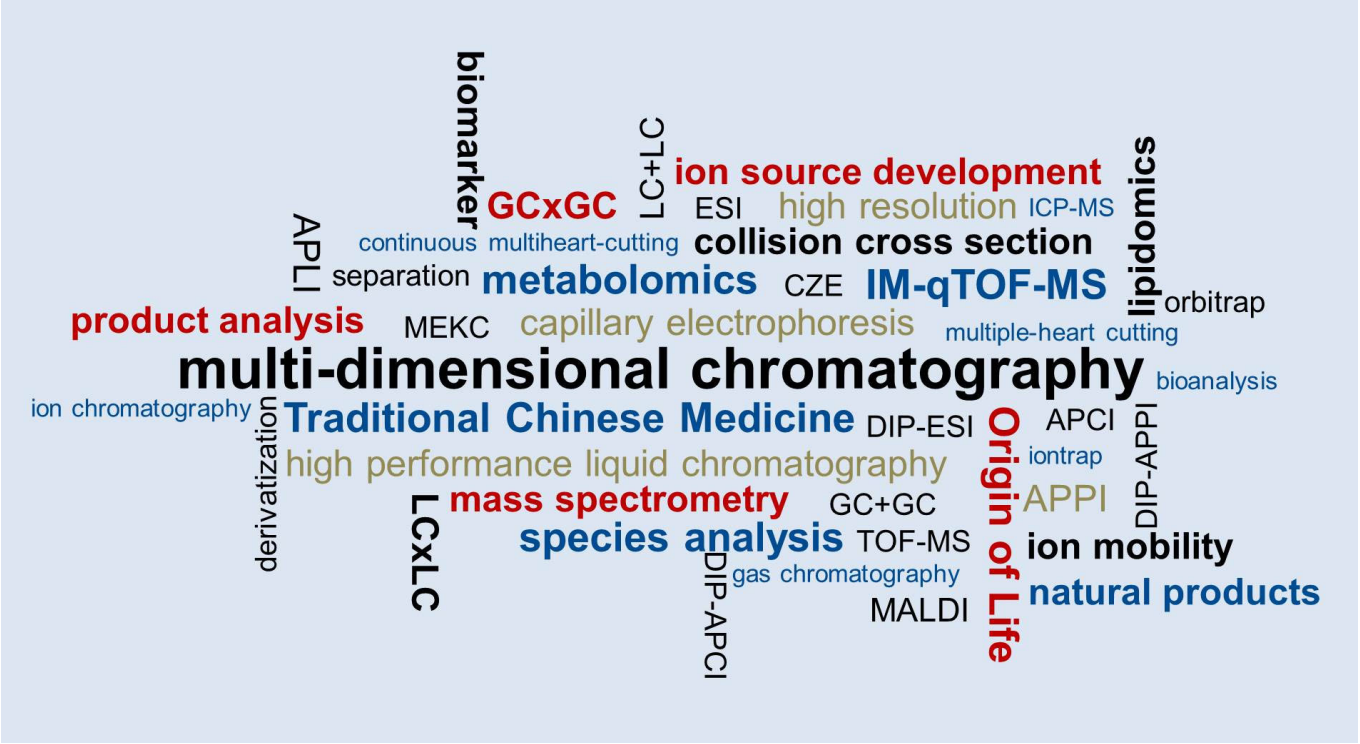
Applied Analytical Chemistry (AAC)

Annual Report 2022

AAC
applied analytical chemistry

Applied Analytical Chemistry

Annual Report 2022



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Applied Analytical Chemistry
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Applied Analytical Chemistry

2022 will certainly be remembered as the year of disasters. After 2 years, it seems that Corona is slowly coming to an end and we can then get back to the big problem of climate change. But no, in Russia they had the idea to attack a neighboring independent state, which will not only cause endless suffering among the Ukrainian (and also Russian) population but also plunge us into an unprecedented energy crisis. In addition, due to poor corona policy in China, we are again facing the possibility of new virus mutants spreading. And then some hackers had nothing better to do with their talent than to paralyze the University of Duisburg-Essen for weeks. I have rarely looked forward to the end of a year as much as I did in 2022, hoping that 2023 can only get better.

The Applied Analytical Chemistry (AAC) is part of the Faculty of Chemistry at the University of Duisburg-Essen (UDE). The AAC exists since September 2012 with the main focus on the development of novel ion-sources for mass spectrometry, the non-target analysis of complex samples by multi-dimensional separation techniques in combination with ion mobility and high-resolution mass spectrometry, metabolomics/lipidomics and investigation about origin-of-life.

2021 was the tenth-year of the Applied Analytical Chemistry research group at the University of Duisburg-Essen and – despite all the real problems – a very successful one.

The most important thing in 2022 was that we renewed old collaborations and started some important and forward-looking collaborations with different groups. I would like to highlight three new cooperation partners here. First, we started a successful collaboration with the group of Prof. Alpaslan Tadogan from the University Hospital in Essen (Germany) and the group of Prof. Ömer H. Yilma from MIT (USA) on metabolomics and another one with the group of Prof. David Chen from British Columbia University (Canada) in the field of CE-MS. In addition, cooperation talks are underway with the German Aerospace Center (DLR).

In addition, there were two other drastic experiences for the AAC. Dr. Lidia Montero and Dr. Juan Ayala Cabrera left the AAC at the end of the year and accepted long-term research positions in Spain. We will certainly miss their scientific expertise and their collegial and friendly nature but will continue to be connected through joint projects. But we also have some new additions. For example, our team has been strengthened by Dr. Florian Stappert and Dr. Tatjana Tishakova (Ukraine), whose expertise in ion sources and bioassays, respectively, we can make very good use of. In addition, four new PhD students, Jonas Rösler, Ling Tang (exchange with Hunan University), Katherina Wetzel and Marvin Häßler have recently started their PhD thesis.

In 2022 we managed to publish twelve scientific papers in peer-reviewed journals, an additional one in LCGC and three further manuscripts are in the review process and five in preparation. 11 posters at national and international conferences were presented (one poster prize (Lidia Montero) at HPLC 2022 in San Diego) and three lectures at international conferences and two in national seminars were given.

In addition, one PhD, five master's, and eight bachelor's theses were completed in 2022 in AAC and several projects, funded by BMBF, DFG, VW, and industry were started or continued, e.g. development and optimization of new ion sources (ESI, LC- , GC- and GCxGC-LTP), a new Multi 2D-LCxLC-MS platform for complex samples, and investigation of the metabolome/lipidome of various cells, bacteria, and archaea.

In 2020, because of the inability to hold presentations in attendance at the UDE and the lack of conferences, we have decided to create a TRC forum together with Agilent, where internationally renowned analysts give a digital presentation on 10-12 dates per year. The TRC-Forum started in the winter semester 2020 and is still continuing.

I want to take this opportunity to thank the entire AAC team and all co-workers for their excellent work in the lab in this difficult year 2022 as well as Agilent Technology and Hitachi High-Tech and the many collaborators in and outside the University of Duisburg-Essen for pleasant and efficient collaborations.

In case you see possibilities for future collaborations, I would be happy to discuss them with you.

We wish you all the best, good health, happiness, and success for the year 2023.

Essen, December 23, 2022

Applied Analytical Chemistry – Staff

Regular Staff

Prof. Dr. Oliver J. Schmitz	Head
Dr. Sven Meckelmann	Senior Researcher
Dr. Florian Stappert	Senior Researcher
Dr. Florian Uteschil	Senior Researcher
Constanze Dietrich	Technician / Lab
Astrid Gieselmann	Secretary

Post-Docs

Dr. Juan Ayala Cabrera, Dr. Lidia Montero, Dr. Tatjana Tishakova

Ph.D. Students

University Duisburg-Essen

Maha Alhasbani	Kristina Rentmeister
Janosch Barthelmes	Katharina Wetzel
Yildiz Großmann	Pia Wittenhofer
Paul Görs	
Marvin Häßler	External
Claudia Hellmann	Tingting Li
Claudia Lenzen	Dominic Mähler
Christian Lipok	Anneke Niehuus
Martin Meyer	Simon Schastok

M.Sc. Students

Yvonne Isabelle Gisela Ardic, Frau Fariha Firoz Bristy, Pascal Kadej, Peter Lars Stahlkopf

B.Sc. Students

Laura Angela Kiesewetter, Dorian Klaucke, Constantin Krempe, Michael Christian Lieberum, Sebastian Löbbecke, Frau Priscilla Nhan, Christoph Schakau, Marie Carolin Stempel

Guest Scientists

Prof. David Chen (British Columbia University, Vancouver, Canada), Véra Dosedělová (Erasmus student), Prof. Abdalla Elbashir (Khartoum University, Sudan), Yassine Oulad El Majdoub (University of Messina, Italy), Assoc. Prof. Dr. Abul Khayer Mallik (AvH-fellower), Dr. Taher Sahlabji (King Khalid University, Saudi Arabia)

Apprentices

Tom Maxion, Enola Sobel

Major News 2022

Teaching and Research Center for Separation

In 2018, we entered into a partnership with Agilent Technologies. In the course of this cooperation, Agilent provides us with a variety of analytical systems. And in 2021 we had the opportunity to exchange these fantastic instruments for the latest versions.

Without this outstanding equipment, much of the work in this report would not have been possible. Therefore, a big thank you to Agilent Technologies at this point.

Teaching and Research Center for Separation

"old" equipment

"new" equipment

In addition to research, the focus of the center is on teaching students and industry employees – from technicians to managers, graduates to postdocs – about separation science and training them in the use of modern analytical equipment.

For more information visit our website www.trc-separation.com

HPLC 2023 in Düsseldorf, Germany

Now it will soon finally start. The 51th HPLC (Chairmen: Prof. Michael Lämmerhofer and Prof. Oliver J. Schmitz), postponed by Corona, will finally take place in June 2023. The Congress Centre in Düsseldorf (Germany) has been chosen as the venue, guaranteeing a professional environment for the conference and exhibition.

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Since the first HPLC conference in 1973, the HPLC Symposium Series has established itself as the world's leading conference for chromatographic analysis techniques and their coupling with mass spectrometry. The event will be held at the Congress Center Düsseldorf (CCD) as an attendance event and will mainly consist of five program parts:

(i) A total of more than 170 scientific presentations are planned in the form of plenary lectures, keynote lectures and presentations by congress participants, which will be offered in four parallel sessions. In the plenary lectures, renowned scientists will present the latest topics of current research in the field of separation techniques. Keynote lectures will serve to present new technologies and application areas in more detail.

ii) More than 500 expected poster contributions will provide an opportunity for congress participants to present their latest results and discuss them with other participants during the event. Prizes will be awarded to the best posters after selection by a jury.

iii) To contribute to science communication, an HPLCtube and a Science-Slam will be organized. Young scientists will present their research topics to the public and the press within a given time via film or lecture. The focus is on the popular scientific communication of scientific content in an entertaining way. The best contributions will be awarded prizes by a jury.

iv) The latest technical, instrumental and methodological developments in the field of separation techniques will be presented in the industrial exhibition and at the industrial

seminars. The presence of industry representatives will be used to set up a job fair for young scientists to establish contact with possible future employers.

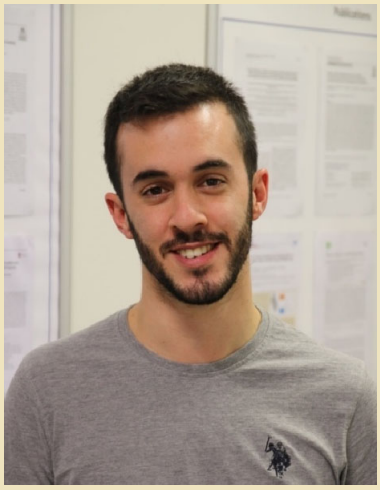
v) Especially for newcomers in the field of separation techniques, a training and education program will be offered, consisting of 12 half-day and one full-day workshop introducing special techniques, as well as eigth tutorial lectures summarizing focused current topics.

The program of HPLC 2023 covers all aspects of separation science in liquid phases and supercritical fluids. The conference focus ranges from fundamentals and theory to new separation materials and column technologies to innovations in the field of microfluidics. The latest developments in the (bio-) pharmaceutical, chemical and food chemical industries, environmental and forensic analysis, including the respective aspects of quality assurance, will be presented. The lively exchange of information through workshops, lectures, posters, tutorials and discussion panels will enable participants to gain a comprehensive overview of the worldwide status quo of separation techniques. The large number of world-leading analysts at the meeting will help to provide important impulses for innovative new approaches in the field of separation methods to be presented to the participants.

Mark your calendar! We look forward to your participation.

For more information visit our website www.hplc2023.com

Dream Team of the Year 2022



Dr. Lidia Montero and Dr. Juan Francisco Ayala Cabrera

They are now for about 5 and 3 years, respectively in the AAC working group and enriches it immensely.

Besides their excellent publications Lida and Juan are very successful in working on projects funded by industry and DFG about 2D-LC, metabolomics and ion source development (GC-APPI, GC-LTP, LC-LTP).

Their above-average commitment in the laboratory is impressive and their friendly nature arr a great enrichment for the Applied Analytical Chemistry.

List of Projects 2022

(Abstracts of these projects within the next pages)

Automated Extraction of Lipids using Green Solvents
Pia Wittenhofer, Lidia Montero, Sven W. Meckelmann

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Juan F. Ayala Cabrera, Sven Meckelmann, Florian Uteschil, Lidia Montero

Analysis of phthalate ester in drinking water by GC-TPI-HRMS (qTOF)
Sebastian Löbbecke, Alexandra Pape, Florian Uteschil, Lidia Montero, Juan F. Ayala Cabrera

Development of the new analytical platform GC × GC-TPI-HRMS/MS using flow modulator for the chemical characterization of vermouth aroma profile
Lidia Montero, Taher Sahlabji, Juan Francisco Ayala Cabrera

Analysis of Fatty Acids in Archaea by Gas Chromatography coupled to Atmospheric Pressure Chemical Ionization Mass Chromatography
Paul E. Görs, Sven W. Meckelmann

Post-Column Paternò-Büchi Reaction for the Simultaneous Quantification and Identification of Double Bond Position of Fatty Acids by Gas Chromatography-High Resolution Mass Spectrometry
Paul E. Görs, Juan F. Ayala-Cabrera, Sven W. Meckelmann

Synthesis of β-Alanine-Derived Stationary Phase for Mixed-Mode Chromatography
Abul K. Mallik, Lidia Montero

Quantification of local anesthetics in tattoo creams
Juan Francisco Ayala Cabrera, Lidia Montero

Non-targeted HPLC-HRMS approach to face the analysis of ancient samples related to the origin of life
Lidia Montero, Isabelle Ardic, Juan F. Ayala Cabrera

Analysis of Polyamines in Cancer Cells
Sven W. Meckelmann, Pia Wittenhofer

Differences in Metastasis – Using Untargeted Metabolomics to Elucidate Organotropic Effects in the Metastasis of Cancer Cells
Jonas Rösler, Sven Meckelmann, Alpaslan Tasdogan

Development of a heart-cutting LC method (LC - LC) for the analysis of short-, medium, and long-CoA esters
Constantin P. Krempe, Lidia Montero, Paul E. Görs, Delia Castilla-Fernández, Sven W. Meckelmann

Development of a 2D Heart-Cut LC-LC-MS/MS Method to Characterize the Biosynthesis of Cholesterol in Cancer Cells
Pia Wittenhofer, Sven W. Meckelmann

Multidisciplinary study of the use of black currant fruits, juice and by-products: comprehensive chemical characterization and neuroprotective activity
Lidia Montero, Priscilla Nahn, Juan Francisco Ayala Cabrera

A novel implement for maximizing the separation power of multidimensional liquid chromatography: Multi-^{2}D-LC × LC
Lidia Montero, Fariha F. Britz, Juan Francisco Ayala Cabrera

Investigation of Maillard reaction by using thermogravimetry hyphenated with an orbitrap mass spectrometry
Maha Alhasbani

Automated Extraction of Lipids using Green Solvents

Pia Wittenhofer, Lidia Montero, Sven W. Meckelmann

Lipids represent thousands of diverse molecules and are involved in various biological processes. However, in many diseases an imbalance of lipids can be observed. In addition to analytic conditions, sample preparation is important in order to obtain precise and quantitative results. Many of the currently applied extraction methods use solvents that are harmful to the environment or are based on finite raw materials. Therefore, green alternatives such as ethanol, ethyl acetate, or limonene are being increasingly used. Here we developed an automated extraction protocol using ethylacetat and ethanol as green solvents for global lipidomics extraction. Moreover, the protocol was compared to the typically used MTBE (tert-butyl methyl ether) extraction (Matyash et al. J. Lipid Res. 2008) as well as an modified hexane extraction (Meckelmann et al. Circ Genom Precis Med. 2020). All protocolls were applied to different matrices such as human plasma, human serum, and HepG2 cells and recovery rates were determined for all major lipid classes (Fig. 1).The ethyl acetate and MTBE protocol showed good recoveries for a broad range of lipids while the hexane protocol is more suitable for non polar lipids. However, the highest recoveries were achieved for the developed ethyl acetat protocol. Especially for highly polar lipids such as lyso-phosphatidylcholins (LPC) and lyso-phosphatidylethanolamines (LPE) ethyl acetate is providing better recoveries.

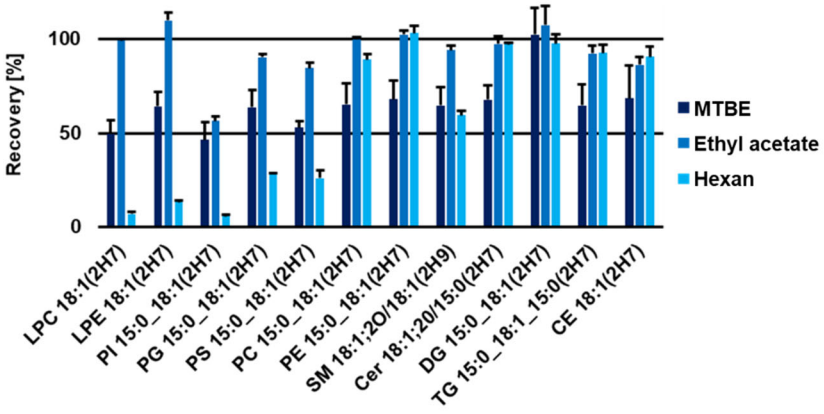


Fig. 1: Recovery rates of EquiSplashMix in plasma using MTBE, ethyl acetate and hexan for sample preparation.

Funded by: Deutsche Forschungsgemeinschaft (DFG) - ME 5800/1-1

Further development of an inverse low temperature plasma ion source for liquid chromatography mass spectrometry

Alexandra B. U. Pape, Juan F. Ayala Cabrera, Florian Uteschil, Florian Stappert

A plasma consists of ions, free electrons, neutral atoms and molecules, and usually reaches temperatures of up to several thousand degrees. The here employed “Low Temperature Plasma” (LTP) has temperatures of less than 30 °C. The plasma is created by applying a high voltage to an electric circuit, where either one or both electrodes are covered by an insulating material, also called “dielectric barrier”. When enough fast changing high voltages are applied to the electrode, the insulator is polarized. In between the two insulators, the carrier gas, here argon, is ignited, meaning that the highly energetic electrons excite the abundant gas molecules and atoms.

This plasma is used in plasma ion sources for mass spectrometry to ionize the analyte molecules. There are different types of LTP ion source configurations, like the inverse LTP (iLTP) used in this project which has a high-voltage needle electrode and a ring electrode, as depicted in Fig. 1, or the Tube Plasma Ionization (TPI), where there is no ring electrode used.

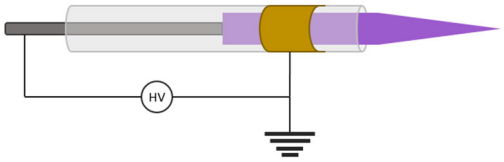


Fig. 1: Schematic set-up of an iLTP

In an effort to enhance the plasma ionization, a new iLTP was developed, called capsuled iLTP (ciLTP) as shown in Fig. 2. The capsule does not only make the operation safer, but the new configuration also allows the plasma to be ignited and operated at lower voltages. Instead of a ring electrode fixed on the dielectric barrier quartz tube, the whole top of the capsule functions as the ring electrode.

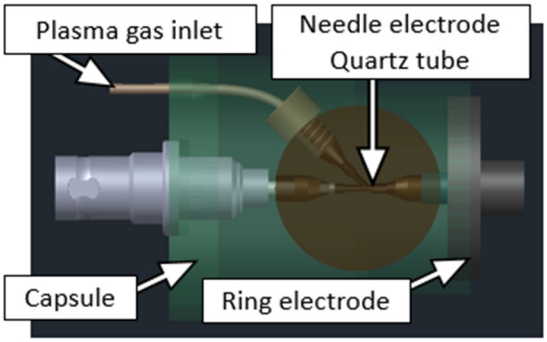


Fig. 2: Schematic set-up of the novel ciLTP

Preliminary results show that the ciLTP operated with a gold needle elctrode has an increased ionization efficiency at lower operating voltages in comparison to the previous iLTP. In further investigations, the geometry of the ciLTP will be optimized, including important parameters like the quartz tube and needle lengths and the distance between the electrodes.

Collaborative Project – Project Partner: Hitachi High-Tech Corporation, Tokyo, Japan.
Funded by: Hitachi High-Tech Corporation, Tokyo, Japan.

Experimental studies to clarify the ionization mechanism of an argon plasma based ion source

Florian Stappert, Alexandra B. U. Pape, Juan F. Ayala Cabrera, Florian Uteschil

The ionization represents a crucial step in mass spectrometric investigations, which can be adjusted depending on the analytical problem. Therefore, new ion sources are constantly being developed and optimized. An understanding of the underlying chemical and physical processes in these ion sources is of great importance as this offers the possibility of a targeted optimization and supports in reliably interpreting the ionization patterns obtained.

In the last years, different plasma-based ion sources operating under atmospheric pressure (AP) conditions have been developed in our group. In experimental studies of a homemade tube plasma ionization (TPI) source, argon turned out to be the ideal plasma gas. This is different from the typically used helium, which, however, resulted in a lower ionization efficiency in our setups. The ionization mechanism in a helium plasma under AP conditions is widely understood and recognized, while the mechanism using argon plasma under AP conditions is still controversial in analytical community. From a plasma physics point of view, it seems very likely that charged argon species are formed in the plasma and represent the primary species of the ionization mechanism, but this has not yet been clearly demonstrated.

In cooperation with the Physical and Theoretical Chemistry of the university of Wuppertal we plan to clarify this unclear situation experimentally by investigating an argon plasma under well-defined conditions. Since even small contaminations with water ensure that the reactive species are quenched, a water-free system aspired. Therefore, an external turbo pump will be used for cleaning the reaction area. Subsequently, the pressure will be increased to AP conditions (water-free) and an argon plasma will be ignited under comparable conditions like in our ion sources. The primary ions will be analyzed by mass spectrometry and by stepwise increasing the water ratio, the ionization mechanism of water should be enlightened.

The theoretical planning of the experimental setup has been finalized to a large extent, and currently final components are assembled, designed, and manufactured.

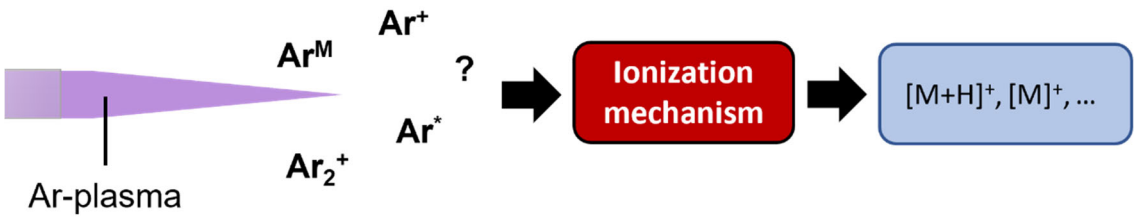


Fig. 1: Reactive species from an Ar-plasma that initiate an ionization mechanism from which, among other things, (protonated) analyte ions ([M]$^+$, [M+H]$^+$) are formed.

Collaborative Project – Project Partner: Prof. Thorsten Benter (Physical Chemistry, University of Wuppertal, Germany)

New Tools in Cancer Metabolomics – Ion Source Development for Single Cell Analysis

Jonas Rösler, Florian Uteschil, Alpaslan Tasdogan

Metastasising of cancer cells is responsible for about 90 % of cancer related deaths and therefore key target in cancer research. A major challenge in this field is to unravel the mechanisms of metabolic reprogramming of cancer cells during metastasis, which allows for efficient adaptations to the changing chemical environment. For now, cancer metabolomics still relies on bulk analysis technologies, which are not capable to picture the heterogeneity of the disease and by this lose a big part of the desired information. [1] The emerging field of single cell metabolomics is aiming to cover this gap, but for challenges in sensitivity and keeping the cells metabolome unaffected no reliable technology has been reported yet.

The project is aiming to setup and apply a new ion source for an Orbitrap mass spectrometer capable for single cell analysis. For the ionization the system relies on a low temperature plasma ionization (LTP) provided as SICRIT ion source by Plasmion GmbH. This ionization technique has been proven adequate for single cell analysis elsewhere [2], while the cell introduction system still remained challenging. Therefore, a self-build cell introduction system is used, relying on ultrasonic nebulization of single cell droplets for combination of efficient cell lysis and fast transfer into the mass spectrometer. A working prototype for cell introduction has been constructed. The sample droplet (5) gets placed on top of the ultrasonic horn (1). By turning on the device the sample gets nebulized in the spray chamber (2) and the gas stream (3) transports the sample through the heated transfer line (4) into the ion source. It was shown, that the system is successfully vaporizing liquid samples and providing a rapid transfer into the SICRIT ion source. This prototype is representing a new kind of liquid introduction system for mass spectrometry.

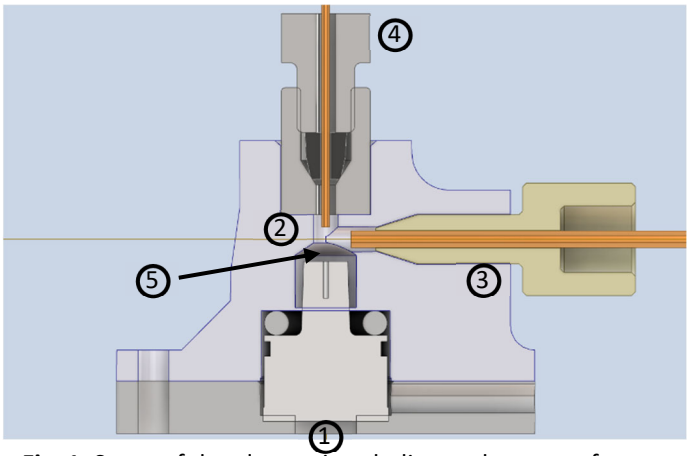


Fig. 1: Setup of the ultrasonic nebulizer as key part of the ion source design.
(1) Ultrasonic Horn, **(2)** Spray Chamber, **(3)** Gas Inlet, **(4)** Heated Transfer Line to the SICRIT ion source, **(5)** Sample droplet

The performance of the new device has been evaluated using various standard solutions indicating a low sensitivity of this method. For example, Phencyclidine was detected at a concentration of 23 nM, which is in range of the desired in-source concentrations needed for single cell analysis.

References:
[1] Martins Nascentes Melo, L. et al., Trends in cancer (2022) 8:988-1001
[2] Liu, Q. et al. Angew. Chem. Int. Ed. (2021) 60:24534-24542

Funded by: A. T. was funded by an Emmy-Noether Award from the German Research Foundation (DFG, 467788900) and the Ministry of Culture and Science of the State of North Rhine-Westphalia (NRW-Nachwuchsgruppenprogramm)

Application of a TPI Source for the Analysis of Sterols

Pia Wittenhofer, Juan Cabrera, Sven W. Meckelmann

Electrospray ionization has a wide range of applications in liquid chromatography. However, for non-polar molecules this offers only a limited ionization capability. Therefore, APCI is also used in sterol analysis for these molecules. Low temperature plasma ion sources offer an alternative to increasing sensitivity for challenging analytes such as sterols. In the current setup, argon gas is converted into a plasma in a glass electrode via an applied voltage with a specific frequency and pulse width. To transfer the ions into the gas phase an APCI vaporizer is used and located above the plasma cone inside the source housing. This ionization is a soft method resulting in abundant molecule ions and low in-source fragmentation.The previously developt LC-ESI-QqQ-MS method was adapted to the TPI source. The Figure shows a comparison of the ionization using TPI and ESI. Preliminary results indicated increased intensities for cholesterol and all biosynthetic precursors. Currently, the ionization conditions were optimized prior to a complete characterization of the method according to the EMA guidelines for bioanalytical method validation.

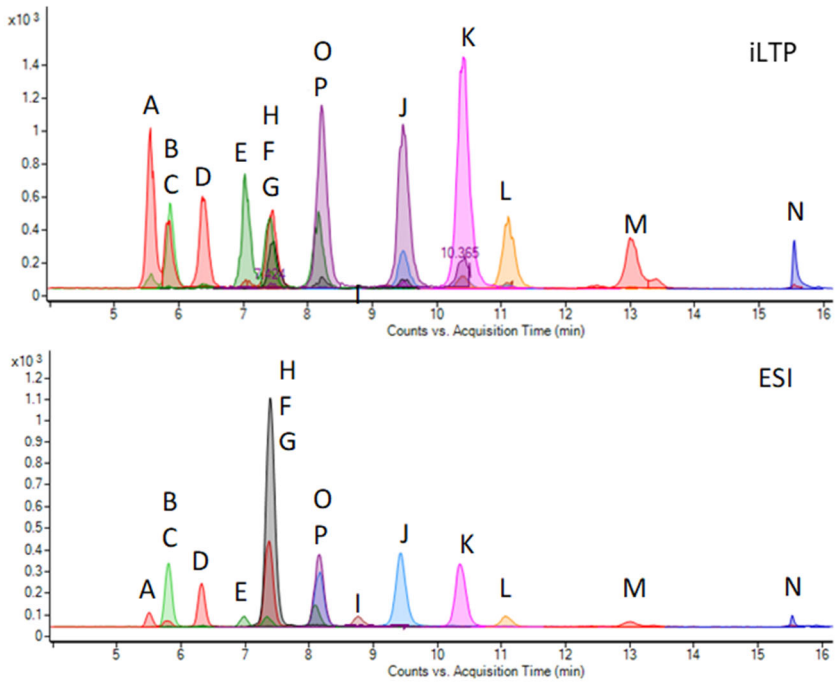


Fig. 1: Chromatographic separation of sterols of the cholesterol biosynthesis. Chromatographic separation was carried out using a Kinetex PFP-column as a stationary phase. Ionization and detection was performed by TPI-QqQ-MS (top) or ESI-QqQ-MS (bottom). Zymosterol (A), dehydrodemosterol (B), dehydrolathosterol (C), desmosterol (D), zymostenol (E), FF-MAS (F), lathosterol (G), 7-hydrocholesterol (H), cholesterol (O), T-MAS (P), 2,3-oxidosqualene (I), dihydro FF-MAS (J), dihydro T-MAS (K), dihydrolathosterol (L), lanosterol (M), squalene (N).

Collaborative Project – Project Partner: Prof. Dr. Annette Paschen and Dr. Barbara M. Grüner, (Molekulare Tumorimmunologie, University Hospital ssen, Germany)
Funded by: Deutsche Forschungsgemeinschaft (DFG) - ME 5800/1-1 and SCHM 1699/30-1

Differentiation of herbal liqueurs by GC-qTOF-MS platforms integrating EI and TPI sources

Juan F. Ayala Cabrera, Sven Meckelmann, Florian Uteschil, Lidia Montero

Non-targeted analysis (NTA) requires of powerful analytical platforms that can ensure a good identification of a wide range of compounds with a high confidence level. For the analysis of more volatile compounds, gas chromatography-mass spectrometry (GC-MS) using electron ionization (EI) is the gold standard methodology since it allows to ensure the identification of the analytes by means of well-stablished mass spectral libraries such as NIST. However, the high fragmentation achieved with this ion source could lead to wrong identifications when complex matrices such as herbal liqueurs are analyzed. In this sense, the use of GC-MS platforms integration atmospheric pressure ionization (API) sources could help to overcome this limitation. API sources provide a soft ionization which largely preserve the molecular or quasi-molecular ion, overcoming the compromise between sensitivity and selectivity required with EI as well as promoting the coupling with high-resolution mass spectrometers (HRMS) initially thought for liquid chromatography applications.

Here, we evaluate the potential of combining GC-qTOF-MS platforms integrating EI and a homemade API source called tube plasma ionizaiton (TPI) for the characterization and differentiation of herbal liqueurs. As can be seen in the Fig. 1 for homopterocarpin, the softer ionization achieved with TPI as well as the possibility to do tandem mass spectrometric experiments allows to ensure the identification of the analytes, increasing the confidence on the indentification or even correcting the results achieved by EI, especially with coeluting compounds. Using this strategy, seven herbal liqueurs could be differentiated by partial least-squares discriminant analysis, being the samples UF and RI the herbal liqueurs that presented more different profiles. The use of these platforms also helped to identify potential biomarkers to discriminate between different samples. For instance, the feature *m/z* 153.0546, identified as methyl salicylate was proposed as a biomarker for UG herbal liqueurs.

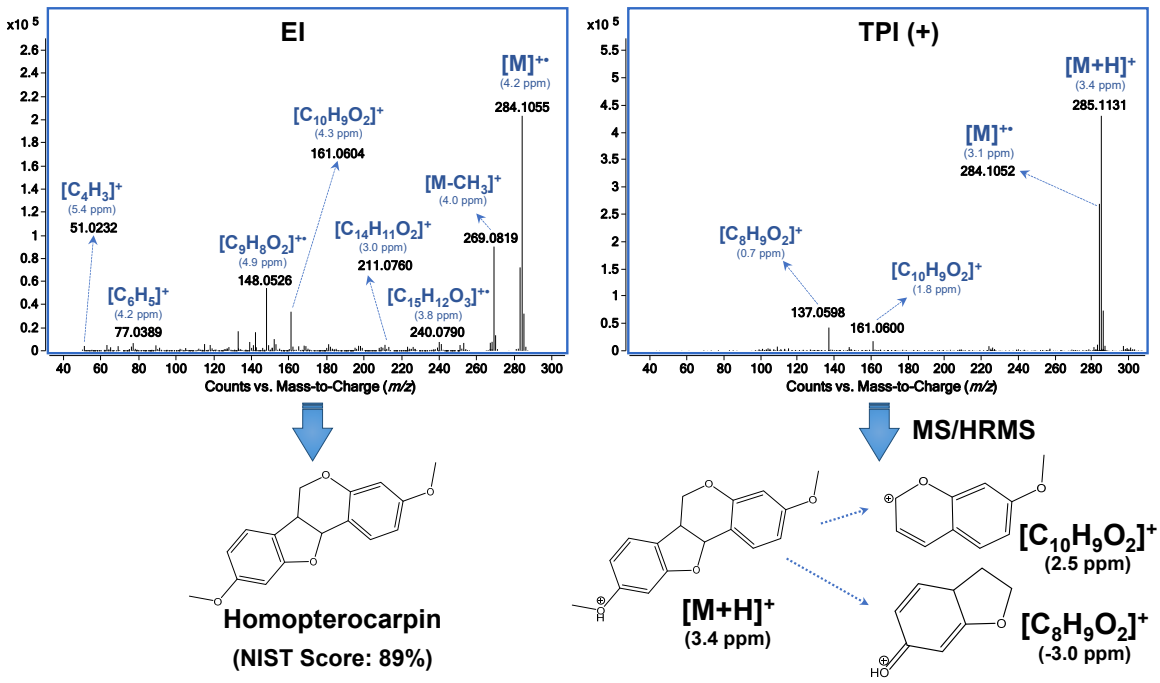


Fig. 1: GC-HRMS mass spectra of homopterocarpin by EI (left) and TPI (right) in herbal liqueur extract.

Collaborative Project – Project Partner: Dr. Ana B. Martínez-Piernas (University of Jaén, Spain)

Analysis of phthalate ester in drinking water by GC-TPI-HRMS (qTOF)

Sebastian Löbbecke, Alexandra Pape, Florian Uteschil, Lidia Montero, Juan F. Ayala Cabrera

Phthalic acid esters (PAEs) are synthetic organic compounds derived from 1,2-denzenedicarboxylic acid with dialkyl, alkyl or aryl side chains. They have been widely used in the industry in personal care products, dietary supplements, medical supplies or as plasticizers in food packaging, among others. However, their widespread distribution, bioaccumulation ability as well as their harmful effects to the environment and living organisms has led to the regulation of their concentration levels. The analytical determination of PAEs is challenging since due to the risk of a high background contamination as well as the low selectivity achieved in their determination due to the high fragmentation observed by gas chromatography-mass spectrometry (GC-MS) using the gold standard electron ionization (EI). Recently, the AAC group introduced an atmospheric pressure ionization (API) so-called tube plasma ionization (TPI) which consists of a half dielectric barrier discharge based on an inverse low temperature plasma configuration where the high voltage is applied to a pin electrode and the "virtual" grounded electrode is the housing itself. This TPI source can ionize a wide range of compounds by means of the molecular ion or the protonated molecule, thus improving both the selectivity and the detection capability of the methodologies. Thus, the aim of this project lies on the evaluation of the capabilities of TPI to efficiently ionize the PAEs.

The ionization of PAEs by TPI led to a significanly lower in-source fragmentation than that observed by EI, where the phthalic acid ion (*m/z* 149) is the base peak of the mass spectrum. As can be seen for the diethyl phthalate, the protonated molecule and the loss of one alkyl chain (i.e., $[M\text{-}C_2H_5]^-$) were the base peaks of the mass spectra in positive and negative ion mode, respectively.

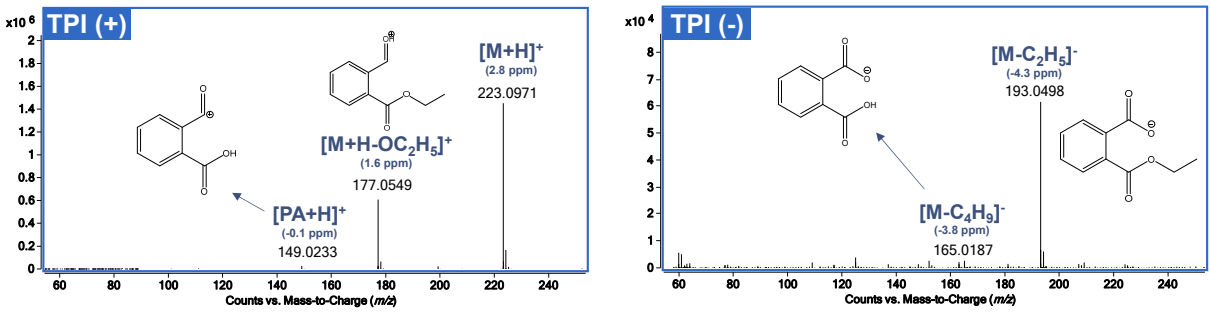


Fig. 1: Mass spectra of diethyl phthalate (DEP) by tube plasma ionization in positive (left) and negative (right) ion mode

Moreover, it was observed that the addition of certain modifiers in the gas-phase such as methanol, water or ammonia could help to improve the ionization efficiency of the analytes. Thus, the GC-qTOF-MS methodology using TPI in positive ion mode (0.02-0.7 µg L^{-1}) provided better instrumental limits of detection than those achieved by APCI (0.6-70 µg L^{-1}) and APPI (1.4-80 µg L^{-1}) and similar to those obtained by EI (0.01-0.4 µg L^{-1}). Moreover, the GC-TPI-qTOF-MS showed good quality parameters, achieving a good linearity (R^2 < 0.97), high precision (RSD < 5), and trueness (Rel. Error < 14). The methodology was finally applied to the evaluate the migration of PAEs from plastic bottles to water. Among the PAEs found, DEP showest the highest concentrations in water. Moreover, recycled PET and the softness of the plastic seems to be key factors for a higher migration of PAEs.

Development of the new analytical platform GC × GC-TPI-HRMS/MS using flow modulator for the chemical characterization of vermouth aroma profile

Lidia Montero, Taher Sahlabji, Juan Francisco Ayala Cabrera

The aroma profile of complex food samples is composed by the mixture of hundreds of volatile organic compounds (VOCs) in a very high concentration range. Moreover, the chemical identification of all the compounds responsible for the aroma of these products is an analytical challenge due to the presence of a huge variety of compounds that involves both compounds with very similar chemical structures and isomers, and compounds that present a large variability in their structures. Therefore, advanced analytical techniques, able to provide high separation power and capability of detection are necessary. In this work, vermouth was selected as a sample characteristic to present a complex aroma composition due to the presence of the VOCs from different plants extracted during the maceration of those plants in wine. For the complete characterization of this aroma profile a comprehensive two-dimensional gas chromatography using the new reversed flow modulator designed by Agilent Technologies and coupled to a novel tube plasma ionization (TPI) and a high resolution QTOF mass spectrometer (GC × GC-TPI-HRMS/MS). Several advantages were achieved for the separation of the vermouth VOCs using this new analytical technique. On one hand, an increased peak capacity was achieved by the optimized GC × GC separation, on the other hand, the flow modulator helped to automate the GC × GC method since it does not require cryogenic solvents like liquid N_2. Moreover, the TPI ionization as atmospheric pressure ionization (API), has been demonstrated to generate a soft ionization that can be coupled to GC analysis, in comparison to the conventional electron impact (EI) ionization process that are usually coupled to GC separations, TPI provided a simpler MS spectrum were the molecular ion ($[M]^{-\bullet}$ or $[M]^{-\bullet}$) and/or the protonated molecule ($[M+H]^+$ or $[M-H]^-$) were obtained for all the separated compounds. Besides, the use of the TPI allowed the use of typically high GC flow rates in the second dimension without the need of any flow splitting, which would drastically decrease the sensitivity and the detectability mainly of low abundant compounds. Thanks to the optimization of this novel approach, approximately hundred compounds were separated by the GC × GC method and tentatively identified by the TPI-HRMS/MS. Figure 1 shows the 2D separation of the VOCs that build up the aroma of the vermouth sample obtained under these conditions. Thanks to the soft ionization provided by the TPI very simple and clear MS spectrum were achieved, which allowed the easy elucidation of the molecular formula of each compound and together with the tandem MS caried out during the analysis, the tentative identification of the structure and the name of the compound using several MS libraries.

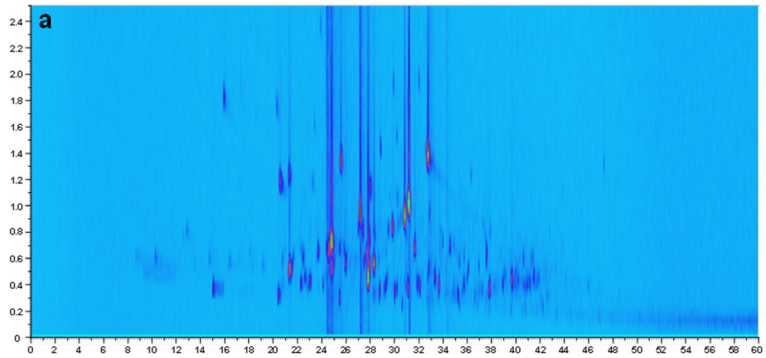


Fig 1.: 2D plot of the GC × GC-TPI-HRMS/MS separation of the volatile compounds present in the vermouth sample

Analysis of Fatty Acids in Archaea by Gas Chromatography coupled to Atmospheric Pressure Chemical Ionization Mass Chromatography

Paul E. Görs, Sven W. Meckelmann

In eukarya and bacteria, fatty acids (FAs) fulfill various important roles in biological systems. In archaea, there has only been evidence for the presence of FAs, but proof by metabolic labeling using ^{13}C-labeled substrate has not yet been provided.

Due to the low concentrations at which FAs were expected to be present in archaea, a method for sensitive analysis was developed. For this purpose, derivatization of FAs with pentafluorobenzyl bromide (PFB) was performed, and the PFB-derivatives obtained were then ionized with Atmospheric Pressure Chemical Ionization (APCI).

The archaea examined in the study were grown on ^{13}C-labeled glycerol as the sole carbon source by our project partners. The ^{13}C-labeling made it possible to distinguish between FAs formed by the archaea and contaminants, enabling a sensitive analysis of the archaeal fatty acids.

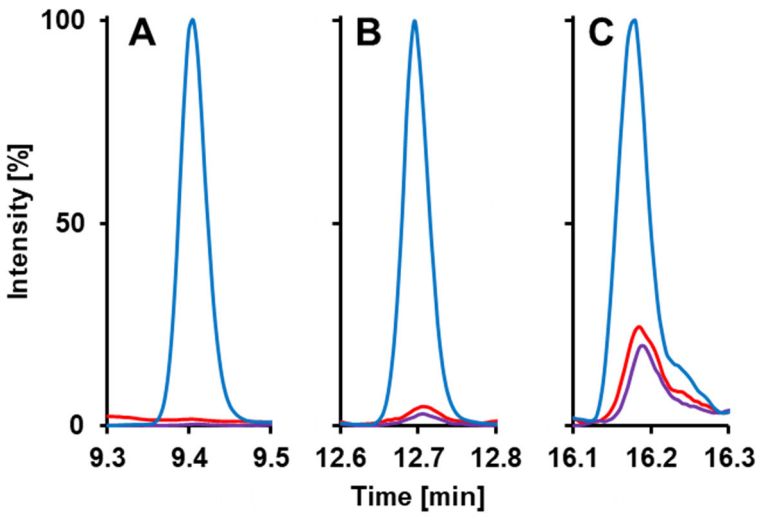


Fig. 1: Metabolic labeled ^{13}C fatty acids found in archaea MW00G using ^{12}C-labeled substrate (red), ^{13}C-labeled substrate (blue) as well as in a knock-out mutant grown on ^{13}C-labeled substrate (violet). The cells were hydrolyzed, extracted according to Matyash et al. (J. Lipid Res. 2008; 49:1137-1146) and measured by GC-APCI-QqQ-MS. The amount of ^{13}C fatty acids found in the wild type MW00G (A: FA 8:0, B: FA 10:0, C: FA 12:0) is increased compared to the control samples grown on a ^{12}C-labeled substrate, and the knock-out mutant grown on a ^{13}C-labeled substrate.

Fig. 1 shows the presence of the fatty acids FA 8:0 (A), FA 10:0 (B), and FA 12:0 (C) after metabolic labeling. Moreover, in a knock-out experiment, a gene related to proposed FA biosynthesis was performed. The results show that the knock-out mutant contains a similar amount of FAs compared to the control samples, and less FAs than the previously investigated wild-type MW00G.

Collaborative Project – Project Partner: Prof. Dr. Bettina Siebers (University Duisburg Essen, Essen, Germany)
Funded by: VolkswagenStiftung

Post-Column Paternò-Büchi Reaction for the Simultaneous Quantification and Identification of Double Bond Position of Fatty Acids by Gas Chromatography-High Resolution Mass Spectrometry

Paul E. Görs, Juan F. Ayala-Cabrera, Sven W. Meckelmann

The biological effects of unsaturated fatty acids (FAs), which contain one or more double bonds, depend not only on the number, but also on the position of the double bonds. For instance, the ratio of omega-3 to omega-6 FAs plays an important role in nutrition. Therefore, selective methods are needed for achieving both quantification of FAs and identification of the position at the same time.

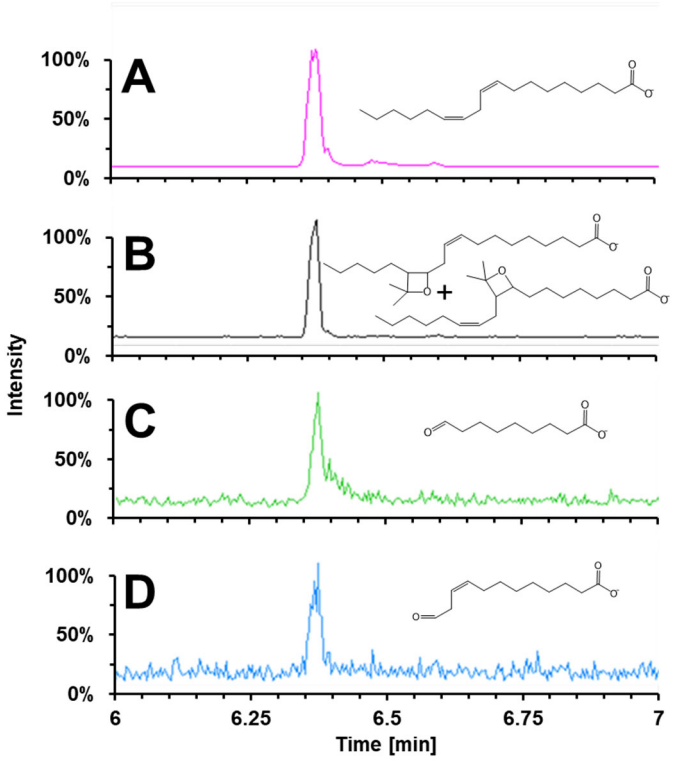


Fig. 1: Paternò-Büchi Reaction at the example of linoleic acid. A: Unreacted Fatty Acid [M-PFB]$^-$ ion (m/z 279.2330); B: PB product [M-PFB+acetone]$^-$ ion (m/z 337.2748); C: First R=O diagnostic fragment (m/z 171.1027); D: Second R=O diagnostic fragment (m/z 211.1340)

One possible approach is the Paternò-Büchi (PB) reaction. This reaction involves a [2+2] photocycloaddition of a ketone to a double bond, which can subsequently be cleaved into diagnostic fragments using collision-induced dissociation (CID). Unlike the often-used ozonolysis, no ozone or other aggressive chemicals are used that could potentially damage the mass spectrometer.

Here we are analyzing FAs after derivatization with pentafluorobenzyl bromide (PFB), and subsequent gas chromatographic separation. Ionization and quantification are carried out by APCI and monitoring the [M-PFB]$^-$ ions (**Fig.1A**). Despite that GC is capable of separation positional isomers no further mass spectrometric confirmation can be acquired and authentic standards are necessary to confirm which FA is present in the sample.

To achieve the simultaneous FA quantification and the identification of the double bond position, the APCI source used for ionization was modified and equipped with a mercury lamp enabling the PB reaction. To promote this reaction, the auxiliary gas was saturated with acetone, leading to stable source conditions that facilitate the formation of the [M-PFB+acetone]$^-$ ion (**Fig.1B**), while keeping the [M-PFB]$^-$ ion as the base peak of the mass spectrum. Moreover, under these conditions, in-source fragmentation of the PB-derivates was also observed (**Fig.1C and D**). These diagnostic ions allow the identification of the double bond position, thus leading to a simple approach to simultaneously obtain qualitative and quantitative information for FAs.

Funded by: VolkswagenStiftung

Synthesis of β-Alanine-Derived Stationary Phase for Mixed-Mode Chromatography

Abul K. Mallik, Lidia Montero

The application of high-performance liquid chromatography (HPLC) has been increasing as an analytical tool in various fields like pharmaceutical, chemical, drug treatment monitoring, and biomedical analysis. However, in most of the cases a single column can separate specific type of analytes. Therefore, the development of new organic phase with incorporating various interaction sites is desiarable for the separation of versatile analytes with a single column with high selelctivities.

Here we synthesized (Fig. 1a), characterized, and applied new embedded polar groups (urea and amide) containing stationary phase (Sil-Ala-C18) from β-alanine. The new phase was characterized by elemental analysis, TGA, FT-IR, SEM, and ^{13}C CP/MAS NMR spectroscopy. The materials were packed into stainless steel column (150 x 2.1 mm) and applied for the separation of various analytes in RPLC and HILIC modes (Fig. 1b). Fortunately, the new phase showed better separation compared to the commercial embedded polar group containg reference column (Ascentis RP-Amide) for the separation of terphenyl isomers and triphenylene in RPLC. Moreover, a mixture of uracil, propranolol, butylparaben, dipropylphthalate, naphthalene, amitriptyline, and acenaphthene was separated within a very short time. Furthermore, nucleosides and nucleobases were separated with the same column in HILIC mode (Fig. 1b).

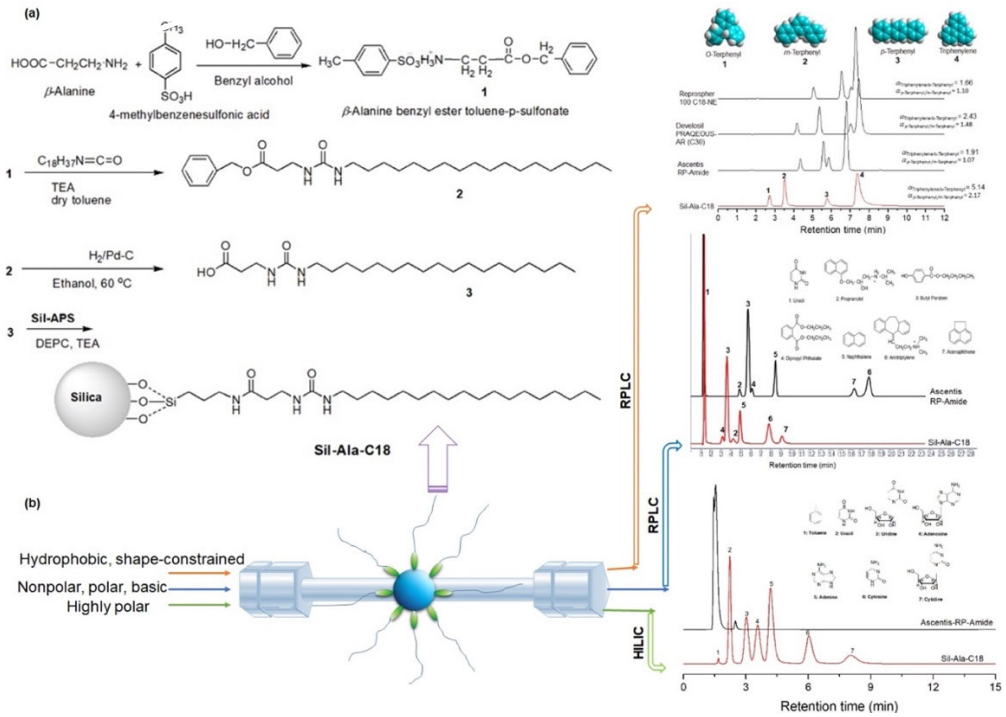


Fig. 1: Synthesis of the embedded polar groups (urea and amide) containing stationary phase (Sil-Ala-C18) from β-alanine (a). Application of the phase for separation of the mixtures of hydrophobic and shape-constrained isomers, nonpolar, polar, and basic analytes in RPLC, and highly polar analytes in HILIC mode (b).

Funded by: Alexander-von-Humboldt Foundation

Quantification of local anesthetics in tattoo creams

Juan Francisco Ayala Cabrera, Lidia Montero

Local anesthetic creams are used in intact skin for minor surgeries. The two main anesthetics compounds used in these creams are lidocaine (LIDOC) and prilocaine (PRILOC). However, LIDOC can be metabolized to 2,6-dimethylaniline (DiMetANI) and PRILOC to orto-toluidine (O-TOL) which are more toxic metabolites than their corresponding products and are related to potential cancerogenic activity in humans. Therefore, the control and quantification of these metabolites in commercial products is of vital importance. One of the uses of these local anesthetics creams is their application during tattooing. Therefore, in this study thirteen tattoo creams were analyzed to quantify the concentration of the two main anesthetics and their metabolites. An LC-MS analysis was optimized to quantify the presence of O-TOL, DiMetANI, LIDOC, and PRILOC in the tattoo creams. To maximize the sensitivity of the method, an electrospray ionization (ESI) coupled to a triple quadrupole mass spectrometer (QqQ) was employed. The ionization and collision parameters were optimized to maximize the signals and therefore the sensitivity of the method.

After optimizing the analysis of local anesthetics and their metabolites, the figures of merit of the UHPLC-MS/MS method were determined. Instrumental limits of detection (iLODs) range at the medium ng L^{-1} which was low enough to detect these compounds in tattoo creams. Moreover, the method provided a good linearity along the working range (0.05-500 µg L^{-1}). The precision (estimated as the relative standard deviation (RSD) of each calibration point, n=3) and the trueness (estimated as the relative error (RE) between the theoretical and the found concentration for each calibration point, n=3) was lower than 8% and -13%, respectively. Besides, the ion ratio (IR, q/Q) defined as the ratio between the response for the selective reaction monitoring transitions selected for confirmation (q) and quantification (Q) were established for all the compounds as an additional criterion for confirmation.

These figures of merit show the good performance of the developed UHPLC-MS/MS methodology for the analysis of local anesthetics. Then, the thirteen tattoo creams were analyzed by this method for the quantification of the local anesthetics in the sample. The theoretical results reported in the label of the tattoo creams did not match with the content found for both lidocaine and prilocaine in most of the cases. Only one cream showed similar concentrations than those reported by the manufacturer. These results may confirm the mislabeling of the products by the manufacturers. Additionally, O-toluidine could be quantified in three of the samples, although the found concentrations were very low (ca. 0.3-0.6 mg g-1). Figure 1 illustrates the detection of the local anesthetics in four of the thirteen samples with different content of LIDOC, PRILOC and even O-TOL.

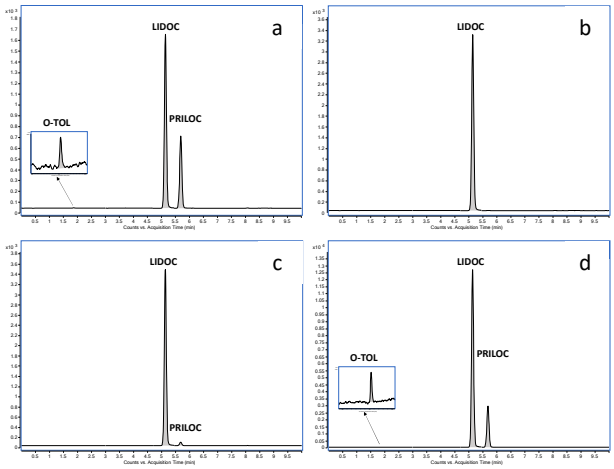


Fig. 1.: Detection of Lidocaine and prilocaine concentration in four of the thirteen samples. In samples a) and d) also orto-toluidine was detected and quantified.

Collaborative Project – Project Partner: Elisabeth Weber and Prof. Elmar Richter† (Munich, Germany)

Non-targeted HPLC-HRMS approach to face the analysis of ancient samples related to the origin of life

Lidia Montero, Isabelle Ardic, Juan F. Ayala Cabrera

The origin of life remains an unsolved question for sciences. Throughout history, different theories have been proposed although they have shown some weak points that could not support the established hypotheses. Recently, Schreiber *et al.* suggested that early steps in the development of life could have occurred in the deep-reaching tectonic faults. Organic molecules can be included in fluid inclusions of minerals, grown in the hydrothermal environment of tectonic faults of the upper continental crust. Under these conditions, these sensitive organic compounds are well protected against UV radiation and could undergo complex reactions in a two-phase system formed by hot H_2O and supercritical CO_2. Thereby, these minerals might have entrapped small amounts of the fluid phase containing the formed compounds that may represent the original composition of the prebiotic planet stage.

In this project, archaic hydrothermal quartz crystals from the Jack Hills (Western Australia) dating from the prebiotic times were analyzed using a non-targeted high performance liquid chromatography-high-resolution mass spectrometry (HPLC-HRMS) approach. To do that, each sample has been analyzed by two different separation mechanisms by using a reverse (Zorbax SB C18, 100 x 2.1 mm; 1.8 µm) and a hydrophilic liquid interaction chromatography (ZIC-HILIC, 150 x 1 mm;3.5 µm) column. This strategy helps to increase the confidence level on the identification of the compounds coming from the fluid inclusions. For instance, as can be seen in Figure 1, the *m/z* 152.0567 showed a different retention in both chromatographic columns. Combining this information with tandem mass spectrometry experiments and the monoisotopic mass measurement, it was possible to tentatively identify this compound as guanine (level of confidence 2a) after matching with a mass spectra library (*mzCloud*).

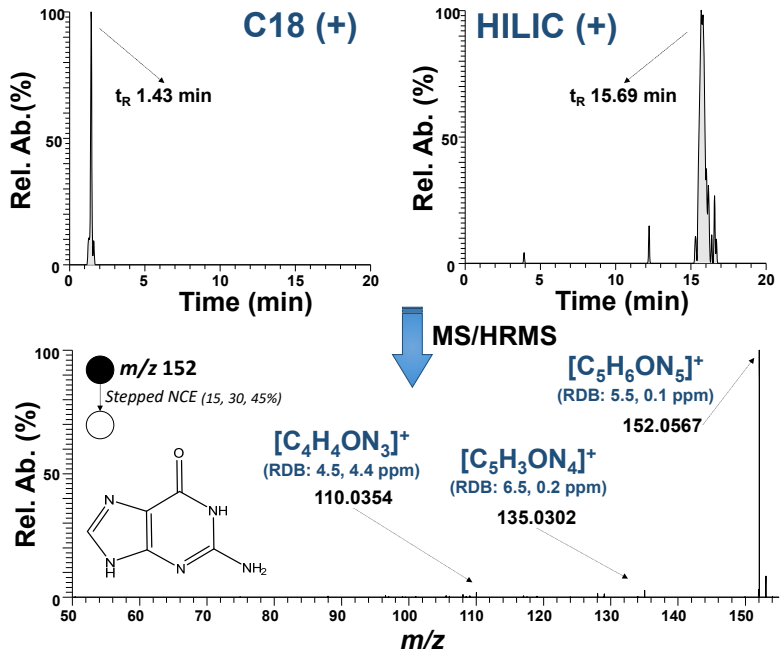


Fig. 1: Extracted ion chromatograms of guanine in a C18 and a ZIC-HILIC column as well as the tandem mass spectrum achieved with a qExactive plus with enhanced resolution

Collaborative Project – Project Partner: Prof. U. Schreiber and Prof. C. Mayer (University of Duisburg-Essen)

Analysis of Polyamines in Cancer Cells

Sven W. Meckelmann, Pia Wittenhofer

Polyamines are a group of important metabolites that are involved in various biological processes such as nuclein and protein biosynthesis, cell development as well as autophagy. The process is necessary for a balance between the production of new cell components and the degradation of old ones. Autophagy is induced when cells are staving and are forced to use up internal resources more efficiently.

Here we were analyzing polyamines to characterize the effects of fasting and post-fast refeeding on tumorigenesis in crypt stem cells from mice. Therefore, we developed an LC-ESI-QqQ-MS method that allowed the sensitive and selective detection of polyamines after derivatization with dansyl chloride. For the separation, we used a ZORBAX Eclipse Plus C18 RRHD column (50x2.1mm, 1.8µm) and water (A) and ACN/water 90/10 (B) both with 0.1% formic acid as eluents. The method allowed a fast quantification of all important polyamines (Figure 1 left). As can be seen from the quantitative results, fastening is reducing the levels of puterescine, spermidine, and spermine in the samples (Figure 1 right).

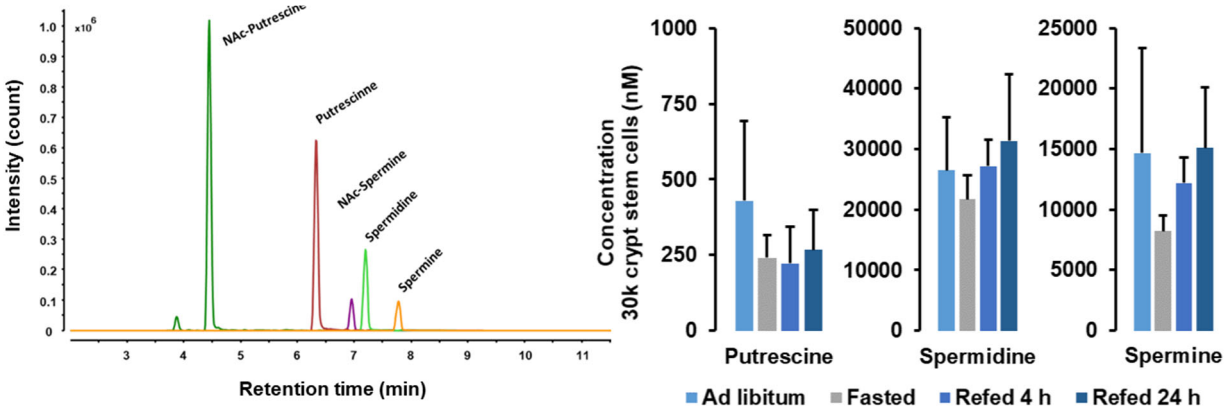


Fig. 1: Separation of polyamines analyzed by means of LC-ESI-QqQ-MS (left). Quantitative results for the three detected polyamines putrescine, spermidine, and spermine (n=5, right).

Collaborative Project – Project Partner: Prof. Dr. Alpaslan Tasdogan (Institut for Dermatology, University Hospital Essen, Germany) Ömer H. Yilma (Koch Institute for Integrative Cancer Research at MIT, Cambridge, USA)

Differences in Metastasis – Using Untargeted Metabolomics to Elucidate Organotropic Effects in the Metastasis of Cancer Cells

Jonas Rösler, Sven Meckelmann, Alpaslan Tasdogan

The hazard of cancer diseases is highly related to the process of metastasising. In order to survive the metastatic cascade, cancer cells need to undergo continuous metabolic adaptations to the changing chemical microenvironment. This leads to a strong correlation between the cell's metabolome and the properties of the metastatic site, causing preferences in metastasis to specific organs for each cancer type also known as organotropism. To gather more information about the influence of organotrophic effects in the metastatic cascade, this project aims to compare the global metabolic profile of different metastatic sites with their primary tumour. The used method was designed for untargeted metabolomics and consisted of a liquid extraction followed by HILIC separation using an *Agilent AdvanceBio MS Spent Media* column and data dependent MS/MS analysis by *Thermo qExactive Orbitrap* MS. Received data was initially processed in *MSDial* and subsequently filtered. The final dataset was evaluated for differences in the metabolic profile of the primary tumour and the corresponding metastases using *Simca* and *Metaboanalyst*. The analysis was conducted on 42 mouse samples consisting of subcutaneous injected primary tumours and corresponding lung, liver and kidney metastases. Injected cells originated from the four cell lines A375, M405, M481 and UT10. Every sample was measured as biological triplicate. Preliminary results indicate a significant difference especially between the primary tumours and their lung metastases as pictured above. Also, the cell lines show an influence on the metabolic pattern unique to specific organs. These global differences in the metabolic profile will be further evaluated by tracing them to alterations in specific pathways, which could enable new possibilities in cancer treatment by targeting cancer progression.

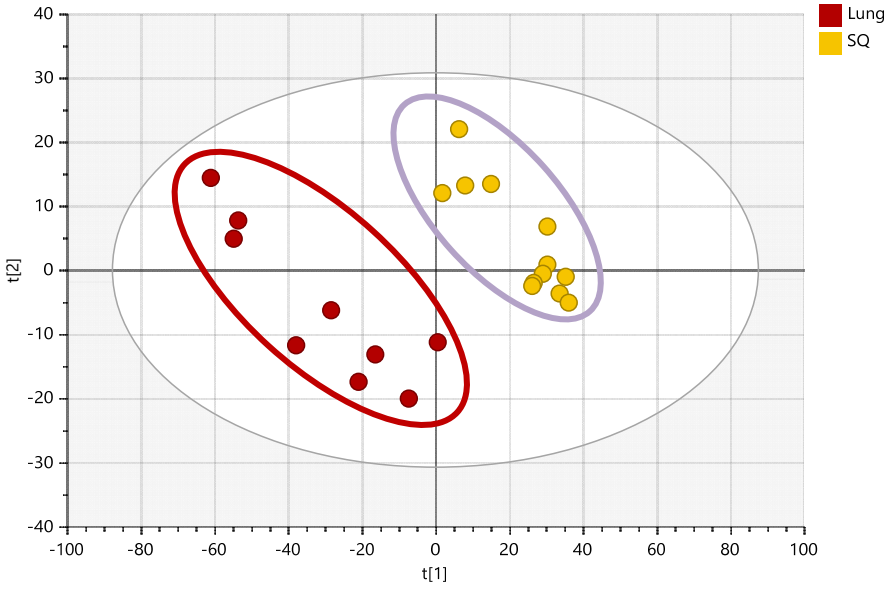


Fig.1: Partial least square – discriminant analysis (two major components) of all Lung and primary tumour (SQ) samples. Metabolic differences between primary tumour and metastases visible as formation of sample groups.

Funded by: A. T. was funded by an Emmy-Noether Award from the German Research Foundation (DFG, 467788900) and the Ministry of Culture and Science of the State of North Rhine-Westphalia (NRW-Nachwuchsgruppenprogramm)

Development of a heart-cutting LC method (LC - LC) for the analysis of short-, medium, and long-CoA esters

Constantin P. Krempe, Lidia Montero, Paul E. Görs, Delia Castilla-Fernández, Sven W. Meckelmann

CoA esters have a key role in the synthesis and degradation (β-oxidation) of fatty acids as well as they are important metabolic regulators in several metabolic pathways like citric acid cycle, lipid, amino acid, and carbohydrate metabolisms. Therefore, the analysis of CoA esters is of great interest for the determination of these metabolic pathways and the identification of possible markers of metabolic disorders. The chemical structure of CoA esters consisted of one fatty acid, a 3'-phospho-AMP linked to phosphorylated pantothenic acid and cysteamine. The chemical variety of CoA esters in the natures relies on the fatty acid chain that determines the classification of these compounds in short-, medium, and long-CoA esters. Besides of the big range of CoA ester metabolites, another challenge for the determination of these compounds is their relative low concentration in biological samples in comparison to other lipids.

For this reason, currently most of the analytical methods developed for the analysis of CoA esters consist of the use of sample pretreatment to clean and concentrate the sample, for instance using solid phase extraction (SPE), and the chromatographic analyses are focused only in part of the CoA ester groups (short-, medium, and long-CoA esters). In this work, a multidimensional heart-cutting liquid chromatography method (LC – LC) is developed for the analysis of the whole range of CoA esters in biological samples without the need of a pre-fractionation of the sample. To do so, a HILIC column was used in the first dimension (^{1}D) due to the ability of this separation mode to separate lipids by families, thus the aim of this ^{1}D was to optimized the separation of the sample so that all CoA esters eluted in one peak. That way, the CoA-ester peak containing all the CoA standards could be modulated in one fraction by means of a hearth cutting modulation. For the second dimension (^{2}D), a C18 EVO for the separation of the individual CoA esters accordingly to their fatty acid chain. The first challenge to solve was the reduction of breakthrough in the ^{2}D separation caused by the injection of the CoA ester fraction into the ^{2}D column dissolved in a strong solvent. To avoid this distortion of the ^{2}D septation several actions were taken: i) use of a trapping column in the interface with a similar ^{2}D retention mechanism (C18) that allowed the focusing of the CoA esters; ii) a make-up flow with a highly aqueous composition was introduced before the trapping column to weaken the strength of the solvent; iii) a deep pH optimization was done for the make-up solvent and the ^{2}D mobile phase. Thanks to all this actions a good separation of a large range of CoA compounds (from free CoA to long 24C fatty acid chain CoA esters) was achieved (Fig. 1). Regarding the detection of the CoA esters, an electrospray ion source (ESI) coupled to a triple quadrupole mass spectrometer was selected due to its high sensitivity. As the expected concentration of CoA esters in real samples is very low, a careful optimization of the ESI conditions was optimized by an experimental design to maximize the ionization of a big range of CoA compounds.

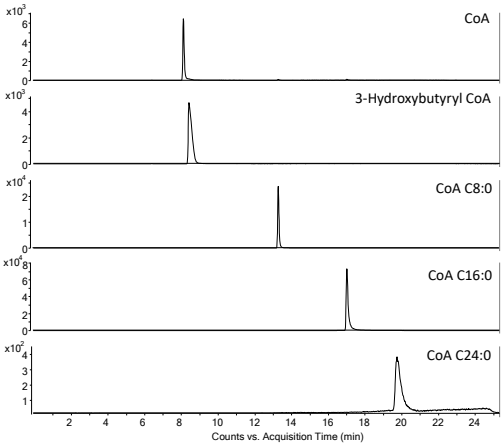


Fig. 1: CoA ester separation achieved after the optimization of the LC – LC method (from free acid to long fatty chain CoA esters)

Development of a 2D Heart-Cut LC-LC-MS/MS Method to Characterize the Biosynthesis of Cholesterol in Cancer Cells

Pia Wittenhofer, Sven W. Meckelmann

There is increasing evidence that cholesterol homeostasis is altered in cancer. Current studies have reported increased levels of cholesterol in cancer cells. However, not all precursors in cholesterol biosynthesis are usually monitored due to various difficulties in the analysis. One challenge in monitoring cholesterol biosynthesis is based on the large concentration differences of precursors to cholesterol. Depending on the sample, cholesterol can occur in a 1000-fold higher concentration compared to its precursors such as lathosterol or lanosterol. Moreover, most sterols are structural similarity which is challenging for selective detection. For example, some molecules differ only in the position of a double bond and selective detection by mass spectrometry only can not be achieved. In addition, interference between analytes and matrix are causing poor reproducibility

In this project, we developed a 2D LC-LC-MS method to analyze the whole pathway of the cholesterol biosynthesis. For this purpose, a column screening was performed. In total, 42 different columns with different stationary phases (C4, C8, C18, EC-C18, EVO-C18, PFP, Biphenyl, Phenyl-Hexyl), inner diameters (1 to 4 mm), lengths (30 to 150 mm) and particle sizes (1.3 to 5 µm) were used under the same conditions. The best separation was achieved by using a PFP column. Due to the expected concentration differences, a heart-cut method was developed to separate the cholesterol peak from the precursor molecules. To focus cholesterol during the heart-cut, a trapping column was used instead of a loop. Figure 1 shows a separation of 14 different sterols that are part of the cholesterol biosynthesis within 22 minutes. Detection was carried out by using an Agilent 6470 QqQ-MS in scheduled reaction monitoring mode. Currently, the method is characterized according to the EMA guidelines for bioanalytical method validation.

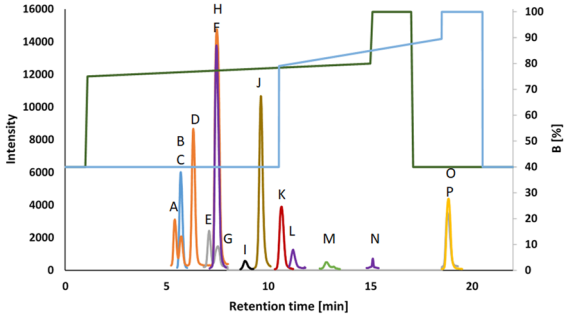


Fig. 1: Chromatogram of the 2D measurement of the cholesterol biosynthesis, deposited with the percentage B of the gradient of 1. dimension (green) and 2. dimension (light blue). Elution order is zymosterol (A), dehydrodemosterol (B), dehydrolathosterol (C), desmosterol (D), zymostenol (E), FF-MAS (F), lathosterol (G), 7-hydrocholesterol (H), 2,3-oxidosqualene (I), dihydro FF-MAS (J), dihydro T-MAS (K), dihydrolathosterol (L), lanosterol (M), squalene (N), cholesterol (O), T-MAS (P). LC-LC was carried out using a Kinetex PFP-column and a Kinetex EC-C18 -column

Collaborative Project – Project Partner: Prof. Dr. Annette Paschen and Dr. Barbara M. Grüner, (Molekulare Tumorimmunologie, University Hospital Essen, Germany)
Funded by: Deutsche Forschungsgemeinschaft (DFG) - ME 5800/1-1

Multidisciplinary study of the use of black currant fruits, juice and by-products: comprehensive chemical characterization and neuroprotective activity

Lidia Montero, Priscilla Nahn, Juan Francisco Ayala Cabrera

Black currants are fruits with a myriad of bioactive compounds that present a unique and complex phytochemical composition. They are particularly rich in phenolic compounds, highlighting their content in anthocyanidins. Black currants are mostly consumed as fruit juice. However, the consumption of whole fruits instead of fruit juice is known to enhance the related health-beneficial effects because during juice production, a high amount of the bioactive compounds present in the seeds, pulp, and peel remain in the pomace, which usually is discarded.

In this work, a comparison of the antioxidant and neuroprotective activities of black currant fruits, juice and the remaining pomace after juice extraction are evaluated. To do so, two different green extraction techniques were used, pressurized liquid extraction (PLE), and supercritical liquid extraction (SFE). Moreover, the chemical composition of all the PLE and SFE extracts was characterized by two-dimensional liquid chromatography coupled to tandem high resolution mass spectrometry (LC × LC-DAD-MS/HRMS). Regarding the extraction procedure, PLE provided higher extraction yield than SFE. The high polarity of the solvent used in PLE fostered the extraction of the target compounds present in the fruit samples (mainly phenolic compounds). The antioxidant activity, in terms of total phenolic content (TPC) and total flavonoid content (TFC), showed that the pomace extracts obtained with both PLE and SFE are the fractions with higher phenolic compound concentration. Regarding the neuroprotective activity, the best activity was observed for the pomace and natural juice samples extracted with PLE, although all the tested extracts showed a modest activity. The chemical characterization of these extracts by LC × LC-DAD-MS/HRMS revealed a very complex profile of the three samples extracted by PLE and SFE. The most intense peaks corresponded to anthocyanidins, as can be seen in Figure 1. Interestingly, it was observed that fruits and pomace presented a very high anthocyanidin concentration while the content of these important phenolic compounds was drastically reduced in the juice sample.

These results revealed that during the juice process, the anthocyanidins remained in the pomace fraction, giving rise to a poorest juice in some phenolic compounds such as anthocyanidins. So, the consumption of the whole fruit could be recommended to intake all the beneficial compounds present in the black currant. Besides, a valorization of the waste products generated in this industry could provide new high added value products.

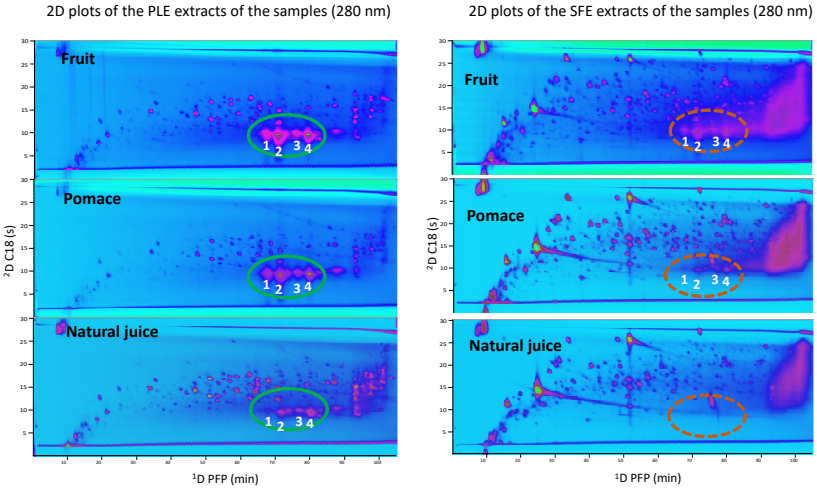


Fig. 1: 2D plots of the fruit, pomace and natural juice black currant samples. Peak 1: delphinidin 3-O-glucoside; peak 2: delphinidin 3-O-rutinoside; peak 3: cyanidin 3-O-glucoside; peak 4: cyanidin 3- O-rutinoside.

Collaborative Project – Project Partner: Dr. Miguel Herrero (Foodomics laboratory, CSIC, Spain)

A novel implement for maximizing the separation power of multidimensional liquid chromatography: Multi-^{2}D-LC × LC

Lidia Montero, Fariha F. Britz, Juan Francisco Ayala Cabrera

The characterization of food samples has an increasing interest in the scientific field. Food authentication and food bioactivity are probably the disciplines where the complete characterization of food samples has more impact. Very powerful separation techniques are required to obtain chemical information about a food complex samples like multi-analytical platforms able to maximize the acquisition of high-quality data for unequivocal identification. The use of several analytical techniques may be expensive and time consuming. In this work, we have developed a new analytical implementation consisting of a comprehensive two-dimensional liquid chromatography (LC × LC) where two different columns act alternatively as second dimension (^{2}D) separation. These two columns should provide complementary separation for all the compounds present in the sample. In this way, fractions coming from the first dimension (^{1}D) that are not well retained and separated in one of the ^{2}D columns are directed towards the other ^{2}D column that provides better selectivity for them, and vice versa, getting an improved orthogonality level. This novel setup has been called multi-^{2}D-LC × LC. For the development of the multi-^{2}D-LC × LC, vermouth was chosen as complex food matrix. Vermouth is a highly complex phenolic compound mixture. This beverage is a fortified wine whose production consists of the maceration of several parts of aromatic plants in wine and a neutral spirit. For the optimization of the multi-^{2}D-LC × LC analysis of vermouth a PFP column was selected for carrying out the separation in the ^{1}D. Then, two conventional LC × LC methods using HILIC and C18 columns in the ^{2}D were carefully optimized. However, after a deep evaluation of all the parameters that affect the 2D separation, neither the PFP × C18, nor the PFP × HILIC couplings provided the complete separation of the sample. As can be seen in Fig. 1a, the most polar compounds eluted at the beginning of the PFP-^{1}D column were very well separated when using HILIC as 2D, but they did not show any retention in the C18 ^{2}D column. On the other hand, the medium-polar compounds were completely separated with high orthogonality using the C18-^{2}D column, but a big breakthrough was observed when the HILIC column was selected as ^{2}D. Therefore, the HILIC-^{2}D and the C18-^{2}D showed a complementary separation. Hence, the use of the separation power of both separation modes were coupled in the multi-^{2}D-LC × LC. In this way, from 0 to 30 min the ^{2}D separation was carried out using the HILIC column and from 30 min to the end of the analysis, the C18 column was selected. The chromatogram obtained after the multi-^{2}D coupling is depicted in Figure 1b where it is possible to observe how the multi-2D separation obtained with the HILIC and C18 column was exactly preserved as the separation obtained with the single setups.

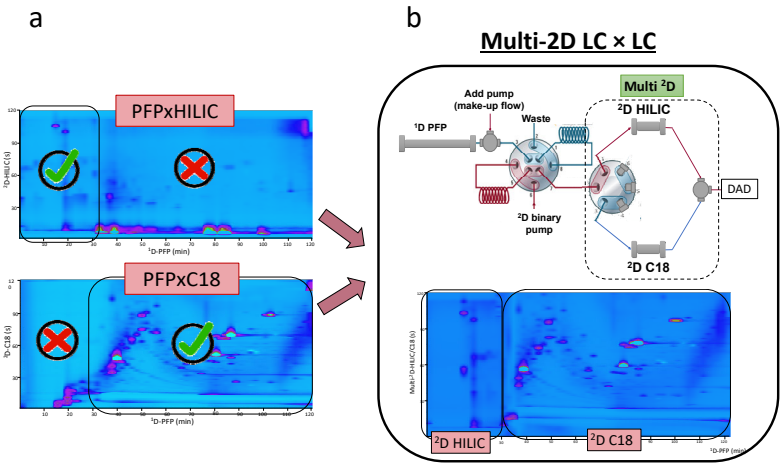


Fig. 1: a) Maximum separation of the vermouth sample achieved using conventional PFP × HILIC and PFP × C18 methods. b) Multi-^{2}D-LC × LC scheme and separation coupling the HILIC-^{2}D column from 0 to 30 min and the C18-^{2}D column from 30 min till the end of the analysis.

Funded by: Deutsche Forschungsgemeinschaft (DFG)

Investigation of Maillard reaction by using thermogravimetry hyphenated with an orbitrap mass spectrometry

Maha Alhasbani

Maillard reaction produces flavor and aroma while cooking and creates brown pigments in cooked food in a very specific way. It occurs when amino acids and some sugars are arranged in rings and collections of rings that give the food a brown color. An equal concentration of glucose with asparagine and glycine was placed in a crucible for analysis. The solvent used was water. In order to optimize the analysis parameters and obtain a large number of high intensity signals, a temperature rise of 65 °/min was chosen to more clearly identify individual reaction steps of the Maillard reaction. The TIC for the reaction between glucose and glycine at 12 minutes of analysis time is shown in Figure 1, along with the mass spectrum between 4 and 12 minutes. Based on literature data, volatiles of the Maillard reaction were searched for using the respective EICs. A number of compounds belonging to different groups were found: Pyrazines, Furans, Pyrroles, Pyridines, Pyrolidines and Pyrolizines. The same compounds were searched for in both glucose+asparagine and glucose+glycine, and more than 40 compounds were found to be formed in both reaction mixtures. In order to also analyze real samples, various food samples were placed in the crucible for analysis. These samples include: Milk, bread, potatoes, salami and onions. In addition to mass results, thermal results such as degradation phases, reaction types, melting points, and mass losses were also examined.

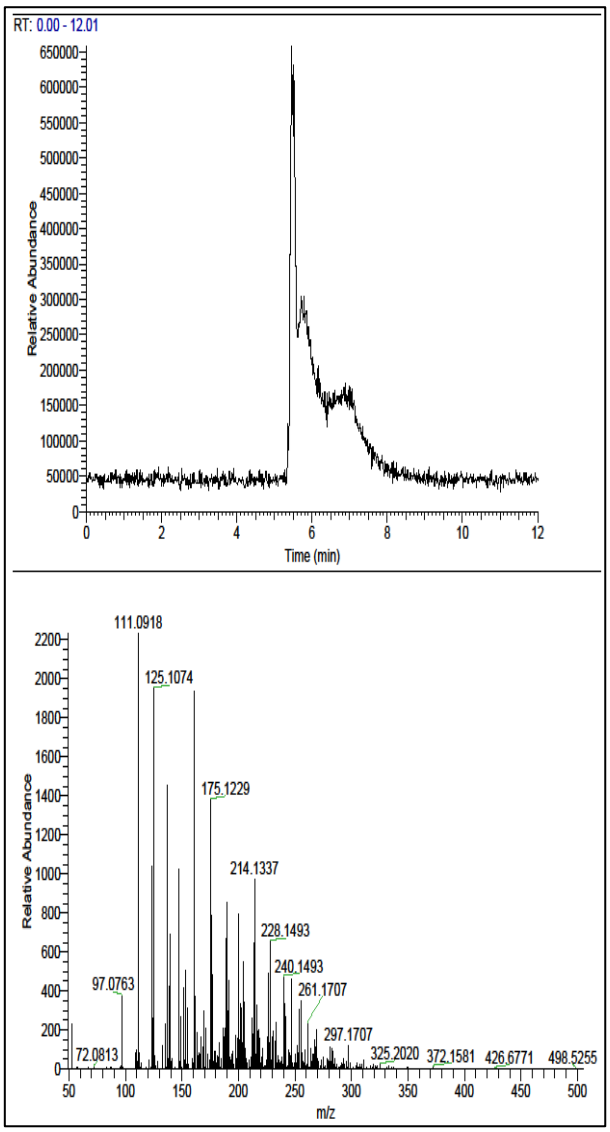


Fig. 1: TIC and mass spectrum of the reaction between glucose and glycine under the rate 65 °/min and 12 min analyzing time

Funded by: Hitachi High-Tech (Tokyo, Japan) and Konrad Adenauer Foundation.

Doctoral Thesis accomplished 2022

Dr. Christian Lipok

Development and optimization of an ion source for chemical ionization at atmospheric pressure

A new atmospheric pressure chemical ionization source design was developed. The in-house developed ion source is made of a sealed ionization chamber which enables the coupling of a gas chromatograph and a mass spectrometer with atmospheric pressure interface. The ion source performance was investigated and optimized to increase precision. The introduced design allows the control and optimization of the ion source temperature, humidity, corona needle position, capillary column position and the flow rate of an additional make-up gas. It was found that the column position, humidity and make-up gas flow rate affect the sensitivity and repeatability of the ion source and the GC-MS coupling. The ion source performance was compared with a commercially available GC-APCI ion source. The comparison was done by the analysis of chemical standards of different polarity and proton affinity. The determined limits of detection for these standards were in the same order of magnitude (pg on column). Furthermore, a reproducibility with RSD values < 16 % were determined for all compounds. That is significant smaller compared to the commercial GC-APCI ion source which shows RSD values up to 55%.

The ionization behavior of methyl esters and pesticides like organochlorine, organophosphorus, organonitrogen, herbicide methyl esters and pyrethroids compounds during APCI was investigated. It was observed that most of the analyzed pesticides were detected as $[M+H]^+$ and $[M]^+$. Furthermore, the elimination of halogens and water from the analytes were observed. In addition, mechanisms like Retro Diels Alder occurred. The analysis of the ion source fragmentation revealed that the fragmentation of the analytes is not only based on excess energy of the protonation. To predict fragmentation, the transition states and the enthalpy of formation must be considered. Furthermore, it has been shown that the conditions in the ion source can lead to adduct formation. Benzyl alcohol and related compounds showing reactions with the chemical background (phthalates) and will be detected with APCI as adduct ion with $[M+72]^+$.

For a performance test under real conditions, the new APCI ion source was used for the determination pesticides in commercially available coffee beans from Vietnam. The described ionization behaviour was used for the GC-MS/MS method development and for most of the analytes $[M+H]^+$ or $[M]^{+\cdot}$ ions were detected. The developed GC-MS methods revealed for pesticide's limits of detection between 1 - 250 pg on column and relative standard derivations < 16 % for all compounds. The used ultrasonic-solid-liquid-extraction yielded recovery rates of approximately 60 to 100 %. Residues of herbicide methyl esters, organophosphorus compounds and organonitrogen compounds have been detected in the analysed coffee beans.

Master's Theses Accomplished 2022

Yvonne Isabelle Gisela Ardic
Optimization of a non-target HPLC-HRMS workflow to determine polar compounds related to the origin of life

Fariha Firoz Bristy
Analysis of the polar fraction of vermouth wine by using two-dimensional liquid chromatography

Pascal Kadej
Development and application of an automated sample preparation for target and non-target lipid analysis

Peter Lars Stahlkopf
Design of a novel second dimension setup for 2D LC analysis of very complex samples

Bachelor's Theses Accomplished 2022

Laura Angela Kiesewetter
Development of a 2D-LC-ESI-IM-qTOF-MS method for cholesterol biosynthesis

Dorian Klaucke
Development and application of a Paternò-Büchi post-column derivatization for GC-MS to determine the position of double bonds in fatty acids.

Constantin Krempe
Development of a two-dimensional heart-cutting liquid chromatographic (LC-LC) method for the characterization of CoA-esters.

Michael Christian Lieberum
HPLC column characterization of newly synthesized packing materials for improved performance in RP mode

Sebastian Löbbecke
Analysis of phthalate esters in drinking water by GC-TPI-MS

Priscilla Nhan
Phenolic compound profiling of black currant juice by comprehensive two-dimensional liquid chromatography (LCxLC)

Christoph Schakau
Characterization of an ultrasonic nebulizer unit for liquid-injection-mass spectrometry.

Marie Carolin Stempel
Application and further development of "low-temperature" normal-phase chromatography

Scientific Publications 2022

Original Paper / Peer-reviewed

D. Maehler, S. Hoefgen, U. Münchberg, O. J. Schmitz, J. Rautschek, Y. Huang, E. Freier, V. Valiante, **Time-resolved multiparameter analytics on a cell-free production platform for acyl-CoA precursors**, Analytical Science Advances (2022) https://doi.org/10.1002/ansa.202200021

J. F. Ayala-Cabrera, L. Montero, S. W. Meckelmann, F. Uteschil, O. J. Schmitz, **Review on atmospheric pressure ionization sources for gas chromatography-mass spectrometry. Part II: Current applications**, Analytica Chimica Acta (2023) 1238:340379; 10.1016/j.aca.2022.340379

J. F. Ayala-Cabrera, L. Montero, S. W. Meckelmann, F. Uteschil, O. J. Schmitz, **Review on atmospheric pressure ionization sources for gas chromatography-mass spectrometry. Part I: Current ion source developments and improvements in ionization strategies**, Analytica Chimica Acta (2023) 1238:340379; 10.1016/j.aca.2022.340379

L. Kuschmierz, M. Meyer, C. Bräsen, J. Wingender, O. J. Schmitz, B. Siebers, **Exopolysaccharide composition and size in Sulfolobus acidocaldarius biofilms**, Frontiers Microbiology (2022) 13:982745; 10.3389/fmicb.2022.982745

V. Dosedělová, M. Laštovičková, J. F. Ayala-Cabrera, J. Dolina, Š. Konečný , O. J. Schmitz, P. Kubáň, **Quantification and identification of bile acids in saliva by liquid chromatography-mass spectrometry: Possible non-invasive diagnostics of Barret's esophagus?**, Journal of Chromatography A (2022) 1676:463287; 10.1016/j.chroma.2022.463287

S. K. Heuser, A. LoBue, J. Li, Z. Zhuge, F. Leo, T. Suvorava, A. Olson, R. Schneckmann, D. D. Guimaraes Braga, T. Srivrastava, L. Montero, O. J. Schmitz, J. P. Schmitt, M. Grandoch, E. Weitzberg, J. O. Lundberg, J. Pernow, M. Kelm, M. Carlström, M. M. Cortese-Krott, **Downregulation of eNOS and preserved endothelial function in endothelial-specific arginase 1-deficient mice**, Nitric Oxide (2022) S1089-8603(22)00067-2; 10.1016/j.niox.2022.06.004

Y. Großmann, U. Schreiber, C. Mayer, O. J. Schmitz, **Aliphatic aldehydes in the Earth's crust – remains of prebiotic chemistry?** Life (2022) 12: 925; https://doi.org/10.3390/life12070925

J. F. Ayala-Cabrera, J. Turkowski, F. Uteschil, O. J. Schmitz, **Development of a tube plasma ion source for gas chromatography-mass spectrometry analysis and comparison with other**

atmospheric pressure ionization techniques Analytical Chemistry (2022) 94:9595-9602; 10.1021/acs.analchem.2c00582

T. Koehler, J. Wingender, M. Lueling, S. W. Meckelmann, U. Telgheder, O. J. Schmitz, **Characterization of the extracellular volatile metabolome of Pseudomonas aeruginosa applying an in vitro biofilm model under cystic fibrosis-like conditions**, Frontiers in Bioscience – Landmark (2022), 27:156; 10.31083/j.fbl2705156

A. R. Ziefuß, T. Hupfeld, S. W. Meckelmann, M. Meyer, O. J. Schmitz, W. Kaziur-Cegla, L. K. Tintrop, T. Schmidt, B. Gökce, S. Barcikowski, **Ultrafast cold-brewing of coffee by picosecond-pulsed laser extraction**, npj Science of Food (2022) 16:19; 10.1038/s41538-022-00134-6

L. Montero, S. Meckelmann, H. Kim, J. F. Ayala-Cabrera, O. J. Schmitz, **Differentiation of the cannabinoid and phenolic compounds of industrial hemp varieties by LC×LC-HRMS**, Analytical and Bioanalytical Chemistry (2022); https://doi.org/10.1007/s00216-022-03925-8

Misc. Publications

S. W. Meckelmann, P. Wittenhofer, K. Tötsch, O. J. Schmitz, **Supercritical Fluid Chromatography coupled with Drift Time Ion Mobility Quadrupole Time-of-Flight Mass Spectrometry as Tool for Lipid Characterization of HepG2 Cells,** LCGC Europe (2022) 35:207-212

Poster Presentations

L. Montero, O.J. Schmitz, S. W. Meckelmann, **Analysis of ultra-complex food samples by multidimensional analytical platforms**, Young Scientist Researchers Meeting of the Spanish Society of Mass Spectrometry (SEEM), Miraflores de la Sierra, Spain, March 2022

J. F. Ayala-Cabrera, J. Turkowski, F. Uteschil, O. J. Schmitz, **Development of a tube plasma ion source for GC-MS**, Young Scientist Researchers Meeting of the Spanish Society of Mass Spectrometry (SEEM), Miraflores de la Sierra, Spain, March 2022

J. F. Ayala-Cabrera, L. Montero, F. Uteschil, S. W. Meckelmann, O. J. Schmitz, **Tube plasma: a soft ionization for the GC-MS analysis of complex food samples**, EUROFAST2022, Nijmegen, The Netherlands, April 2022

L. Montero, J. F. Ayala Cabrera, S. W. Meckelmann, O. J. Schmitz, **Multi-^{2}D comprehensive liquid chromatography (multi-^{2}D LCxLC), a new setup for the analysis of extremely complex samples**, 50th International Symposium on High Performance Liquid Phase Separations and Related Techniques (HPLC 2022), San Diego, California, USA, June 2022 (Best Poster Award)

L. Montero, H. Kim, J. F. Ayala-Cabrera, S. W. Meckelmann, O. J. Schmitz, **Industrial Hemp Varieties Differentiation by Comprehensive Two-Dimensional Liquid Chromatography (LCxLC)**, 50th International Symposium on High Performance Liquid Phase Separations and Related Techniques (HPLC 2022), San Diego, California, USA, June 2022

L. Montero, P. E. Görs, D. Castilla-Fernández, C. P. Krempe, S. W. Meckelmann, O. J. Schmitz, **Analysis of CoA Esters using heart-cutting two-dimensional liquid chromatography coupled to mass spectrometry (LC-LC-MS)**, 50th International Symposium on High Performance Liquid Phase Separations and Related Techniques (HPLC 2022), San Diego, California, USA, June 2022

J. F. Ayala-Cabrera, L. Montero, I. Ardic, C. Mayer, U. Schreiber, O. J. Schmitz, **Orthogonal non-targeted HPLC-HRMS approach to face the analysis of ancient samples related to the origin of life**, 50th International Symposium on High Performance Liquid Phase Separations and Related Techniques (HPLC 2022), San Diego, California, USA, June 2022

P. E. Görs, L. Montero, O. J. Schmitz, S. W. Meckelmann, **Targeted Lipidomics of CoA-Esters by means of heart-cutting two-dimensional liquid chromatography coupled to mass spectrometry**, 50th International Symposium on High Performance Liquid Phase Separations and Related Techniques (HPLC 2022), San Diego, California, USA, June 2022

J. F. Ayala-Cabrera, S. Löbbecke, A. Pape, L. Montero, F. Uteschil, O. J. Schmitz, **Tube plasma ionization (TPI): a novel ion source for the determination of environmental pollutants in water by GC-MS**, 5. Mülheimer Wasseranalytisches Seminar (MWAS2022), Mülheim an der Ruhr, Germany, September 2022

J. F. Ayala-Cabrera, C. Lipok, E. Deibel, F. Uteschil, O. J. Schmitz, APCI, APPI, APLI, and LTP: **Uncommon ionization methods for GC-MS**, International Mass Spectrometry Conference (IMSC2022), Maastricht, The Netherlands, September 2022

L. Montero, S. Serio, P. Nahn, J. F. Ayala, O. J. Schmitz, M. Herrero, **Multidisciplinary study of the use of black currant fruits, juice, and by-products: comprehensive chemical characterization and neuroprotective activity**, XXI Scientific Meeting of the Spanish Society of Chromatography and Related Techniques (SECyTA 2022), Almeria, Spain, October 2022

Invited Lectures / Oral Presentations

Prof. Oliver J. Schmitz

APCI, APPI, APLI, and DBD: Uncommon ionization methods for GC-MS
APCE-CECE-ITP-IUPAC Meeting 2022, Angkor Wat, Cambodia, November 2022

2D-LC: Hype or huge Potential?
Micro-, Nano and 2D-LC-Symposium: User meeting for miniaturized and multidimensional chromatography, Frankfurt, Germany, September 2022

Why use GC-EI-MS when you can do better?
International Symposium on Chromatography (ISC), Budapest, Hungary, September 2022

Why use GC-EI-MS when you can do better?
University of Rostock, Rostock, Germany, June 2022

Dr. Sven Meckelmann

Effect of LC-IM-qTOF-MS Data Pretreatment in Targeted and Non-Targeted Lipidomics
50th International Symposium on High Performance Liquid Phase Separations and Related Techniques (HPLC 2022), San Diego, California, USA, June 2022

Award

In June 2022, during the 50th International Symposium on High Performance Liquid Phase Separations and Related Techniques (HPLC 2022), San Diego, California (USA) **Lidia Montero** was awarded with the Best Poster Awards for her poster titled: Multi-^{2}D comprehensive liquid chromatography (multi-^{2}D LCxLC), a new setup for the analysis of extremely complex samples

Institute Colloquium

Prof. Dr. David Chen from the British Columbia University in Vancouver, Canada, visited the Applied Analytical Chemistry (AAC) at University of Duisburg-Essen in December 2022. Beside cooperation talks he gave a lecture about CE-MS.

Miscellaneous

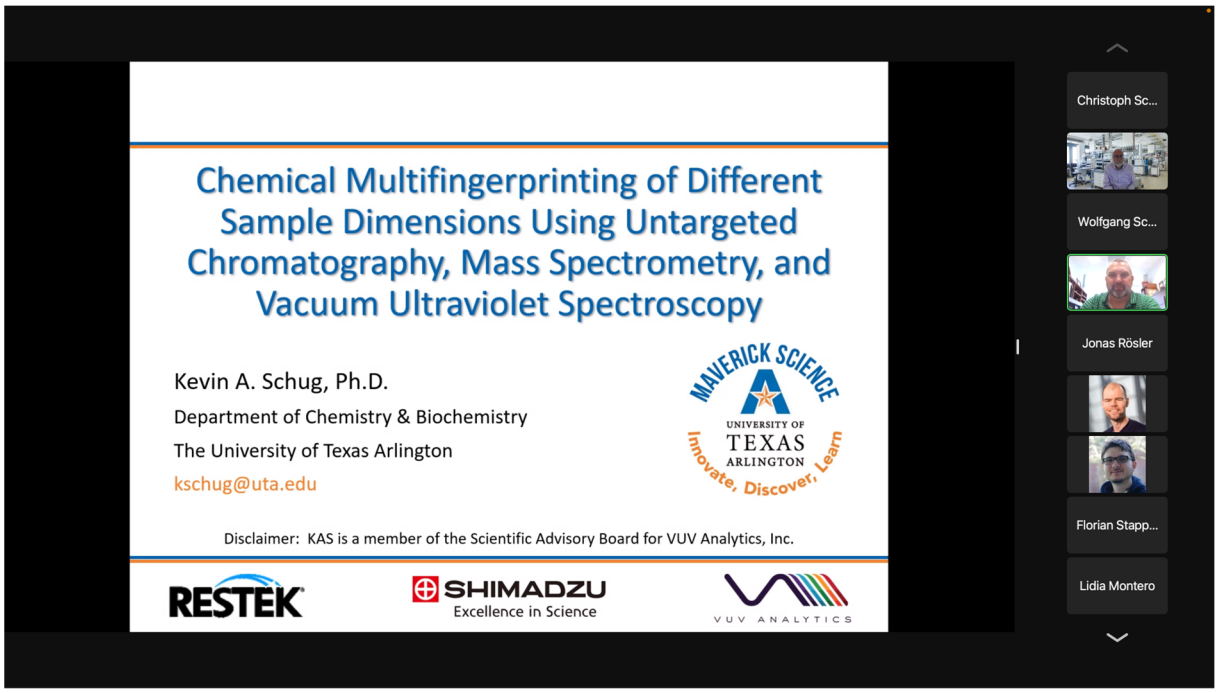
Editorial Tasks by Prof. Oliver J. Schmitz

- Editorial Board member of *Talanta open*
- Editorial Advisory Board member of *Trends in Analytical Chemistry (TrAC)*
- Associate Editor-in-Chief of *Journal of Analysis and Testing*
- Advisory Board member of *Chromatographia*
- Editorial Board member of *Journal of Pharmaceutical Analysis*
- Editorial Board member of *Vietnam Journal of Chemistry*
- Editorial Board member of *Chinese Journal of Chromatography*
- Member of the advisory board of analytica Munich
- Member of the DAAD selection committee (Foreigners from Asia and Oceania)
- Member of the DAAD selection committee (Project-related people exchange with India)
- Member of the committee for the Ernst-Bayer-Price
- Member of the committee for the Eberhard-Gerstel-Price

TRC-Forum

The Teaching and Research Center for Separation, the TRC, is part of Agilent´s global network of world-class Centers of Excellence and besides research in the field of multidimensional chromatography, Ionmobility-mass spectrometry, ion source development, lipidomics and metabolomics we offer three-day-courses on different analytical separation techniques with a practical part. These courses are open for everyone. In addition, a digital seminar, called TRC-Forum is organized. This year speakers from Australia, Belgium, Italy, Switzerland, and USA presented their newest results in the TRC-Forum.

Date [CET]	Title	Speaker
15th February	Doing more with less - smaller, better faster	**Ian D. Wilson** Imperial College London (UK)
3rd May 2022	Chemical Multifingerprinting of Different Sample Dimensions Using Untargeted Chromatography, Mass Spectrometry, and Vacuum Ultraviolet Spectroscopy	**Kevin Schug** University of Texas at Arlington, USA
17th May 2022	Separation Sciences and Multimodal Mass Spectrometry Workflows for Improving Information Content in Omics	**Gerard Hopfgartner** University of Geneva, Switzerland
24th May 2022	Where to go Next with Particles, Columns and Instruments?	**Gert Desmet** Vrije Universiteit Brussel, Belgium
31th May 2022	Guidelines for tuning the macropore structure of monolithic columns for high-performance liquid chromatography	**Sebastiaan Eeltink** Vrije Universiteit Brussel, Belgium
17th June 2022	Expectations beyond Design? The Innovation and Introduction of Comprehensive Two-Dimensional Gas Chromatography	**Philip Marriott** Australian Centre for Research on Separation Science, School of Chemistry, Monash University, Australia
5th July 2022	Innovative Advanced Analytical Methods in Biomedical Sciences	**Luigi Mondello** University of Messina, Italy



The TRC-Forum is organized via Zoom and I would like to invite you to have a look at the presentations and discuss them with us. If you are interested please send an email to my secretary (constanze.dietrich@uni-due.de). This can be done informally by simply stating your name. You will then receive a link to the respective lecture as soon as possible. Of course, the event is free of charge.

The next TRC-Forum will start in October 2023. You will find the program on the following homepage:

https://www.trc-separation.com/trc-forum

Please note that the times given are German time, i.e. Central European Time (CET).

Teaching

Chemistry (B.Sc. / M.Sc.)

Lecture Analytical Chemistry I (in German, Prof. Dr. O. J. Schmitz)

Tutorial Analytical Chemistry I (in German, Dr. S. Meckelmann)

Lecture Analytical Chemistry II (in German, Prof. Dr. O. J. Schmitz)

Tutorial Analytical Chemistry II (in German, Dr. S. Meckelmann)

Lecture Modern analytical methods for systems medicine (in German, Prof. Dr. O. J. Schmitz)

Seminar Modern analytical methods for systems medicine (in German, Prof. Dr. O. J. Schmitz)

Lecture Chemistry and analytics of food and their authenticity (in German, Dr. S. Meckelmann)

Seminar Chemistry and analytics of food and their authenticity (in German, Dr. S. Meckelmann)

Lecture Foodomics: Biochemistry of nutrition and analysis of functional foods (in German, Dr. S. Meckelmann)

Seminar Foodomics: Biochemistry of nutrition and analysis of functional foods (in German, Dr. S. Meckelmann)

Water Science (B.Sc. / M.Sc)

Lecture Analytical Chemistry I (in German, Prof. Dr. O. J. Schmitz)

Tutorial Analytical Chemistry I (in German, Dr. S. Meckelmann)

Lecture Analytical Chemistry II (in German, Prof. Dr. O. J. Schmitz)

Tutorial Analytical Chemistry II (in German, Dr. S. Meckelmann)

Lecture Applied Analytical Chemistry (in English, Prof. Dr. O. J. Schmitz)

Tutorial Applied Analytical Chemistry (in English, Prof. Dr. O. J. Schmitz)

Lecture Modern analytical methods for systems medicine (in German, Prof. Dr. O. J. Schmitz)

Seminar Modern analytical methods for systems medicine (in German, Prof. Dr. O. J. Schmitz)

Lecture Chemistry and analytics of food and their authenticity (in German, Dr. S. Meckelmann)

Seminar Chemistry and analytics of food and their authenticity (in German, Dr. S. Meckelmann)

Laboratory Technician Training

Instrumental analytical chemistry (in German, Prof. Dr. O. J. Schmitz)

Seminar

Analytical-chemical seminar
(in German/English, Prof. Dr. O. J. Schmitz in cooperation with Prof. Dr. T. Schmidt)

Practical Courses

Practical course analytical chemistry (Prof. Dr. O. J. Schmitz and Dr. S. W. Meckelmann)

Research practical courses (Prof. Dr. O. J. Schmitz and Dr. S. W. Meckelmann)

Teaching and Research Center for Separation

Course 1: Basic course HPLC (in German, Prof. Dr. O. J. Schmitz)

Knowledge Transfer (by Prof. Dr. O. J. Schmitz, in German)

Basic course LC-MS-Hyphenation (digital), February 2022

Basic course LC-MS-Hyphenation (digital), March 2022

Method school: HPLC for beginners (digital), August 2022

Method school: HPLC for advanced users (digital), August 2022

Basic course HPLC, Essen, Germany, September 2022

Basic course HPLC, Kronshagen, Germany, September 2022

Basic course GC-MS, Essen, Germany, November 2022

Basic course LC-MS (digital), November 2022

HPLC for advanced users (digital), December 2022

Master course GC-MS, Essen, Germany, December 2022

Annual Report 2022

University of Duisburg-Essen
Faculty of Chemistry
Applied Analytical Chemistry
Universitaetsstr. 5

2022