complex sample analysis.

One of the newest and most exciting approaches is cryogenic zone compression (CZC) GC×GC-HRMS. The first experiments using the CZC approach in combination with Magnetic Sector MS for Dioxins and POPs were realized at the CDC laboratories in Atlanta. In brief, the entire peak of interest is cryotrapped in a single event in one column before being reinjected into the second column (2). The approach produces a very tight, highly-focused peak and gives investigators the option of increasing the sensitivity of the system for particular compounds, as required.

The latest technical advance by Thermo Fisher Scientific developed CZC further into what is now called time-controlled cryogenic zone compression or "t-CZC" (3) see Figure 1. CDC has found that t-CZC gives a clear gain in sensitivity, and furthermore is user-friendly in that you can change between t-CZC and normal operation without needing to change the hardware – even special software is not mandatory. Today, time-controlled CZC is an ongoing development project within Thermo Fisher Scientific, working towards a potential commercially available solution. CDC and other collaborators have been involved for testing and application of this approach on different analytical challenges.

The development of these kinds of techniques – and the extraordinary sensitivity they confer – is allowing us to measure ever lower in terms of detection sensitivity, below the femtogram level and into the attogram range. Soon, we'll be able to test John Taylor's hypothesis that "...concentrations of 1 in 1018 of almost any substance can be expected to be present in almost any sample." We are close to being able to do that now. There's still work to be done on improving the repeatability and reliability of the new systems and to make them commercially available. But will we get there? Yes, I think we will.

Donald G. Patterson Jr. is Principal, Earth and Environmental Practice, at Exponent, Atlanta, Georgia, USA.

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15. Nexera UC

A combination of SFE with SFC or LC separation technologies and MS/MS detection

Produced by Shimadzu

The Nexera UC chromatography system is the world's first unified and fully automated instrument that combines supercritical fluid extraction (SFE) with supercritical fluid chromatography (SFC). The SFE/SFC-MS platform combines quick and easy online sample preparation with advanced chromatographic analysis and high sensitivity detection.

The Nexera UC serves a wide range of applications; for example, in food control, biopharmaceutical research, and environmental analysis. It enables reproducible extraction and stable analysis even of unstable samples prone to oxidation or dissociation when exposed to light or air.

Not limited to SFC analysis, the Nexera UC is also capable of analyzing extracted samples by HPLC, if a conventional reversed phase separation is preferred.

Potential impact

The Nexera UC system can eliminate the need for complicated sample pre-treatment and enables reliable and stable analysis of delicate samples. Furthermore, the fully automated Nexera UC system has a high target analyte recovery rate and reduces the possibility of human error during analysis when compared with conventional manual systems.

In addition, the Nexera UC system significantly reduces the quantity of organic solvents used for applications in normal phase mode or chiral analysis of enantiomers.

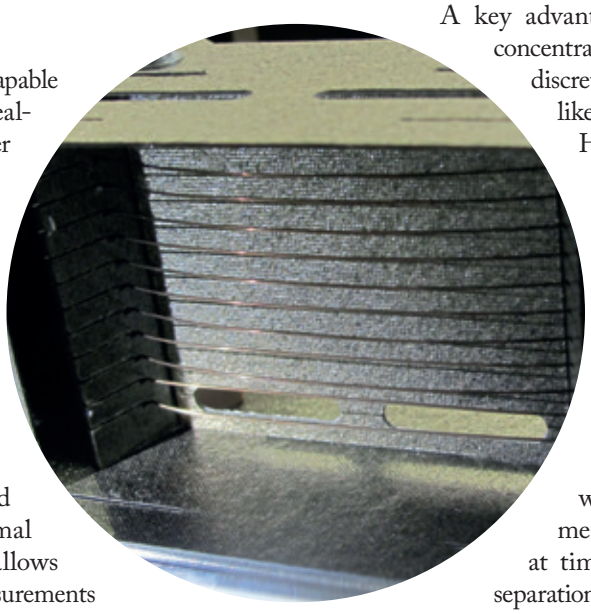
What the judges say:

"[The Nexera UC] considers sample preparation and analysis as one integrated process. And that is the way we should look at it. Both steps influence each other and we should not optimize them in isolation."

14. IONICON fastGC

Adds near real-time chemical separation to PTR-TOFMS trace gas analyzers

Produced by IONICON



IONICON PTR-TOF systems are capable of measuring trace gas samples in real-time with a high mass resolving power and low detection limits in the sub-ppt-range. The new "fastGC" module adds an optional chemical pre-separation step before the analysis. The module consists of a short GC column with an advanced heating concept for ultra-fast heating and equally fast cooling rates, which makes this pre-separation step nearly real-time.

The fastGC module is integrated with the PTR-TOF and the normal sample gas inlet is utilized. This allows researchers to perform real-time measurements and add fastGC runs at time points of interest for enhanced separation and identification.

A fastGC's spectral run is accomplished in less than one minute, which brings GC separation much closer towards real-time analysis and adds another dimension to IONICON's PTR-TOFMS series products. The fastGC is available as upgrade to existing instruments.

Potential impact

A key advantage of PTR-MS is to see trace concentrations in real-time. Compared to the discrete sample analysis in GC-MS, this is like comparing classical photography to a HD movie. However, even though high-resolution PTR-TOFMS systems can separate and identify isobaric compounds (same nominal mass, but different chemical composition), the separation of isomeric compounds (same chemical composition) has remained an advantage of GC-MS. This has now been overcome with the introduction of IONICON's fastGC add-on. Being fully integrated with the analyzer, it enables real-time measurements and add fastGC runs at time points of interest for enhanced separation and identification.

What the judges say:

"Practical, fast separations."

"Many chemical processes are fast, too fast for regular GC – this device combines the strengths of PTR with those of fast GC."

13. 5D Ultra-e (LC-GC×GC-QqQ MS/FID)

A powerful unified separation-science tool

Produced through collaboration between Shimadzu, Chromaleont, and the University of Messina.

The 5D Ultra-e is a unified system that combines comprehensive two-dimensional gas chromatograph and triple quadrupole mass spectrometer/flame ionization detector with an HPLC system connected online. The instrument can be used in seven different combinations ranging from one-dimensional HPLC with a photodiode array detector to on-line LC×GC×GC-QqQ MS/FID. In the latter configuration, it is possible to set different LC, PTV, GC×GC, and QqQ MS conditions during the same run. The online HPLC system enhances the power of comprehensive GC×GC analysis and simultaneously improves productivity by increasing automation. Furthermore, GC×GC system combined with an ultra fast triple quadrupole mass spectrometer allows both untargeted analysis as well as targeted analysis of components in complex samples. The 5D Ultra-e was developed with the principal involvement of Luigi Mondello (University of Messina) and Mariosimone Zoccali (Chromaleont).

Potential impact

The on-line nature of the system, compared to off-line approaches (e.g., LC//GC×GC, solid-phase extraction//GC×GC), reduces the risks of sample contamination, improves run-to-run precision, and enables the setting of batch-type applications, increasing laboratory productivity. The system can be used in a variety of configurations, depending on the specific analytical requirements. Practically all of the requirements of any GC-based application can be covered along the line of the possible operational modes.

What the judges say:

"Many food and life-science samples are extremely complex and no single chromatographic method can separate them. Two-dimensional methods have their limitations, but this system allows easy access to an even higher dimensional study of the sample: three chromatography dimensions and one MS step."

12. Polyarc Reactor

A catalytic microreactor that converts all organic compounds to methane prior to reaching the FID.

Produced by Activated Research Company

The Polyarc Reactor is a catalytic microreactor that enhances existing gas chromatographs (GC) with flame ionization detectors (FID) by converting all carbon-containing species to methane molecules prior to their detection by the FID. Its seamless integration into GC/FID systems eliminates standard time-consuming and costly calibrations, enables quantification of compounds with unavailable commercial standards, and increases FID sensitivity to select molecules.

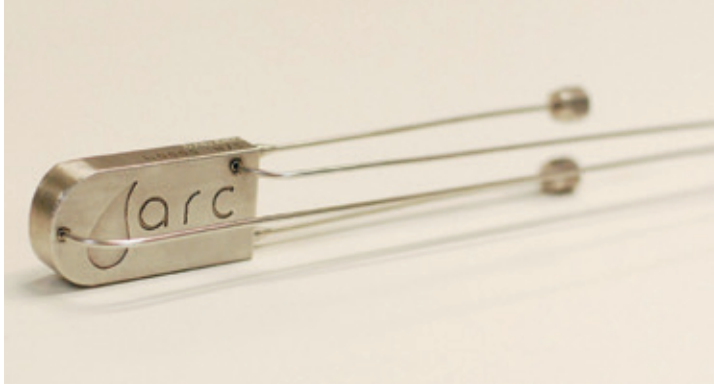
Potential impact

The Polyarc Reactor is a universal carbon detector technology revolutionizing chemical analysis for GC/FID users within a variety of industries. In the petroleum and natural gas industries, scientists and engineers can now detect CO, CO_2, formaldehyde, formic acid, and many additional compounds that previously had little or no visibility in the standard FID in the presence of sulfur, halogens, and other heteroatoms. The food science and pharmaceutical industries can now quantify compounds where standards are prohibitively expensive or simply not available. Academic labs are improving the speed and ease with which they analyze compounds allowing them to perform research better, faster and cheaper than before. The unique advantages of the Polyarc Reactor continue to impress customers and bring value and time saving to a variety of applications and industries.

What the judges say:

"Improves the performance of FID for a range of analytes, in a very simple way."

"Solves a problem that is as old as GC."



11. Pegasus GC-HRT 4D

A marriage of high-resolution time-of-flight mass spectrometry and GC×GC

Produced by LECO

The Pegasus GC-HRT 4D combines the highest performance GC×GC and the most accurate TOFMS on the market together with High Resolution Deconvolution (HRD). Users are able to find more analytes than ever before and identify components with confidence. LECO's integrated all-in-one ChromaTOF-HRT brand software controls all hardware elements, automatically calculates mass accuracies, and identifies second dimension peaks. With innovative features and functions based on years of experience in GC×GC, the software efficiently delivers a great deal of chemical information per sample.

Potential impact

With the integration of two high performance technologies, the Pegasus GC-HRT 4D gives users an unprecedented ability to interrogate complex samples. No matter the industry, from petrochemical to metabolomics, the Pegasus GC-HRT 4D will transform the gas chromatography landscape with its superior sensitivity and peak capacity potential. The Pegasus GC-HRT 4D will help users to fully explore their sample down to the most intricate details (and find what they have been missing), discovering breakthroughs in a variety of markets.

What the judges say:

"Combines two of the most important developments in GC: GC×GC and accurate mass MS."

10. MicroCal PEAQ-ITC

A new generation of isothermal titration calorimeters for quantifying biomolecular interactions

Produced by Malvern Instruments

The MicroCal PEAQ-ITC and MicroCal PEAQ-ITC Automated are sensitive, low volume isothermal titration calorimeters for the label-free, in-solution study of biomolecular interactions. Designed to enhance laboratory efficiency, these calorimeters deliver direct measurements of all binding parameters in a single experiment, using as little as 10 µg of sample. A key feature is the control software and data analysis package, which offers simple operation, enhancing accessibility to life science users.

The MicroCal PEAQ-ITC Automated system has high throughput and the low sample consumption, providing fully walkaway, unmanned ITC measurements. The result is quicker secondary screening, faster hit validation and greater analytical productivity. Integrated MicroCal PEAQ-ITC analysis software offers experiment design simulation, batch evaluation of large data sets, automated assessment of data quality and a streamlined user interface that guides the user to final figures and presentation quality graphs quickly and easily.

Potential impact

ITC is now an essential tool for the life sciences, most importantly in drug discovery where it is used for hit validation and lead optimization. These pioneering new systems increase the robustness of the technique, increase lab productivity and extend accessibility so that even non-experts can routinely generate reliable information. The instrument control software uniquely incorporates all of the tools that the user needs to move efficiently from experimental design to final results, including user-friendly guided workflows with embedded video tutorials. The MicroCal PEAQ-ITC Automated system has the capacity to run four 96-well plates unattended. By combining the excellent data quality and reproducibility with high speed, unattended operation, this system can provide early indications of high quality hits while freeing researchers for other tasks, thereby potentially enhancing the speed and productivity of drug discovery projects.

What the judges say:

"Miniaturization and automation of a powerful tool."

9. PhysioTel HD-XG

A fully implantable telemetry device that continuously monitors blood glucose

Produced by Data Sciences International

The HD-XG is a fully-implantable telemetry device for use in research animals. It allows continuous, real-time monitoring of glucose directly in arterial blood. The implant also continuously monitors body temperature and physical activity, transmitting second-to-second changes in physiology. The glucose sensor is based on a proven technology using glucose oxidase as a catalyst to convert glucose and oxygen into gluconic acid and hydrogen peroxide, which in turn interacts with a noble metal electrode to give up electrons and create a current proportional to the amount of glucose available in whole blood. The HD-XG's primary use is drug discovery and basic research related to diabetes and other metabolic diseases. It is also relevant to other research areas, including drug safety assessment.

Potential impact

With implantable glucose telemetry, researchers are no longer limited to monitoring blood glucose using intermittent sampling with test strips, a method that can miss important events and result in variable data. Implantable telemetry is the gold standard for preclinical physiologic monitoring because it allows researchers to monitor numerous physiologic traits without anesthesia or restraint, decreasing stress to animals while increasing the accuracy of data and allowing for a reduction in the number of animals needed. This new platform will allow development of more accurate disease models, new treatments, and new drugs to improve the quality of life for the increasing population of people with diabetes.

What the judges say:

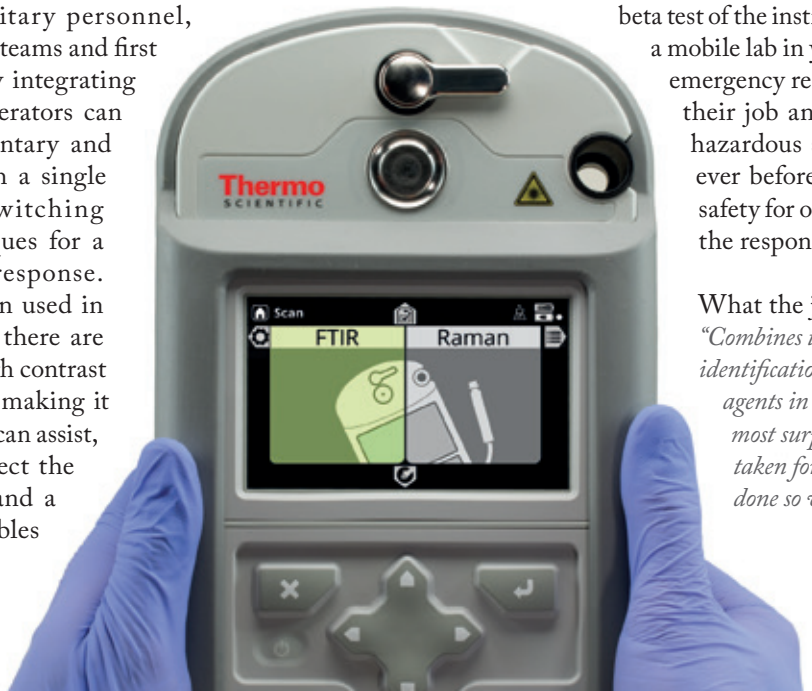
"A clever tool for in-vivo monitoring."

8. Thermo Scientific Gemini Analyzer

A rugged, portable instrument with dual technologies for chemical identification

Produced by Thermo Fisher Scientific

The Thermo Scientific Gemini handheld analyzer is the first to integrate FTIR and Raman spectroscopy in a rugged, handheld instrument for chemical identification in the field. FTIR and Raman spectroscopy are the two leading chemical ID technologies for field-based analysis, widely deployed by military personnel, bomb technicians, hazmat teams and first responders worldwide. By integrating the two technologies, operators can easily conduct complementary and confirmatory testing with a single instrument, quickly switching between analysis techniques for a faster, more confident response. As the instrument is often used in hazardous environments, there are built-in safety controls: high contrast and resistive touchscreen, making it easier for users to operate; scan assist, which guides users to select the appropriate technology; and a motorized anvil that enables Raman and an industry-first FTIR scan delay. The analyzer requires minimal training for proficiency with clear results that eliminate subjective user interpretation.



Potential impact

When elite military forces and first responders need to quickly and safely assess a hazardous situation, they need rugged, compact and easy-to-use instruments for better and fast decision making. The Gemini analyzer is smaller and lighter than two single-technology instruments, and as one EOD (explosive ordinance) technician noted during beta test of the instrument, "it's like having a mobile lab in your pocket." It enables emergency response personnel to do their job and secure a potentially hazardous situation quicker than ever before, leading to improved safety for our communities and for the responders themselves.

What the judges say:

"Combines two critical techniques for identification of potential harmful agents in a single device. What is most surprising is how long it has taken for this to be done – and done so well."

7. Bond Elut Enhanced Matrix Removal – Lipid

A sorbent that selectively removes lipids for efficient, reproducible sample clean-up.

Produced by Agilent Technologies

Current methodology for clean-up of high matrix food samples can be inefficient, time-consuming and/or have high variability in results for LCMS and GCMS analysis. To date, there have been no sample preparation products that effectively remove the most challenging component of complex food samples, lipids, leaving scientists to modify or implement multi-step sample preparation techniques.

In listening to food scientists needs, we have developed a new sorbent, Enhanced Matrix Removal-Lipid, that selectively targets lipids using a rugged, easy to use QuEChERS type protocol. This unique water activated sorbent selectively traps and removes lipids from high fat samples based on two interactions: hydrophobic and size exclusion. Lipids are trapped by the particle due to the long hydrocarbon chains, while most analytes cannot interact with the particle because due to size. The result is a sorbent that can efficiently remove lipids from complex samples, while maintaining high recovery for analytes of interest.

Potential impact

Lipids impact separations and data quality, obscuring target analytes and causing time-consuming review of data. Lipids can also build up, affecting instrument performance, causing ion suppression in mass spectrometric analysis and variability of results.

EMR – Lipid sorbent efficiently removes up to 92 percent of interfering matrix, a considerable improvement upon current techniques. As a result, the separation of target analytes is improved, resulting in faster data analysis, better reproducibility and higher data confidence. Fewer interferences also improves sensitive detection of low-level analytes. Cleaner samples allow for improved instrument performance with less downtime from sample-related maintenance, improving productivity and lab operating costs.

What the judges say:

"The importance of sample preparation is too often ignored. The Bond Elut material removes lipids effectively, addressing a particularly challenging issue in sample preparation."

6. Thermo Scientific Q Exactive GC Orbitrap GC-MS/MS

Gas chromatography combined with high-resolution/accurate mass Orbitrap MS detection for comprehensive sample characterization.

Produced by Thermo Fisher Scientific

The Thermo Scientific Q Exactive GC Orbitrap GC-MS/MS system defines a new chapter in the gas chromatography/mass spectrometry space by combining the power of high-resolution gas chromatography (GC) and high-resolution/accurate mass (HR/AM) Orbitrap mass spectrometry. This technology is designed to advance chemical analyses in laboratories limited by older GC-MS systems. The system offers the highest selectivity in full scan through high resolution, as well as routine delivery of sub-1-ppm mass accuracy for confidence in identification. Add to this the high sensitivity and linear dynamic range for quantitation, and the result is a powerful full-scan GC-MS system.

Potential impact

Thermo Fisher Scientific expects the Q Exactive GC system will allow laboratories to have a much deeper understanding of their samples than they've had before – with the highest degree of clarity. This improved clarity will have a major impact in metabolomic studies, untargeted screening experiments, and sample profiling in a wide range of application areas. Joshua Coon, University of Wisconsin, Madison, applies GC-MS to metabolomic studies to understand complex biological systems. "The introduction of the Q Exactive GC system is a game changer in this space," he said. "The combination of fast, predictable GC separations with accurate mass capabilities will translate to an increased ability to profile entire metabolomes."

What the judges say:

"Accurate mass capability has clearly demonstrated its strengths in liquid chromatography. This instrument is the long awaited expansion into GC."

"Brings a new dimension to GC-MS – especially for the analysis of complex samples, such as those used in metabolomics."

5. MS-PECD

Direct mass spectrometric detection of chiral molecules without any prior enantiomeric separation.

Produced by MassSpecpecD

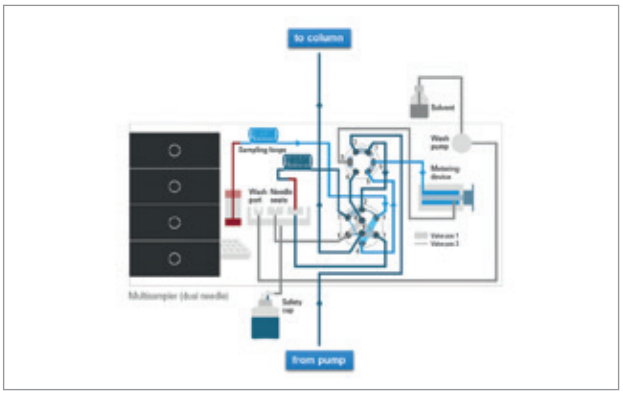
MS-PECD can analyze multi-component mixtures of chiral molecules by direct mass spectrometry using correlated electron-ion imaging. A circular polarized pulsed laser ionizes the gaseous chiral molecules. The three-dimensional angular distribution of photoelectrons is measured on a time- and position sensitive particle detector. The molecular ion is also detected in coincidence with the electron on a time-sensitive particle detector, providing the mass from the time-of-flight. Each electron that is detected is tagged by the mass of the ion that it originates from. The forward-backward asymmetry of the electron distribution along the laser beam (PhotoElectron CircularDichroism, PECD) is measured on the electron-imaging detector in correlation with the time-of-flight of the ion. The (electron, ion) correlation provides the direct MS indentification and enantiomeric excess of the enantiomers present in the multi-component chiral mixture.

Potential impact

- PECD has large enantiomeric sensitivity, on the order of 1-10 percent, a factor of 100-1000 larger than absorption CD, VCD or ROA.
- The correlated mass-tagged PECD gives direct enantiomeric selectivity.
- Direct mass spectrometric measurement of the enantiomeric excess of chiral molecules in multi-component mixtures.
- No prior enantiomeric separation of the sample, like GC, HPLC, SFC or IMS, is needed before MS-detection.
- No prior clustering of the sample with chiral ligands is needed before MS-detection.
- Laser ionization via intermediate vibronically excited states provides additional spectral selectivity, identification and sensitivity.
- The electron kinetic energy provides additional spectroscopic identification and enantiomeric selectivity.

What the judges say:

"Provides simultaneous identification and chirality information – much better then trying to correlate different separations performed for identification or chirality determination."



4. Dual-needle Technology for LC-autosamplers

Two independent flow paths within a single LC-autosampler module

Produced by Agilent Technologies

The Agilent Dual-needle option provides two flow paths within one autosampler by doubling the needle, the sample loops and the needle-seats and by adding a second valve. It allows increased injection cycle speed, providing background activities, such sample prep steps, draw samples, wash injection needles to remove carryover, and so on, all while an actual run is ongoing.

It can also be used to gain flexibility by adding two different sample-loop volumes (for example, 20 µl loop on one side and up to 500/900 µl on the other port), which allows switching from small analytical injections at minimized system delay volumes to large injections without a need to change hardware.

Scientists now have two injection ports to either use separately for specific applications or to reserve one as an ultra-clean reference port.

Potential impact

The Agilent Dual-needle has shown already close to 60 percent time savings for a sequence of analytical runs with smart overlapped injections and automated column regeneration when compared to the same Agilent Multisampler using a standard single injector port.

The flexibility aspect with two different sample volumes allows for very large linear dynamic range of injections using the same instrument and calibration avoiding comparison of analysis done by two systems or at least two different hardware setup of the same machine.

What the judges say:

"This innovation looks very simple, but simply addresses a complex problem."

"This development increases the versatility of LC instrumentation – and that is good; LC itself is much more versatile than current LC instrumentation, which requires frequent reconfiguration of instrumentation."

"Solves the real problem of the rate-limiting step in high throughput LC."

3. Thermo Scientific Orbitrap Fusion Lumos Tribrid Mass Spectrometer

A high-performance mass spectrometer with enhanced sensitivity

Produced by Thermo Fisher Scientific

The Fusion Lumos Tribrid mass spectrometer is designed to achieve proteome-wide coverage by combining the versatility of a tribrid system with the selectivity of Orbitrap technology. The instrument sets new standards for performance for the most challenging research applications in advanced proteomics, biopharma and metabolomics.

The instrument features enhanced sensitivity resulting in improved analyte detection, characterization, and quantitation, enabling scientists to perform more comprehensive sample analyses faster and with better accuracy than ever before. It incorporates:

- a brighter ion source for increased sensitivity
- a segmented quadrupole mass filter with improved selectivity and ion transmission
- Advanced Vacuum Technology for improved ion transmission of high molecular weight ions to the Orbitrap mass analyzer
- higher-capacity electron transfer dissociation (ETD) fragmentation.

The Tribrid instrument excels in the most challenging applications, including analysis of low-level post translational modifications, multiplexed relative quantitation using isobaric tags, intact protein characterization, as well as MSn analysis of small molecules.

Potential impact

Scientists rely heavily on data generated from mass spectrometers and require the most advanced technology for deep sequencing analyses. The more sensitive the mass spectrometer, the more accurate the resulting data, which contributes to a more comprehensive analysis of proteomic samples. The advanced sensitivity, and features to improve structural analysis and characterization, enable scientists to gain more expansive and in-depth analytical information; a more comprehensive analysis of proteomic samples can be undertaken, with the multiplex capabilities supporting simultaneous protein quantification. Furthermore, the Fusion Lumos system provides fast and deep proteoform-resolving measurements of samples, including clinical samples to facilitate translational research.

What the judges say:

"Thermo Fisher Scientific continues to innovate with Orbitrap technology – and [the Fusion Lumos Tribrid] is no exception, taking proteomics analysis to a new level in terms of sensitivity and speed."

2. REIMS Research System with iKnife Sampling

A direct sampling ionization technique combined with high performance time-of-flight MS

Produced by Waters

The iKnife hand-held sampling device produces information-rich vapor directly from the sample surface. When analyzed by time-of-flight MS, this provides analysts with an accurate molecular profile in seconds. No sample preparation or chromatography are required, and, by using powerful multivariate statistics tools, users can quickly determine differences within and between samples, and identify molecular markers responsible for these sample differences.

Potential impact

Removing the need for sample preparation and chromatographic separation has the potential to make a huge impact on the time and money required to analyze large numbers of samples by MS. When combined with multivariate statistical analysis, users across a range of disciplines, such as food research, tissue research, and microbiology research, can quickly and easily differentiate samples from one another and confidently identify the differentiating features, allowing greater insight into chemical and biological systems.

The unique handheld sampling device achieves accessibility and ease of use in a way that no other MS technique has done before, with the long, flexible connection between the sampling device and the MS allowing the user to bring the analysis directly to the sample.

What the judges say:

"This is a potential game changer in terms of real-time sampling and practical analysis."

"Sample preparation is difficult, especially if the location of compounds in the sample is also relevant. The iKnife allows easy sampling while simultaneously providing important information on the location of compounds."

1. Full Spectrum Molecular Imaging

A combination of advanced MS imaging technologies, designed to deliver high quality, comprehensive, spatially resolved molecular information.

Produced by Waters

Combining three technologies (MALDI Imaging, DESI Imaging and Ion Mobility) along with high-performance time-of- flight mass spectrometry and powerful informatics tools, Full Spectrum Molecular Imaging delivers multi-layered, information-rich data from a single sample.

Providing more comprehensive, detailed information than from any individual imaging technique, Full Spectrum Molecular Imaging extracts maximum information from minimal sample, enabling research scientists to definitively and objectively interpret molecular distribution information.

Potential impact

The choice of complementary ionization techniques, combined with high performance ion mobility separation and high resolution MS, provides a more complete and comprehensive picture of the sample than with any individual imaging technique, through mapping the spatial distributions of a range of molecule types, including small molecules, drugs and metabolites, lipids and peptides.

Full Spectrum Molecular Imaging therefore has the potential to expand the use of MS imaging across a wide variety of disciplines, from enhancing capability for established applications in health sciences (for example, histopathology research) and pharmaceuticals (for example, DMPK drug distribution studies) to opening up innovative new application areas in the food and environmental and chemical materials fields.

An intuitive, fully integrated software workflow covering experiment set-up, data acquisition, processing and visualization further enhances accessibility and enables scientists to translate complex samples into meaningful answers faster and easier than ever before.

What the judges say:

"Combines a range of MS imaging technologies to improve data analysis capabilities for complex applications – it has the potential to make imaging techniques truly useful."

"In addition to knowing which compounds are present and at what levels, it is crucial to understand where the molecules are in the sample. MS imaging allows us to get that information."

"A powerful combination of MS imaging modes."

Product Showcase

The Multifaceted Diode Array Detector AZURA DAD 2.1L

The KNAUER AZURA DAD 2.1L diode array detector with innovative cartridge flow cell design covers an extensive application range from nano to process liquid chromatography (LC).

By means of straightforward and swift flow cell exchange, this detector can be optimized within seconds for highly sensitive analytical UHPLC/HPLC or for in-line detection at high flow rates (> 10 L/min). Furthermore, with the aid of a world-first fiber optics adapter in cartridge design, the flow cell can be spatially separated from the device up to 10 meters. Key applications of this remote flow cell technology include enhanced security for explosive, radioactive or toxic applications; detection at high temperatures (100 °C); and flexible flow cell installation.

The Berlin based company KNAUER develops and manufactures liquid chromatography equipment for analysis and purification, as well as dosing pumps and flow-through detectors.

www.knauer.net/detectors

KNAUER

BenchTOF-Evolve – high-performance time-of-flight mass spectrometer for GC

A time-of-flight mass spectrometer for gas chromatography delivering 'SIM-like' sensitivity with full spectral information, while keeping your familiar user interface.

BenchTOF-Evolve changes the way in which you think about TOF MS. Its outstanding performance for GC applications, unbeatable productivity and enhanced quality of results come as standard, and its original modular design enables it to provide the flexibility to meet the demands of increasingly complex applications. It expands your laboratory's capability whilst retaining your existing GC–MS workflow and data-processing packages.

Complemented by powerful deconvolution software, BenchTOF-Evolve gives you robust quantitation of trace-level targets and confident identification of unknowns in a single run – making it ideal for routine but challenging applications, such as air monitoring and forensic analysis.

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EXPLORING CHIRALITY IN OUTER SPACE

What is the origin of stereochemical bias – terrestrial autocatalytic processes, extraterrestrial contamination or otherworldly intervention? Here, I review the gas chromatographic tools being used in the search for homochirality in space – the final frontier.

By Volker Schurig, Institute of Organic Chemistry, University of Tübingen, Germany.

Dedicated to the late Professor Emanuel Gil-Av – the pioneer of modern enantioselective chromatography – on the occasion of his centenary in 2016.

Stereochemical bias is considered to be one of the preconditions for the formation of life on Earth. Yet even in our third millennium, we do not know how the preference of the image over its incongruent mirror image was achieved – a phenomenon called molecular homochirality, single-handedness or symmetry-breaking. It is also unclear why evolution exclusively selected L-amino acids and D-sugars as homochiral building blocks of proteins and nucleic acids in all living species, including viruses, bacteria, plants, animals and humans.

The discrimination of chiral biogenic molecules, called enantiomers, may have occurred on Earth by autocatalysis, or may be the result of extraterrestrial contamination with homochiral molecules (caused by the existence of circular-polarized light in interstellar space) or, less likely in my opinion, as a result of parity-violation energy differences. Therefore, various space missions are under way – or are planned – to detect extraterrestrial homochirality. For this challenge, enantiomers, which possess strictly identical (nonchiroptical) properties in a nonchiral symmetric environment, must be resolved. Consequently, the current Rosetta- and Exo-Mars-missions are equipped with enantioselective gas chromatographic columns containing chiral stationary phases (CSPs) to separate and detect volatile enantiomers as biomarkers of life (1, 2).

BREAKTHROUGHS IN ENANTIOSELECTIVITY

The first direct separation of enantiomers by gas chromatography (GC) was described by Emanuel Gil-Av and coworkers in the year 1966 (see Figure 1). They resolved enantiomers of the N-trifluoroacetyl-O-alkylesters of the proteinogenic α-amino acids alanine, valine and leucine on a glass capillary column (100 m x 0.25 ID) coated with the optically-active CSP, N-trifluoroacetyl-L-isoleucine-O-lauryl ester (3). Scientists of the Weizmann Institute in Israel subsequently – and efficiently – mimicked the selective peptide-enzyme interaction based on hydrogen-bonding (4, 5). In 2016, we will celebrate the 50th anniversary of the development of modern chromatographic enantiomeric separation. The Gil-Av approach was consequently used to investigate extraterrestrial material; however, no amino acids were found (at a detection limit of 0.1 ppm) by NASA in lunar samples from the Sea of Tranquility (6).

Another concept for chirality recognition in GC in the realm of metal organic chemistry was also developed at the Weizmann Institute, where the enantiomers of the olefin 3-methylcyclopentene could be resolved on optically-active CSP dicarbonyl-rhodium(I)-3-trifluoroacetyl-(1R)-camphorate (7). The subsequent use of metal(II) ions started the development of chiral complexation GC for the enantiomeric study of chiral pheromones, flavors, fragrances, as well

Figure 1. Three early promoters of enantioselective GC. Ernst Bayer (left), Emanuel Gil-Av (middle) and Volker Schurig (right) at the 3rd International Symposium on Chiral Discrimination, Tübingen, Germany, 1992.

as oxiranes formed by enantioselective epoxidations and on-column enantiomerizations of configurationally labile racemates (8).

A third – nearly universal – tool in enantioselective GC is the use of alkylated/acylated cyclodextrins coated on high-resolution fused silica capillary columns (9, 10). Almost all classes of volatile chiral compounds can be resolved, including unfunctionalized saturated hydrocarbons devoid of any chemical functionality, such as the racemic methylethyl(i) propylmethanes C*HMeEtPr and C*HMeEtiPr (11). In particular, the resolution of chiral alkanes commands interest of the forthcoming search for extraterrestrial homochirality (12). The Cassini-Huygens mission on Saturn's moon Titan detected methane and higher hydrocarbons and chiral entities may either be racemic or enantiomerically enriched.

A breakthrough in enantioselective GC was achieved by Frank, Nicholson and Bayer (see Figure 1) at Tübingen University when they chemically linked the chiral selector N-acyl-L-valine t-butylamide (5) to polydimethylsiloxane (see Figure 2) thus combining the enantioselectivity of valine with the universal gas chromatographic properties of liquid silicones. On the CSP Chirasil-L-Val (coated on an 18 m x 0.3 mm ID glass capillary column) 17 proteinogenic α-amino acids could be simultaneously enantioseparated as N-pentafluoropropanoyl-O-isopropyl esters in less than 30 min (13). All L-amino acids are eluted as the second fraction, but the elution order can be reversed by employing Chirasil-D-Val. Chirasil-Metal (see Figure 2, middle) can be used as the CSP in GC and supercritical fluid chromatography (SFC) (14).

INVESTIGATING ENANTIOMERIC EXCESS

In Chirasil-β-Dex, permethylated β-cyclodextrin is chemically bonded via an octamethylene spacer on polydimethylsiloxane (see Figure 2, right) (14). Its temperature range extends from -10°C to 250°C. One single column (80 cm x 0.5 mm ID) coated with thermally immobilized Chirasil-β-Dex can alternatively be

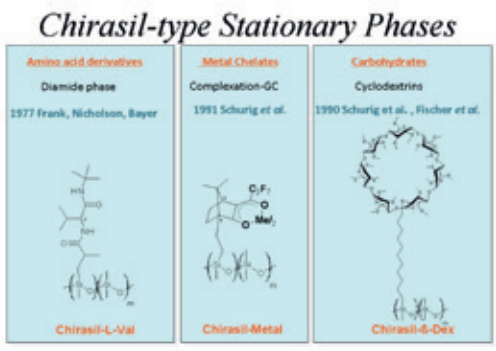

Figure 2. Development of Chirasil-type stationary phases for enantiomeric separations by GC.

used in GC, SFC, liquid chromatography (LC) and capillary electrochromatography (CEC) for the same racemic compounds (in other words, it's a unified approach) (15). In samples from the Murcheson- and Murray meteorites, Chirasil-β-Dex has been employed to detect enantiomeric excess of up to 15.2 percent for L-isovaline (2-amino-2-methyl-butyric acid) (16). The extraterrestrial origin of the enantiomeric bias has been proved using isotopic analysis by GC-combustion isotopic ratio mass spectrometry (GC-C-IRMS) (16).

Chirasil-β-Dex has also been used to correlate dextro-rotatory glyceraldehyde, the key reference compound of stereochemistry, with the absolute configuration of R,R-trans-2,3-dideuterooxirane determined by the novel method of Coulomb explosion imaging (17). Emil Fischer's arbitrary assignment of D-configuration for (+)-glyceraldehyde was thus confirmed once and for all: sugars are D-configurated and α-amino acids are L-configurated on Earth!

In the binary CSP Chirasil-Val-Dex, two complementary selectors are attached to polydimethylsiloxane, allowing a broad enantioseparation spectrum that includes racemic hydrocarbons and derivatized 2-amino acids, which are simultaneously enantioseparated (see Figure 3) (18).

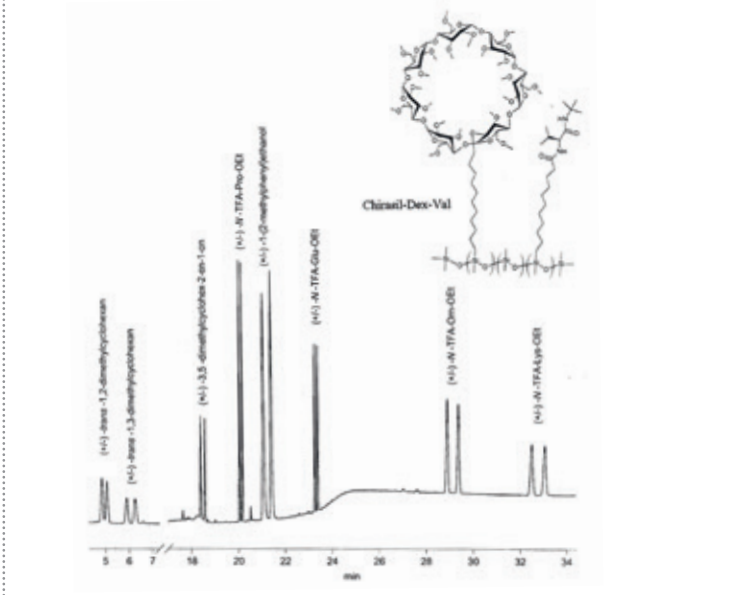

Figure 3. Simultaneous GC enantiomeric separations (signal ratio 1:1) of racemic cycloalkanes, a ketone, an alcohol and the 2-amino acids proline, glutamic acid, ornithine and lysine (as N-trifluoroacetyl-O-ethyl esters) on Chirasil-Dex-Val (insert) on a fused silica capillary (20 m x 0.25 mm ID x 0.25 µm CSP layer) with temperature program and dihydrogen as carrier gas (18).

WHERE NO MAN HAS GONE BEFORE

The European Space Agency (ESA) Rosetta mission and the landing of the robot Philae on the comet 67P/Churyumov-Gerasimenko (nicknamed Chury, pictured on opening page) was awarded 'Breakthrough of the Year 2014' by the American Association for the Advancement of Science (19). The comet Chury is considered to be a remainder from the formation of the solar system 4.6 billion years ago – and as such, it may serve as a model of primordial Earth for bio-astronomers.

As a note for history enthusiasts, the ambitious mission by ESA was named after the inscription-covered Rosetta stone and the temple obelisk Philae, which helped Jean-Françoise Champollion to decipher the Egyptian hieroglyphs in 1822.

Rosetta was launched on March 2, 2004 and Philae landed on the comet on November 11, 2014 at a distance of 510 million kilometers from Earth – signal transmission at that distance takes about half an hour! The Rosetta orbiter and Philae lander are equipped with ten miniaturized measuring devices endowed with low energy consumption.

To detect enantiomerically enriched chiral molecules in interstellar space, GC is the method of choice. It is devoid of liquid mobile phases, instrumentation is simple and shock-resistant, the combination with mass spectrometry (GC-MS) is legion, miniaturization is feasible and due to the enormous separation power of high-resolution capillary GC, multicomponent analysis is straightforward.

GC-MS AT 38 KM/S (TRULY FAST GC)

In fact, Philae contains two GC-MS systems. The British project, Ptolemy, employs three capillary columns (you can read a little more about its inception here: tas.txp.to/1215/

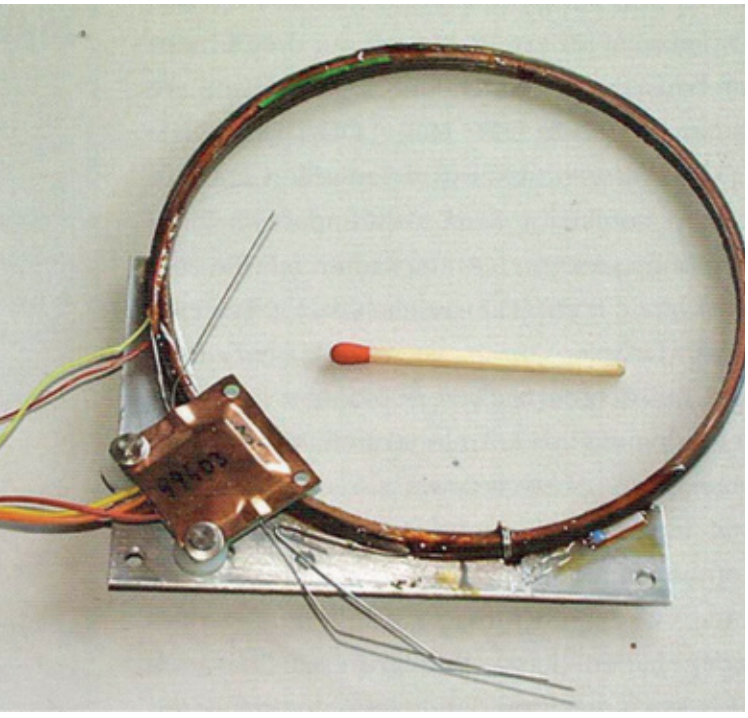

Figure 4. Fused silica capillary column including heating device and thermo conductivity detector as installed on the chirality module of the COSAC instrument onboard Rosetta's lander Philae (Evans). Courtesy of U. J. Meierhenrich.

Ptolemy), but I'd like to focus on the Cometary Sampling and Composition (COSAC) project, which was developed at the Max-Planck-Institute for Solar System Research, Göttingen, Germany. COSAC is based on a GC-time-of-flight (TOF)-MS system (with a mass range of 1-1500 amu), which can analyze samples delivered by the sample drilling and distribution system (SD2) (20, 21). COSAC can also operate in a "sniffing mode", in which the MS accumulates data without active sampling from SD2. COSAC employs a sampling oven heated up to 180°C and a pyrolysis oven, which can reach temperatures of 600°C. The gases originating from the heated samples are analyzed utilizing eight 10–15 m capillary columns connected in parallel, three of them coated with CSPs. The GC uses helium as the carrier gas (refined valve connections are used to keep the helium consumption at a minimum) and is coupled to a thermo conductivity detector.

It was reported in July 2015, that 25 minutes after Philae's initial contact with the cometary nucleus, COSAC carried out its first chemical analysis in the sniffing mode by examining particles that were passively entering the instrument. Sixteen compounds were identified, divided into six classes of organic molecules (alcohols, carbonyls, amines, nitriles, amides and

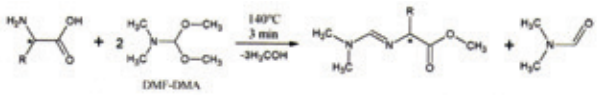

Figure 5. Derivatization of α-amino acids with DMF-DMA (26).

isocyanates). Of these, four were detected for the first time on a comet (methyl isocyanate, acetone, propionaldehyde and acetamide) (22). Investigators concluded, "the complexity of cometary nucleus chemistry and the importance of nitrogen-containing organics imply that early solar system chemistry fosters the formation of prebiotic material in noticeable concentrations..." (22).

Specifically for chirality experiments, COSAC was equipped with three fused silica columns coated with CSPs (20, 21, 23), see Figure 4. Chirasil-L-Val was chosen for chiral α-amino acids and Chirasil-β-Dex was selected for chiral hydrocarbons. Non-bonded 2,6-O-dipentyl-3-O-trifluoroacetyl-y-cyclodextrin (CD-G-TA) (24) was selected for unspecified compounds. In contrast to Chirasil-L-Val, the cyclodextrin selectors are not prone to radio-racemization (25). Unfortunately, native amino acids are involatile and have to be derivatized prior to GC analysis. The traditional two-step protocol to form N-perfluoroacyl-O-alkyl esters appeared unsuitable for space experiments. Hence, the one step reaction with N,N-dimethylformamide/O,O-dimethylacetal (DMF-DMA) (see Figure 5) was developed (26). Notably, only valine, isoleucine, aspartic acid and phenylalanine can be resolved using this method. The Chirasil-β-Dex column was operated shortly after Philae's touchdown on Chury (Uwe Meierhenrich told me), but no data have been disclosed by ESA. Subsequent measurements will only be possible when the batteries of Philae – the lander, which is currently lying dormant – are recharged at an elevated solar altitude. No news on this topic is currently forthcoming...

TO JUPITER... AND BEYOND?

Polymeric Chirasil-β-Dex is insensitive to radiation existing in interstellar space and is considered to be the optimal CSP to detect homochirality on Mars, being exclusively applied for current Mars-science laboratory (MSL) missions (27). Exo-Mars 2018 is a joint mission by the ESA and the Russian Federal Space Agency (Roskosmos) – but the gas chromatography element is being provided by the French space agency, CNES. CNES' Mars Organic Molecule Analyser (MOMA) uses Chirasil-β-Dex in a stainless-steel capillary column and uses helium as the carrier gas and also contains a DMF-DMA kit for the derivatization of amino acids and

hydroxycarboxylic acids (26). Chirasil-β-Dex CSP has also been proposed for GC experiments in the planned NASA mission to Jupiter's moon, Europa.

Whether robotic chirality-experiments in space will succeed is still a matter of conjecture, especially given that the resolution of mirror-image molecules represents a non-trivial task even in earthbound and manned laboratories! But given that our astronautic activities may lead to contamination of the universe with man-made organic material, mass spectrometric isotopic analysis will be required to prove the foreign origin of molecules detected in comets, moons and planets. Whatever the outcome, I believe that the challenge of performing chirality experiments in interstellar space is at least likely to stimulate important terrestrial applications!

Note: fused silica columns coated with Chirasil-β-Dex were first commercialized by Chrompack International, Middleburg, The Netherlands. The brand was later transferred to Varian Inc. and finally to Agilent Technologies.

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Protecting Our Most Precious Resource: Water

New analytical capability can have a significant impact on research direction. In environmental analysis, high-resolution accurate mass (HRAM) mass spectrometry is allowing us to explore uncharted aspects of our increasingly complex chemical world.

In conversation with Heinz Singer, Group leader of Environmental Analytical Chemistry, Eawag - Swiss Federal Institute of Aquatic Science and Technology, Switzerland (by Rich Whitworth).

I've been at the department of environmental chemistry at Eawag for 18 years, though I am very much an analytical chemist at heart. Environmental analysis demands highly sensitive and reliable methods and I love to develop such methods, so my current role is an excellent fit. My interest in analytical techniques is very much linked to the fact that I've always been a technophile – I am fascinated by the capabilities of new technology and systems. René Schwarzenbach, a professor of environmental chemistry at ETH Zurich, also set me off down the right path. I was René's first diploma student and his ambitious and motivated character was infectious.

We all know (but possibly don't often consider) that clean water is our most precious resource. At Eawag we are constantly investigating concepts and technologies that help the world deal sustainably with water bodies. Indeed, we only have one focus at Eawag: water. But many different disciplines – for example, microbiology, engineering, analytical chemistry – must work together to find solutions, which makes Eawag a fantastic place to be. The importance of water will only grow in the future; we use more water than ever before, we're living in an increasingly chemical world, and water is a great solvent.

Hot trends

Around five years ago, people used to believe that we'd learnt all we could about pesticides in water and that we didn't need to push analysis much further – it almost seemed an old-fashioned research area. But I realized that was simply not true. By their very nature, pesticides are designed to harm life in some way, which makes pesticide analysis highly relevant in water analysis – particularly in countries where regulations are less strict. Three challenges drive my interest in this area: (i) the large number of analytes, (ii) low ecotoxicological limits, and (iii) highly dynamic (rain-driven) concentration ranges.

More broadly, the screening of unknown compounds is another hot area right now. There are still unknown compounds in our water, and I don't doubt that they are important. New analytical tools are allowing us to investigate these hidden pollutants like never before.

But perhaps the hottest topic right now is contamination from industrial point sources. At the border between Switzerland and Germany there is a monitoring station, operated by the Cantonal Office of Environment and Energy Basel-City, that conducts non-targeted screening on the river Rhine using our methods and we occasionally witness huge spikes over a short period of time. Contaminants include pharmaceuticals, pesticides, and intermediates of chemical synthesis – and the load can be significant. Many researchers believed this particular problem had been solved by restrictions on industrial wastewater release, but our newfound ability to conduct non-targeted screening has proven us wrong. Evidently, we were not always looking for the right compounds of interest. We've been concentrating on risk assessments based on usage and modeling – but that is clearly not sufficient.

Monitoring industrial point source contamination is particularly challenging because it not only encompasses a huge universe of potential chemicals, but it is also dependent on time and space. Tools that allow us better coverage in terms of all aspects are therefore important.

Pesticides that are not introduced by industrial processes also exist in this complex analytical space. As noted above, concentrations in surface water are highly dependent on time (increasing with rain fall) and also location (not all areas have the same amount of agricultural land, and different crops require the use of different pesticides). This complexity – and the diverse range of pesticides in our environment – stretches our methods to the limit. Moreover, it means that choosing the right sampling technique is paramount.

What's in a sample?

There are essentially two kinds of sampling devices: passive and active. Passive sampling devices are exciting because they can perform sampling and enrichment at the site of sampling (wherever they are needed) and are easy to use. Plus, with the right kind of sorbent material, you can collect both polar and non-polar compounds. Passive sampling results in a time-weighted composite sample, but quantitation demands complex calibration because sampling rate is dependent on river flow, temperature and other factors – so they are not perfect. Active samplers, on the other hand, are more difficult to use, but are the method of choice for quantitative measurements.

Robotic sampling devices that can

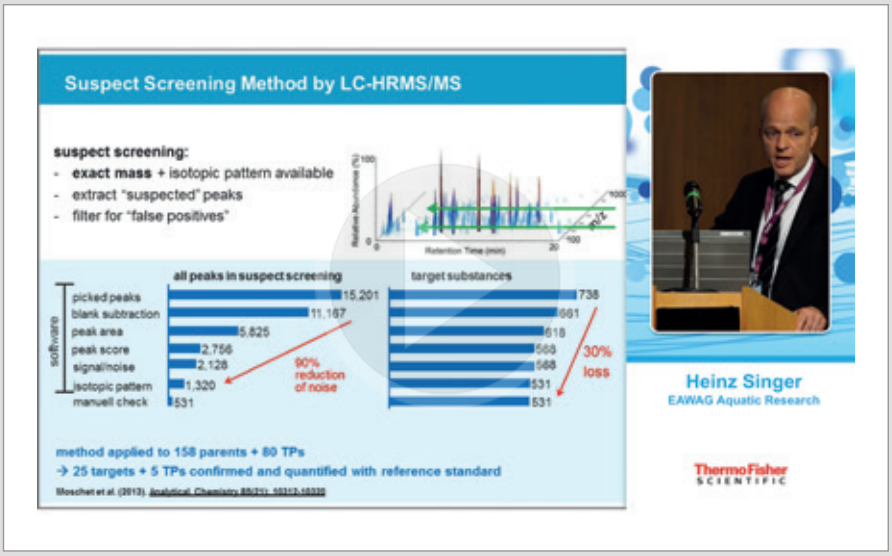
patrol areas or be remotely controlled are likely to present the future of sampling – and some research groups are already experimenting with such technology. An added advantage of remote controlled drones is that you can take horizontal or vertical profiles, which can be important in deeper water bodies, such as lakes. On-board sensors can capture other data and GPS can provide automated and exact location logging. At some point, on-board mass spectrometers would be great for continuous monitoring – but we may have to wait quite a while for that...

And though sampling is clearly important, the power of the analytical instrumentation available to us is critical.

HRAM power

Currently, we rely heavily on LC-Orbitrap™ technology with its combination of accurate mass at very high resolution. The latter is particularly important because it allows you to extract an analyte of interest from a full-scan data set. Moreover, even after measurement, if a new target analyte comes to light, you can go back to the data set and search for that compound. Such retrospective screening essentially means that the number of target analytes is unlimited. And of course, the full-scan nature of the data (with accurate mass and MS/MS information) really lends itself to our non-targeted screening approaches.

I would go as far as to say that the power of this technology has changed our field over the last ten years. We were lucky because we had one of the first Orbitrap-based systems in environmental research (in around 2006) – and the high-resolution capability has really driven our research into new directions. Of course, none of the benefits of HRAM MS would be useful without the sensitivity needed in environmental analysis – and selectivity and reliability are also key. Fortunately, Orbitrap technology ticks these boxes, which is why we have three systems in our lab.



Watch Heinz Singer's presentation at the 1st International symposium on Recent Developments in Pesticide Analysis: http://tas.txp.to/1215/Singer

The unusual suspects

Our work on screening for unexpected compounds sits somewhere between targeted analysis and non-targeted screening. Essentially, we are focusing here on compounds that we believe could end up in the water cycle (through usage data and chemical properties), but for which we might not have standards or even MS spectra available. We can create a list of suspect compounds and then search our full-scan accurate mass data set for potential matches.

Of course, the matching is not straightforward, but using software (blank subtraction, peak area/score, isotopic patterns, and so on) we can reduce the noise level in suspect peaks. In my presentation at the first International Symposium on Recent Developments in Pesticide Analysis in Prague, Czech Republic (online at http://tas.txp.to/1215/Singer) I showed how we can reduce noise by 90 percent while losing only 30 percent of our target substances. For example, we know that pharmaceuticals are used widely in huge amounts, but we only have around 130 on our target list. By assessing 1000 active ingredients using our method, we could identify a limited list of suspect peaks, 60 percent of which we were able to confirm and quantify using reference standards. The result? Thirty or so pharmaceuticals that have never been detected before; some were brand-new blockbuster drugs and others were from manufacturing point sources. In fact, we were surprised to identify drugs that are not even registered for use in Switzerland because they were actually being produced for the global rather than local market.

Addressing blind spots

Environmental monitoring programs are somewhat limited by the fact that we are typically looking for compounds that have been detected by previous monitoring campaigns, and I believe this self-evaluating cycle has created many blind spots. But new technology can increase our scope. For example, increased sensitivity allows us to investigate insecticides, which although not used in large quantities are highly toxic.

Certainly, at Eawag we are always on the look out for new technology that increases our analytical capability – there is no single system that can satisfy all our current and future analytical needs. To that end, it's important to work with a constantly updated toolbox, selecting the best tools for the analytical task at hand.

I strongly believe that fully understanding and embracing new technology can shape our research and allow us to move into previously uncharted territory – and that is the most exciting place to be!

Raising the Bar for Routine Analysis

The Pesticide Explorer Collection comprises four complete workflows that meet the challenges of modern pesticide residue analysis. High-resolution, accurate mass measurements – courtesy of Orbitrap™ technology – represent the ultimate solutions for laboratories that want to take routine analysis to the next level.

We previously introduced the Pesticide Explorer Collection and shared details of the "Standard Quantitation" (see tas.txp.to/1215/standardquan) and "Premium Quantitation" packages (see tas.txp.to/1215/premiumquan). In the final article, we introduce the "HRAM Quantitation" and "HRAM Screening and Quantitation" solutions, both of which benefit from the analytical power of the Thermo Scientific™ Q Exactive™ Focus MS system.

Definitive quantitation

The Orbitrap-based "HRAM Quantitation" configuration uses the Thermo Scientific UltiMate™ 3000 LC system as the separation platform – as do all Pesticide Explorer Collection solutions – but differentiates itself with high-resolution, accurate mass analysis – a unique capability that enables quantitation without compromise in sensitivity, accuracy, precision, and linear dynamic range. When it comes to the complex matrices often encountered in food analysis, high resolving power is particularly useful because it overcomes the masking effects of isobaric interferences, allowing detection of pesticides at very low concentrations.

As with all packages of the Pesticide Explorer Collection, HRAM Quantitation comes with all the workflow components needed, from consumables (including the QuEChERS sample preparation reagent kit and HPLC columns), essential hardware and software. The complete package facilitates method development and ultimately enables fast, accurate and cost effective routine pesticide determinations.. Indeed, pre-configured instrument methods for targeted quantitation enable you to start acquiring data with a lot less time and effort – one of the main focal points during development of the collection, according to Dipankar Ghosh, Global Director for Environmental, Food Safety & Industrial Markets at Thermo Fisher Scientific.

When it comes to data analysis, the addition of the HRAM Spectral Fragmentation Library (fully integrated and searchable using TraceFinder™ software) – with over 2,600 compounds and more than 15,000 spectra – gives you the ability to identify compounds with speed and confidence.

Adding non-targeted screening to the mix

The high-resolution accurate-mass MS/MS spectral library is also key for "HRAM Screening and Quantitation" as it also facilitates screening of non-targeted compounds. But in the ultimate Pesticide Explorer package, it is joined by two other powerful pieces of software: Thermo Scientific Compound Discoverer™ and SIEVE™. Compound Discoverer includes an extensive set of tools to ensure confident compound identification and structural elucidation. And SIEVE enables label-free, semi-quantitative differential analysis of complex LC-MS datasets, allowing you to reproducibly identify components with statistically significant inter-sample differences.

Naturally, it's not all about the software; the HRAM Screening and Quantitation package also fully exploits the power of the Q Exactive Focus system, which allows targeted quantitation and non-targeted screening from a single dataset. With MS/MS HRAM analysis, no sample-specific method optimization is necessary, and the risk of missing important non-targeted compounds is greatly reduced. Once the data has been acquired, it can be reanalyzed retrospectively without the need for sample reinjection.

Ghosh notes the upcoming nature of non-targeted methods, "Though our triple quadrupole MS-based solutions excel in targeted pesticide analysis, the Q Exactive Focus unlocks the door to unknown screening in routine environments, using the power of Orbitrap technology. This is of increasing importance given the globalized nature of the food industry. And, of course, this capability extends well beyond pesticides."

And as Kate Mastovska stated in a recent article on the never-ending challenges of pesticide analysis (visit http://tas.txp.to/1215/Mastovska), "When we consider our ever-expanding list of compounds in our target list (right now, we are currently validating a method that looks at over 500 compounds), the ability of HRAM-MS systems to perform non-targeted analysis starts to look increasingly attractive."

For more information on the Pesticide Explorer Collection, visit: http://tas.txp.to/1215/explorer

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Getting your work published in a high-quality, peer-reviewed journal isn't easy. But if you follow these 40 tips, you could at least avoid common errors that frustrate reviewers.

By Steven Lehotay

I am a frequent reviewer for many analytical science journals, and I love to read a well-organized and well-written manuscript about an interesting study that could be useful to others. I prefer to help authors improve their work rather than recommending rejections, and I appreciate truly applicable work more than "novel" research conducted just for the sake of publication. My favorite recommendation is to "accept as is," but I've experienced this pleasure too few times as a reviewer (or author!) in my career. Moreover, I used to say "yes" to all review requests, but I've had to become more selective lately because the task has too often become a time-consuming grind.

To help reduce reviewer fatigue from submissions requiring too many revisions, I would like to share some common problems that I encounter in manuscripts. For a review of the basics, you can refer to several excellent tutorials about scientific publishing by Kamat et al. (1–4). If you follow the advice, you will save a lot of time and reduce frustration for all involved (the editors, reviewers, readers – and yourself). Realize that everyone is busy – and most journals are inundated with submissions – so a lack of time is not an acceptable excuse for substandard effort in preparing manuscripts.

Beginning with the assumption that the work meets the scientific and ethical standards of the journal, I share the following common examples of mistakes to avoid, including some tips for publishing success.

To the letter

1. Follow the author instructions for the journal. After all, the ability to follow instructions is expected from professionals.
2. Use page numbers and line numbers in the manuscript. As a reviewer, I am annoyed if I can't easily refer to page and line numbers for revisions.

To the point

3. Devise the shortest title possible without using acronyms to convey the purpose and main aspect of the study.
4. The abstract must be a single paragraph capturing the highlights of the work within the journal's word limit.

Reflective referencing

5. Read the literature! Choose high-quality papers. Don't just cut and paste random references from online search services.
6. Look through the references from notable papers to find the original work to cite.
7. Cite good review articles when available rather than several articles on the same topic.
8. Include citations from the journal to which you're submitting (or submit to the journal that you cite the most in your manuscript).
9. Avoid application notes and websites if peer-reviewed papers are available.
10. Double check the numbering and accuracy of all references before submission, know the difference between first and last names, and remove the superscript "a" and/or "*" from author names when cutting and pasting.

Review (and revise) before submission

11. Unless you want to irritate reviewers, read closely and revise your own manuscript at least three times before submission. Ask

trusted colleagues to review it, too.
12. Eliminate obvious grammatical errors, even if you're not writing in your native language. Word processing software typically marks misspelled words, ungrammatical sentences, and poor diction. So, pay attention to the highlights and fix mistakes.

Form and structure
13. Write the first draft from an outline, not rambling text.
14. Organize the work in focused sections and paragraphs, and then remove trivialities and redundancies.
15. Be concise and just give pertinent background information in Introduction, relying on citations to previous work. Unless the article is a review or tutorial, most readers already know the background and subject matter (sometimes better than you).
16. Don't exaggerate the importance of the topic or novelty of your work.
17. Avoid repetition of marketing hyperbole from vendors.

Attention to acronyms
18. Define and use acronyms properly. Don't capitalize words when defining an acronym unless the word is normally capitalized.
19. Once defined, always use the acronym afterwards – and don't define acronyms if they aren't used again.

Make it easy on the reader
20. State the aim of the study clearly in the last paragraph of your introduction ("Our intent for conducting this work was…"). Do not give a summary of what was done – save those points for the abstract and conclusions.
21. Most readers just look at the abstract and tables/figures in publications. Put effort into presenting the most interesting aspects of the work into figures with clearly labeled axes, units, lines, symbols, error bars, and legends that can be seen from a distance (no reader wants to use a magnifying glass).
22. Captions should contain enough information for the reader to understand what is presented without having to study the text, including the number of replicates.

"My favorite recommendation is to "accept as is," but I've experienced this pleasure too few times as a reviewer (or author!)"

Save time and space
23. In the text, don't merely repeat information given in figures and tables, but explain the results if needed. Simply refer to the clearly presented figures and tables and let the information speak for itself.
24. Conserve journal space by presenting only useful information to the reader in tables, and combine similar tables when possible by using landscape layout.
25. Don't include calibration equations.
26. Use supplemental information for long tables listing analytical parameters.
27. Avoid too many significant figures; few analytical methods can actually distinguish 80.1% from 80.2% recovery, or 2.5% from 2.4% RSD, or 187.5 from 187.6 ng/g. Give results to the nearest integer or two significant digits (e.g., 80% recovery with 2% RSD, and 190 ng/g).

Experimental not protocol
28. In "Experimental", list the information needed for a professional analyst to repeat the study – especially unique aspects.
29. Do not include trivialities that all readers already know, such as how to prepare solutions, information found in instrument manuals, calculation of recoveries, etc., or put those details into supplemental information.

Concentrate on concentrations
30. Always give equivalent sample amount in the final extracts (for example, g/mL) and amount analyzed (for example, injection volume). A surprising number of authors don't track sample equivalents properly (usually co-extracted water in the sample is the culprit), which introduces biases.
31. Comparisons of detection limits should consider the relative amounts of equivalent sample analyzed.
32. Refer to concentrations in the original sample (for example, ng/g), not in the final extracts (for example, ng/mL unless the sample is measured in volume), and be clear about what is meant in any case.
33. Don't use ppb or ppm for concentrations because those aren't SI units that distinguish between weights and volumes.

Simple little things

34. It should be "quantification" not "quantitation;" "weighed" not "weighted;" "min" not "minutes;" "s" not "sec" (always use SI units); "method" not "methodology" unless "study of methods" is intended.
35. Mass spectrometry involves analyte "identification" not "confirmation" unless a second analysis specifically confirms the results of the first.
36. Give "rcf" or "× g" in centrifugation because "rpm" is centrifuge dependent.
37. "tR" represents retention time, not "RT" (which usually means room temperature!)
38. Don't start sentences with numerals.
39. "Non," "ultra," "micro," and other non-words need to be part of a longer word or hyphenated.

And finally...

40. Nothing is "proved" in science, only "demonstrated/supported" – or not.

In preparing this article, I went through approximately 50 reviews that I've conducted so far this year, and every manuscript had at least one of the problems listed above. I hope that authors, particularly those who aren't native English speakers, read this list before and after writing their manuscripts. Perhaps journals should include a checklist of common referee comments in their guides to authors, which could ease and speed the publication process, and improve the quality of papers overall.

I shall conclude with one final piece of advice. Don't be afraid to stand up for your good work if reviewers and editors don't recognize its value. Use facts and rational arguments to rebut wrong or even hostile comments. I've had to defend my submissions against mistaken criticisms by referees on many occasions, and I could give some preposterous examples.

The goal of some reviewers is to reject manuscripts, and the power of anonymity can give such reviewers a great deal of nerve to make ridiculous comments. Victoria Samanidou recently touched on this issue in The Analytical Scientist (5), and editors will remain unaware of problems with certain reviewers, if authors don't call attention to improper comments. For example, scientific journal standards for publication do not require use of certain regulatory validation protocols, but I've known authors to accept reviewer comments asking them to follow specific protocols, even though the author used another scientifically acceptable approach. All authors will periodically encounter this type of frustration, and we must try to ensure that scientific reason and fairness prevail. That said, authors must also accept that journals are not obligated to publish their work – and editors make the final decisions.

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Going Further Together

Sitting Down With… Deirdre Cabooter,
Assistant Professor, Faculty of Pharmaceutical Sciences, KU Leuven, Belgium, and HTC-14 committee member.

Busy with HTC-14?

Absolutely. I'm on both the organizing and scientific committees and I am the chairperson of the poster jury so also responsible for organizing the best poster awards. We have a young team and we're all eager to invest time and effort into making the conference a dynamic experience that will surprise the audience with new ideas. We're all extremely determined to create a pleasant and stimulating atmosphere.

Any surprises you can divulge?

Battle of the Gurus! Pat Sandra, Jim Jorgenson and Alexander Makarov will debate the future of chromatography in a lively interactive session. And we have a new approach to the poster session; it will take place during a Belgian beer tasting session so that we can mix socializing with scientific discussion...

Given the youth of the team, are younger scientists well catered for?

Though we've got some very established speakers for the plenary and keynote lectures, one of the three conference streams is actually dedicated to young, emerging scientists – the "YES" stream – so yes! We've spread the YES message far and wide, which has stimulated a great response from scientists aged 25 to 30 years. There'll also be a strong focus on interaction between academia and industry. We have dedicated sessions on separation sciences in industry and we've invited suppliers to pitch their up and coming solutions.

How did you get into analytical chemistry?

I trained as a bioengineer at Brussels University followed by a PhD in chemical engineering under the supervision of Gert Desmet. Then I did a post-doc, spending a year with Gert and a year at Stellenbosch University with André de Villiers. Right now, I am working as an assistant professor at the Department of Pharmaceutical and Pharmacological Science at KU Leuven.

Have you drifted away from fundamental research?

Opportunities in fundamental research are getting scarcer (though a few very strong groups remain, such as those of Gert Desmet, Fabrice Gritti and Ulrich Tallarek, to name just a few). In fact, my own interest in fundamental research is a direct result of working with Gert Desmet, undoubtedly one of the leaders in fundamental chromatography. But now that I've joined the pharmaceutical department, I've found myself in a completely new environment. The problems we face are different – it's much more applied. We are very busy with method development and validation for pharmaceuticals, as well as bioanalytical samples and even environmental analysis. Our work requires different collaborations, so my focus is shifting and broadening.

That said, I still firmly believe in the importance of the link between fundamental and applied chromatography. All analytical scientists must have a solid understanding of chromatographic theory. Whatever the application area, understanding why you are using a certain technique, why you need to use a certain column, or why it's important to invest in UHPLC is essential for success. And explaining fundamentals so that they can be understood by the people who need to use chromatography is as important as ever.

What are the best aspects of your role?

I love the variety – whether it's experimental, teaching or writing. And I'm pretty free to spend my time however I want, on whatever I want – freedom is very important to me. I also like to work together with my students to seek new solutions and overcome obstacles by talking to people, reading and experimenting until we finally discover the best option. It's very rewarding.

And there is still a lot going on in chromatography – it's evolving to meet the demands in complex samples, biomarker research and drug design. We're no longer focusing on single separations and techniques, but looking at new combinations for specific applications. At the same time, we're advancing fundamentals, for example, new column packing structures and packing arrangements. I hope to be able to contribute to these endeavors by establishing and maintaining my own research group of motivated and happy people who are eager to work together to achieve great things.

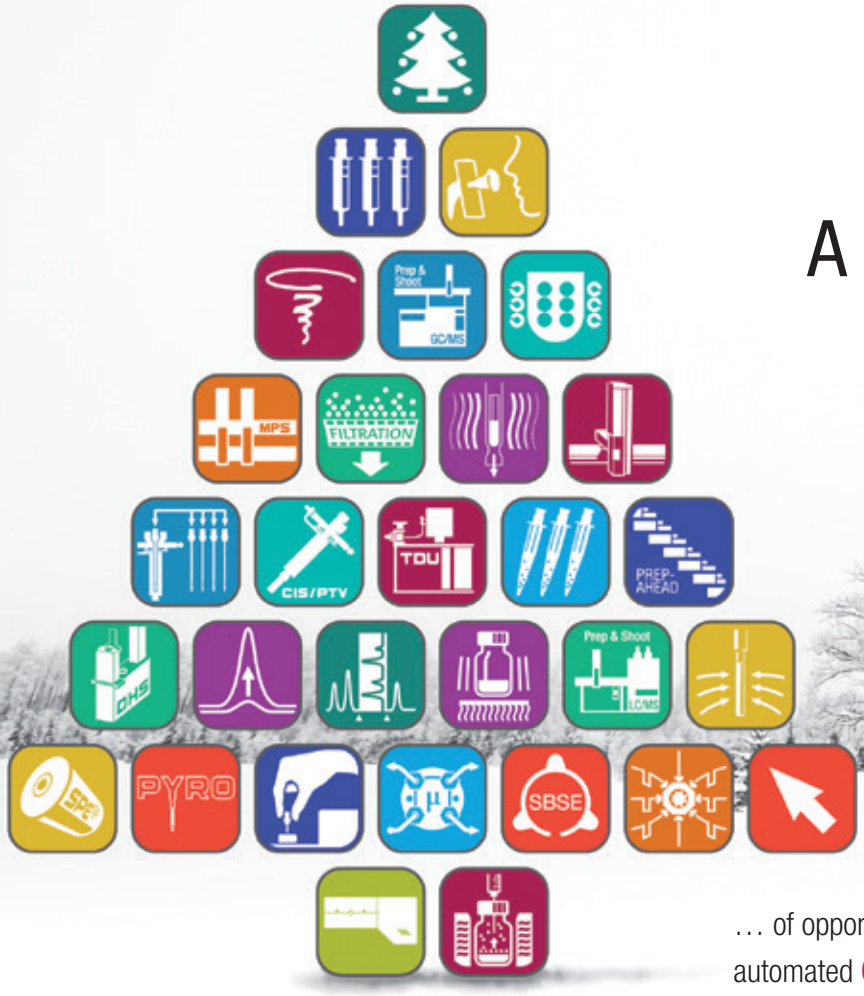
"If you want to go fast, go alone. If you want to go far, go together."

You come across as a real team player...

I've always enjoyed working with likeminded people who are as passionate and driven as me as we go at full throttle towards a common goal. That's really the most gratifying best experience to have. I spent a lot of time in Pat Sandra's lab on a collaborative project, and it was fascinating. The Pfizer Analytical Research Center was based there along with several excellent scientists who were all passionate about their work – and very open about sharing their knowledge.

Gert always stressed the importance of collaboration and openness to me. It's better to do some things together; you get to learn new perspectives. There's a well-known saying: "If you want to go fast, go alone. If you want to go far, go together." There's a lot of truth in that.

A wider field …



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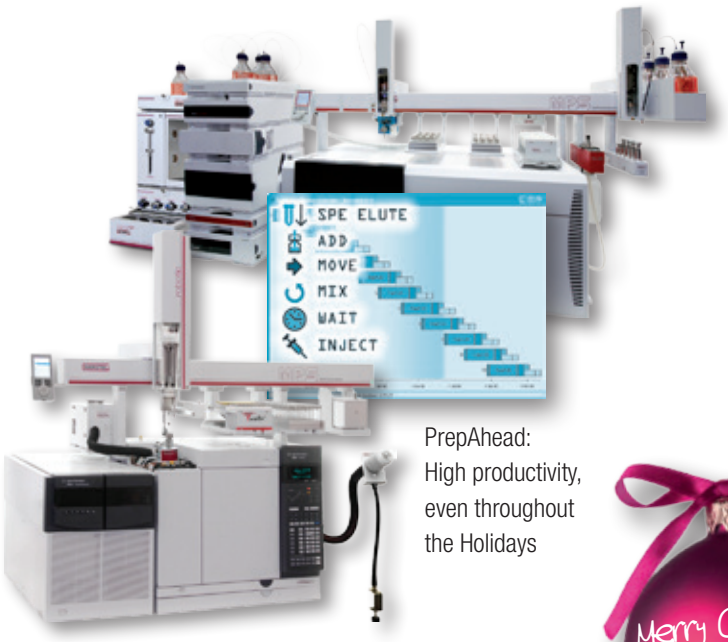

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