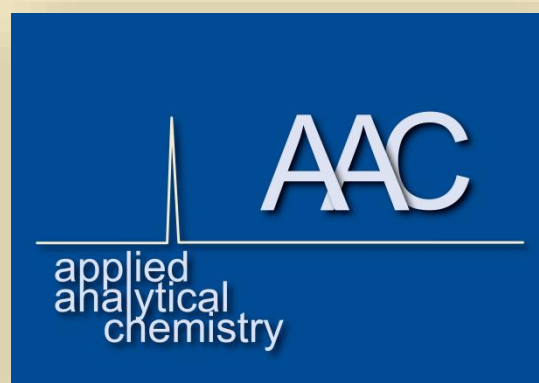


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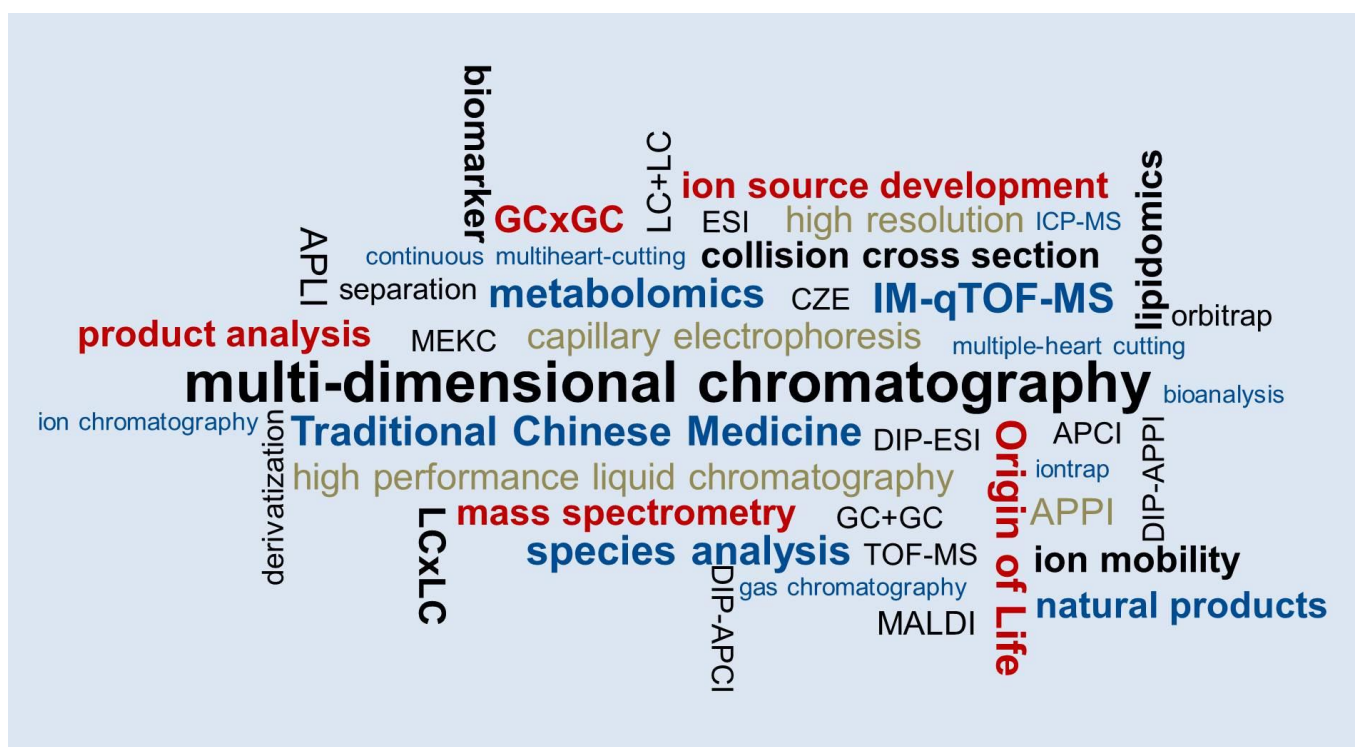
**Applied Analytical Chemistry
(AAC)**

Annual Report 2020



Applied Analytical Chemistry

Annual Report 2020



University of Duisburg-Essen

Faculty of Chemistry

Applied Analytical Chemistry

Universitaetsstr. 5

45141 Essen

Germany

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Applied Analytical Chemistry

What a crazy and historic year! But I would have gladly renounced to become a contemporary witness of this year. However, now the Corona year 2020 is coming to an end and I would like to share our annual report with you.

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.

The most important topic in 2020 was that we have focused our research topics on Metabolomics/Lipidomics. This field will be supported by our further work in ion source development and multidimensional chromatography.

2020 was the eight-year of the Applied Analytical Chemistry research group at the University of Duisburg-Essen and a very successful one.

Twelve scientific papers in peer-reviewed journals with a total impact factor of more than 43, one in a non-peer-reviewed journal, but as the title story (*The Column*), one further manuscript in the review process and five in preparation, four posters, and eight lectures at national and international conferences (digital and in presence) were presented. Two doctoral theses, 3 master's, and 5 bachelor's theses were completed in 2020. Several third-party funds were also successfully raised and further national and international industrial cooperations were extended. Many colleagues have contributed to an exciting year of research, teaching, and last but not least to shouldering many other tasks.

In 2020 several projects, funded by BMBF, DFG, VW, and industry were started or continued, e.g. development of new ion sources (LC-LTP, GC-APCI, and GC-APPI), μ LC+LC-MS for complex samples, and investigation of the metabolome/lipidome of various cells, bacteria, and archaea. We also intensify the cooperation with several working groups from the university hospital Essen and developed workflows in GC-MS and LC-MS for metabolome and lipidome analysis.



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Based on our Origin-of-Life research – together with Prof. Ulrich Schreiber and Prof. Christian Mayer (both University of Duisburg-Essen), we are still analyzing an 18 m long drill core (between 950 and 1000 m depth) near Laacher See in the Volcanic Eifel. This is a region in Germany, that is defined to a large extent by its volcanic geological history. Characteristics of this volcanic field are eg. volcanic tuffs, lava streams, and volcanic craters like the Laacher See. The Volcanic Eifel is still volcanically active today. And yes, we found the expected analytes, which will confirm our theory regarding the formation of life in tectonic fault zones.



Due to 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 12 dates per year. The TRC-Forum started this year in the winter semester and is a lot of fun.

I want to take this opportunity to thank the entire AAC team and all co-workers for their excellent work with all the hygiene regulations in the lab in this difficult year 2020 as well as 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 2021.

A handwritten signature in black ink, appearing to be 'Ulrich Schreiber'.

Essen, December 18, 2020



Applied Analytical Chemistry – Staff

Regular Staff

Prof. Dr. Oliver J. Schmitz	Head
Dr. Martin Sulkowski	Senior Researcher
Dr. Sven Meckelmann	Senior Researcher
Dr. Florian Uteschil	Senior Researcher
Maria Madani	Technician / Lab
Birgit Wöstefeld	Secretary
Constanze Dietrich	Secretary

Post-Docs

Dr. Juan Ayala Cabrera, Dr. Lidia Montero

Ph.D. Students

University Duisburg-Essen	External
Maha Alhasbani	Susanne Brüggem
Janosch Barthelmes	Tingting Li
Dominik Brecht	Wiebke Mehwald
Amela Bronja	Niklas Danne-Rasche
Yildiz Danisan	Dominic Mähler
Paul Görs	Ruzanna Mnatsakanyan
Claudia Hellmann	
Julia Klein	
Timo Köhler	
Claudia Lenzen	
Christian Lipok	
Martin Meyer	
Kristina Rentmeister	

M.Sc. Students

Rezaul Karim Chowdhury, Yulia Dietle, Hyerin Kim, Kendra Majewski (external), Simon Schastok, Pia Wittenhofer

B.Sc. Students

Ashrafal Alam, Zaid Awad, Marc Hauke, Kübra Temel, Jasmin Maria Turkowski, Hannes Schlottmann, Maximilian Specht

Guest Scientists

Apprentices

Lina Lantermann, Kim Verholen

Major News 2020

Teaching and Research Center for Separation

Agilent is developing a global network of world-class Centers of Excellence that can be linked together to broaden scientific collaborations. The University of Duisburg-Essen is world-wide the fifth university to join this network.

As part of the collaboration, Agilent has supported the AAC with a broad range of instruments to equip a new Agilent-sponsored Teaching and Research Center for Separation (TRC). In addition to research, the focus of the center will be 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.



**Teaching and Research
Center for Separation**



Unfortunately, due to the corona situation, we could only hold a course on one- and two-dimensional gas chromatography in March. After that, there was a lockdown and a few months later this was relaxed with strict safety requirements, but no more courses could be held.

The next teaching courses will be given on:

- | | |
|------------------|---|
| 05. – 07.05.2021 | Basic Course Liquid Chromatography (Theory and HPLC) |
| 26. – 28.05.2021 | 1D- and 2D-GC |
| 23. – 25.06.2021 | GC-MS |
| 18. – 20.08.2021 | Advanced Course Liquid Chromatography (2D-LC, LCxLC, SFC) |
| 01. – 03.09.2021 | LC-MS and Ion Mobility-MS |
| 27. – 29.10.2021 | ICP-OES, ICP-MS, and CE |

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

HPLC 2023 in Düsseldorf, Germany

In the last time, you have not heard much about HPLC 2021. We were carefully following and evaluating the worldwide situation regarding the COVID-19 crisis. Unfortunately, this pandemic crisis continues to keep us in trouble and under great uncertainty. We are not very optimistic that international travel can take place unrestricted next year. This would strongly negatively affect the international character of the symposium.

In an intensive exchange about whether a digital event is attractive enough for participants, speakers, and sponsors/exhibitors, together with the Permanent Scientific Committee we concluded that this is not the case.

To maintain the spirit of maximum interactivity at HPLC, which is the strength of this scientific meeting, the chairmen (Prof. Michael Lämmerhofer and me), the GDCh, and the permanent scientific committee have therefore decided to postpone the HPLC 2021 Symposium in Düsseldorf, Germany until June 2023.

We thank you very much for your understanding and hope to see you at HPLC 2023.

The HPLC symposium series is known as the world-leading conference on liquid phase separations and related technologies. Its program covers all aspects of separation sciences in liquid and supercritical fluid phases as well as hyphenation with advanced detection technologies in particular mass spectrometry. The program will span from fundamentals and theory of chromatographic separations and detection principles, over methodological and technological advances including separation materials, column technologies, and instruments, to applications in various fields and quality assurance aspects. The symposium will feature workshops and tutorials, plenary and keynote lectures from the leading scientists in the field. Yet, the majority of lectures will be selected from submitted abstracts to make sure that participants can share and discuss their newest results with the audience. Besides, HPLC 2023 will have a big exhibition and vendor seminars in which attendees can see the latest innovations from the leading vendors in the field.

The conference topics will cover the advances in LC technologies in terms of fundamentals, hyphenation, and application.

Fundamentals

New column technologies, stationary phases and materials, Separation modes, Sample preparation, new instrumentation, mass spectrometric detection methods, Supercritical fluid chromatography, Capillary electrophoresis, and miniaturized formats, Preparative and process chromatography, Biochromatography, Green technologies, future challenges, and trends.

Hyphenated technologies

LC-MS, SFC-MS, CE-MS, microscale LC-MS, nanoLC-MS Ion-mobility spectrometry, Multidimensional separations, Untargeted and targeted analysis technologies Data processing for omics analysis technologies

Applications

Food analysis, environmental analysis, Pharmaceutical analysis, Biopharmaceuticals, biosimilars, monoclonal antibodies, and protein analysis Drug discovery, pharmacokinetics, natural products analysis, Omics technologies and biomarker analysis, Clinical and forensics analysis, doping control



HPLC 2023
51st International Symposium
on High Performance Liquid Phase Separations and Related Techniques
June 18 – 22, 2023 in Duesseldorf, Germany
www.hplc2023-duesseldorf.com

Mark your calendar! We look forward to your participation.

For more information visit our website www.hplc2023-duesseldorf.com

Hero of the Year 2020



This time I would like to thank **Dr. Lidia Montero** very much.

She is now for about 3 years in my working group and enriches it immensely.

Besides her excellent publications, and reviews Lidia is very successful in working on projects funded by industry and BMBF (five projects in parallel).

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

List of Projects 2020

(Abstracts of these projects within the next pages)

Characterization of the metabolome of *P. aeruginosa* in biofilms as a lung infection model

Timo Köhler

Development of a UHPLC-HRMS method to determine CLR01 in biological samples

Juan F. Ayala Cabrera

Non-target analysis of complex natural substances: Industrial hemp (*Cannabis sativa* L.) for food products using 2D-LC-IM-MS

Hyerin Kim, Lidia Montero

Analysis of Sudan plant infusions by comprehensive two-dimensional liquid chromatography

Samuel Thebingbuß and Lidia Montero

Analysis of additives in engine and transmission lubricants by 2DLC-MS

Lidia Montero

Metabolomic study of the Archaea *Sulfolobus acidocaldarius*

Lidia Montero

Thermal and mass spectral analysis of pharmaceutical compounds

Maha Alhasbani, Florian Uteschil

Coupling of thermogravimetry with an Orbitrap-MS

Maha Alhasbani, Florian Uteschil

Comparative study of chromatographic methods for the analysis of carbohydrates in biological samples

Martin Meyer

Analysis of the monomeric composition of exopolysaccharides from archaeal biofilms

Martin Meyer

Origin of Life – Drill core

Yildiz Danisan

Analysis of free fatty acids by GC-APCI-MS and GCxGC-NCI-MS

Paul Görs, Sven W. Meckelmann

Analysis of herbal liqueurs by Liquid Chromatography Coupled with Ion Mobility Quadrupole Time-of-Flight Mass Spectrometry

Sven W. Meckelmann, Lidia Montero

Improving a data analysis workflow for untargeted lipidomics

Kristina Rentmeister, Sven W. Meckelmann

Development of a fast-switching dual (ESI/APCI) ionization source for liquid chromatography-mass spectrometry

Dominik Brecht, Florian Uteschil

Development of a low-temperature plasma ionization source for liquid chromatography-mass spectrometry

Dominik Brecht, Florian Uteschil

Application of a Novel Low-Temperature Plasma Ion Source for the Detection of 13 Drugs of Abuse in an LC-LTP-QqQ-MS Coupling

Simon Schastok, Florian Uteschil

Monitoring of defective Silicone-gel Breast Implants by determination of cyclic volatile methylsiloxanes in human whole blood

Janosch Barthelmes

Characterization of the metabolome of *P. aeruginosa* in biofilms as a lung infection model

Timo Koehler

Cystic fibrosis (CF) is an autosomal recessive hereditary disease that leads to the production of thickened mucus in the infected organ (e.g. lung). Conditions in the infected lung favor polymicrobial infections, such as chronic lung infections with *Pseudomonas aeruginosa*. *P. aeruginosa* is the major pathogenic bacterium that colonizes CF lungs at the end of the lifetime of CF patients. [A. Folkesson et al., Nat. Rev. Microbiol., 2012;10:841–51]

In the *in vitro* biofilm model, confluent biofilms of the strains *P. aeruginosa* ATCC 10145, PAO1, and FRD1 were cultivated under CF-like conditions (see Figure 1, a-c). Cultivation was performed on a solid artificial sputum medium, which was previously developed with the project partners. To characterize the extracellular volatile metabolome (mVOCs) of the *P. aeruginosa* strains under CF-like conditions, the mVOCs were sampled from the *in vitro* model by thin-film microextraction. A significant difference between the three strains used could be demonstrated with an unsupervised PCA (see Figure 1, f), as well as by comparing the peak intensities (see Figure 1, d, e, g, h). When comparing the clinical strains PAO1 and FRD1 (CF-relevant), 31 mVOCs were identified, which show a significant change in peak intensity.

Further *in vitro* studies on the extracellular volatile metabolome of other CF-relevant bacterial pathogens will be conducted in the future. These investigations aim to identify CF-relevant bacteria from CF sputum based on selective metabolites. Furthermore, these results will be used for the development and establishment of a clinical non-invasive "at bedside" breath analysis method for CF patients.

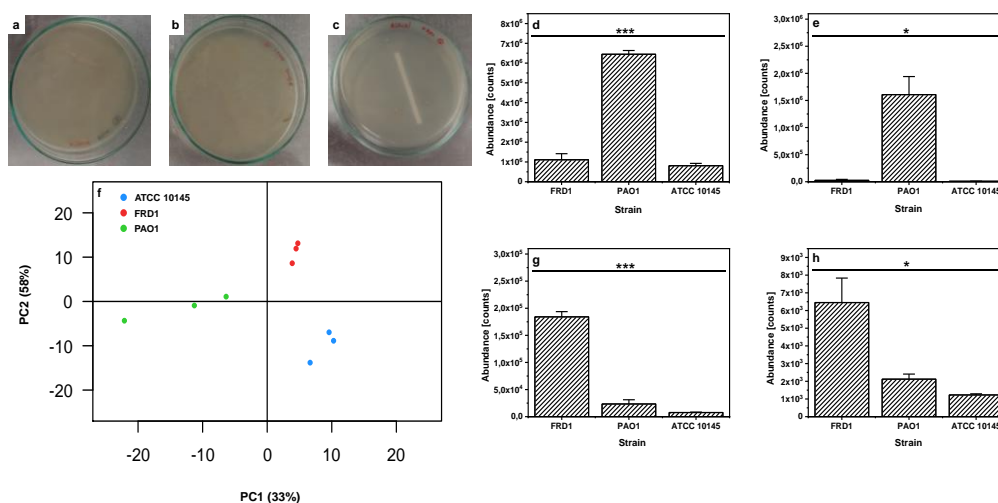


Figure 1: Cultivation of *P. aeruginosa* ATCC10145, PAO1, FRD1 in an *in vitro* biofilm model (CF-like conditions) and subsequent TD-GC-qMS analysis. Fig. a - c: Confluent biofilm growth; Fig. f: scores plot; Bar charts of the significance analysis, d: 2-octanone (confidence level: ***); e: 2-tridecanol (*); g: butyric acid n-butyl ester (***); h: 2-amino-1,3,5-triazine (*).

Collaborative Project – Project Partner: PD Ursula Telgheder (UDE, Essen, Germany) and Dr. Jost Wingender (UDE, Essen, Germany)

Funded by: German Research Foundation (DFG), Bonn, Germany

Development of a UHPLC-HRMS method to determine CLR01 in biological samples

Juan F. Ayala Cabrera

CLR01 is a molecular tweezer that acts as a broad-spectrum inhibitor of abnormal protein self-assembly by binding to Lys residues (Fig. a). This ability has turned CLR01 into a possible therapeutic drug against proteinopathies such as Alzheimer's and Parkinson's diseases among others. Additionally, CLR01 has also demonstrated great potential to inhibit hazardous virus infections like Ebola or Zika. However, the common CLR01 dosage in mice requires a powerful analytical technique to achieve the determination of the analyte at very low concentration levels. Thereby, the main objective of this project lies in the development of a selective and sensitive ultra-high performance liquid chromatography coupled to high-resolution mass spectrometry (UHPLC-HRMS) method to determine CLR01 in biological samples.

CLR01 is analyzed by electrospray in the negative ion mode as the deprotonated molecule. However, this analyte also shows a high tendency to generate adduct ions with mobile phase additives such as acetate. Therefore, high source temperatures (ca. 500 °C) and S-lens RF level (100%) are required to promote the $[M-H]^-$ ion formation. Under these conditions, the full-scan mass spectrum also showed an intense adduct ion with water (Fig. b), which can be also considered to improve the detection capability when working in tandem mass spectrometry. The chromatographic analysis was carried out using a universal gradient in a C_{18} column (50 x 3.0 mm; 1.8 μ m) with a mobile phase consisting of H_2O/CH_3CN (4:1 v/v) and IPA/ CH_3CN/H_2O (70:30:5, v/v), both of them with 0.1% acetic acid and 5 mM ammonium acetate. Under these conditions, the UHPLC-HRMS(/MS) methodology allows a very sensitive detection (Fig. c) achieving an instrumental limit of detection of 0.15 nM which may be low enough to determine CLR01 in biological samples.

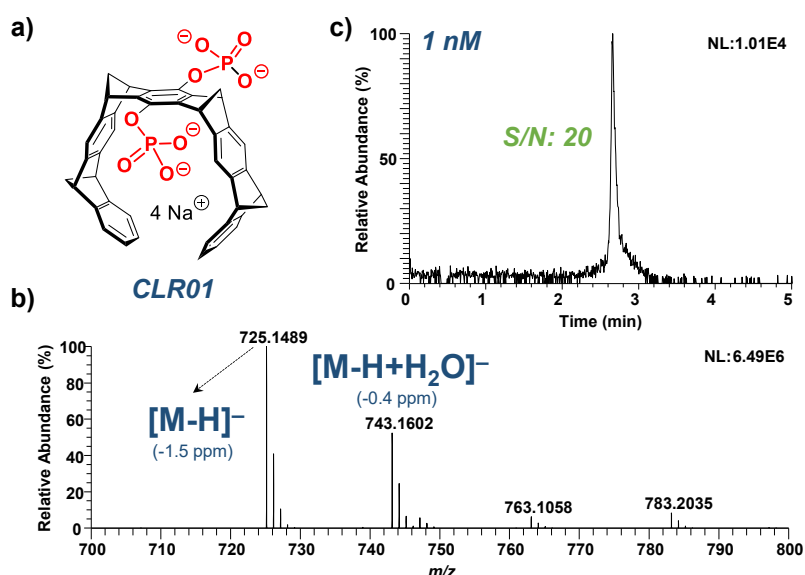


Figure 1: CLR01 a) chemical structure, b) full-scan mass spectrum and c) EIC at 1 nM.

Collaborative Project – Project Partner: Prof. T. Schrader (DUE, Essen, Germany) and Dr. B. Gal (UCLA, Los Angeles, USA)

Funded by: National Institute on Aging (NIA), USA

Non-target analysis of complex natural substances: Industrial hemp (*Cannabis sativa* L.) for food products using 2D-LC-IM-MS

Hyerin Kim, Lidia Montero

With the legalization of the use of industrial hemp, the uses of cannabis in food and cosmetic products are increasing. Unlike conventional marijuana, industrial hemp has a very low concentration of psychoactive substances such as Δ^9 -Tetrahydrocannabinol (THC) but has a higher concentration of cannabidiol (CBD), which is known for its easing effects on anxiety, epilepsy, and cancer. Cannabis is a very complex natural substance, which has more than 700 compounds, including more than 100 different cannabinoids, which are distinctive chemicals in cannabis.

For analyzing and identifying such a complex sample, separation methods with high resolving power are needed. To that point, multidimensional chromatography, like two-dimensional liquid chromatography (2DLC), provides high peak capacity, which allows better identification of the compounds. Furthermore, coupling with other separation methods such as Mass spectrometry and ion mobility spectrometry can contribute to the best separation and identification of complex material.

Therefore, the objective of this work was to develop a method for the chemical characterization of two different hemp-based food products by two multidimensional strategies, LCxLC-QTOF MS and LC+LC-IM-QTOF, to evaluate the complex metabolic profile and the possible differences between them with the largest possible separation power (Figure 1).

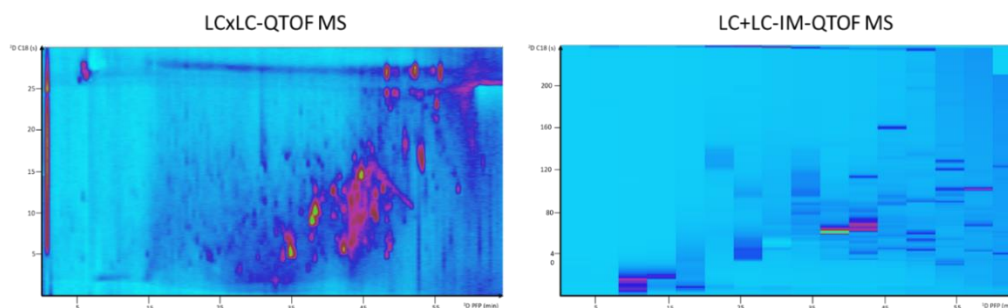


Figure 1: LCxLC-QTOF MS and LC+LC-IM-QTOF 2D plots of the hemp variety used for ice creams recipes.

With these powerful techniques, it was possible to identify different families of compounds like cannabinoids (Figure 2), phenolic compounds, furofurans, terpenes, amino acids, alkaloids.

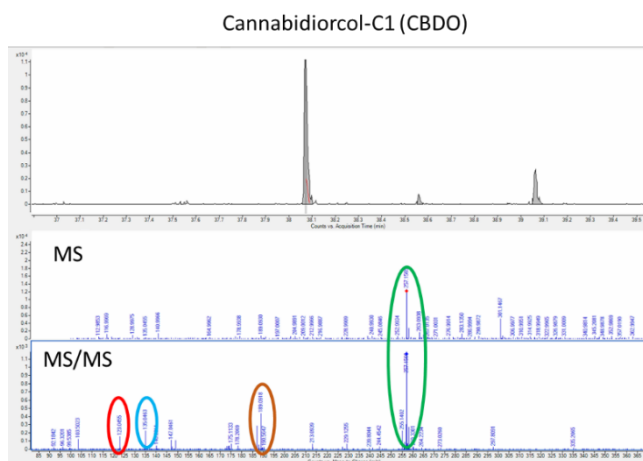


Figure 2: EIC, MS, and MS/MS spectra of the compound cannabidiol found in the hemp variety used for ice cream recipes.

Analysis of Sudan plant infusions by comprehensive two-dimensional liquid chromatography

Samuel Thebingbuß and Lidia Montero

Quality control of herbal medicines is considered a major challenge in analytical chemistry having a wide variety of compounds within a single sample. Since certain tea types have proven to contain therapeutic agents it has gained importance as an alternative to pharmaceuticals and as a source for new beneficial chemical compounds for human health. For instance, infusion constituents potentially carry an antioxidant activity, reduce the risk of cancer and coronary heart diseases.

In this work, infusions of *Guiera senegalensis*, which is a shrub of the savannah region of West and Central Africa, have been analyzed. Its leaves are commonly used in traditional medicine in gastrointestinal disorders, respiratory infections, rheumatism, and as an antimalarial agent. Previous studies showed that the herb extract usually contains two alkaloids (harman, tetrahydroharman, or eleagnine), flavonoids, naphthopyrans, tannins, and a naphthyl butenone (guieranone A).

The comprehensive two-dimensional liquid chromatography (2D-LC) displays a good analytical method for this kind of complex samples as it offers high selectivity and separation efficiency. Furthermore, unknown compounds can be identified by an accurate mass detection through a quadrupole time of flight mass spectrometer (Q-TOF-MS).

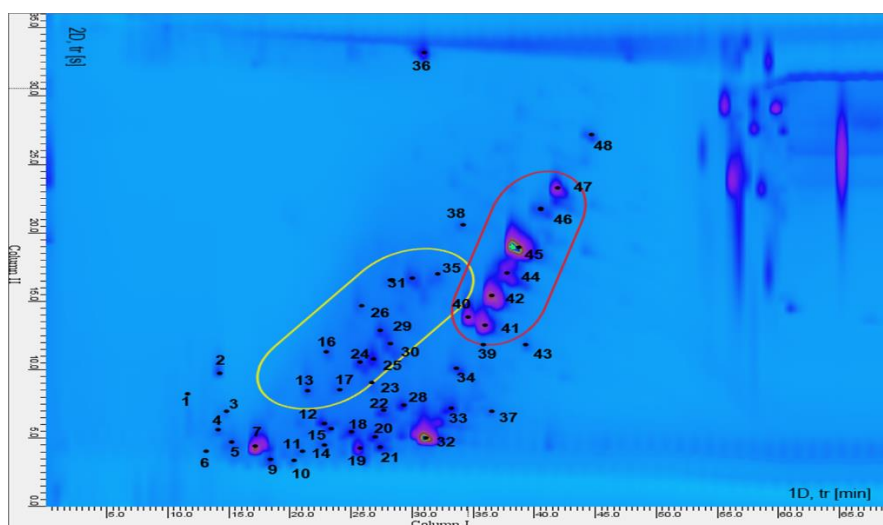


Figure 1: LCxLC analysis of an herbal extract of *G. Senegalensis* leaves through boiled ultra-pure water. Circles show the lowest (yellow) and the highest (red) concentrated compounds.

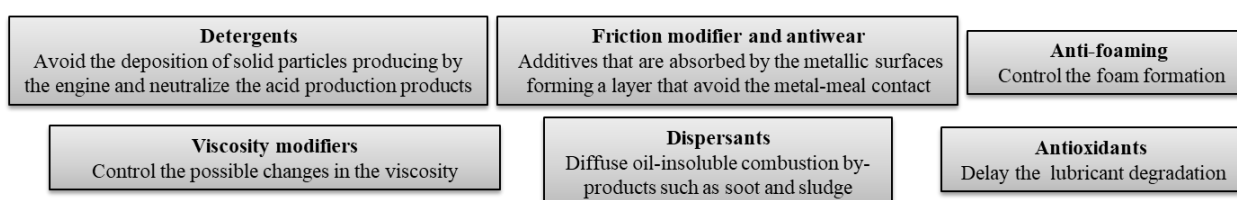
The results indicate a predominant presence of flavonoids, in particular, flavan3-ol within the herbal extract. In this flavonoid fraction, a mixture of (epi)catechin, (epi)gallocatechin, (epi)gallocatechingallate could potentially have been detected. Besides, phenolic acids like galloylquinic acid and caffeoylquinic acid were found.

Analysis of additives in engine and transmission lubricants by 2DLC-MS

Lidia Montero

The engine is the heart of the car, so one of the most important elements to improve the life of our cars is to maintain the engine strong and in optimal conditions. In this regard, lubricants are crucial for engine life. Without lubricants, the engine would be submitted to extreme friction, wear, and overheating conditions that could destroy the internal parts in just minutes.

The composition of commercial lubricants consists of 60-40% of base oil and a 40-20% fraction of additives. Among this fraction, different additives are used in lubricants with different and specific purposes. For example:



The combination and the final composition of the additive fraction determine the quality of the lubricant.

In this work a 2DLC-MS method was developed for the analysis of additives in three different lubricants: marine lubricants for boats and automotive and transmission lubricants for cars.

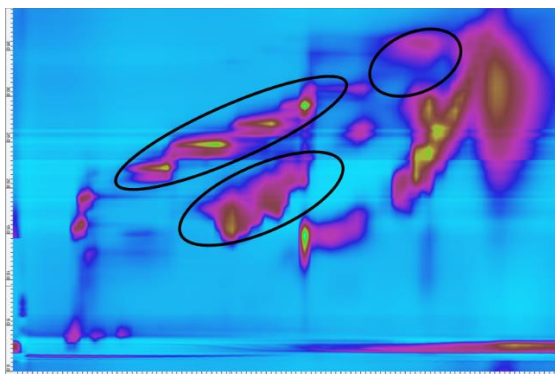


Figure 1: Different groups of additives separated in marine lubricants

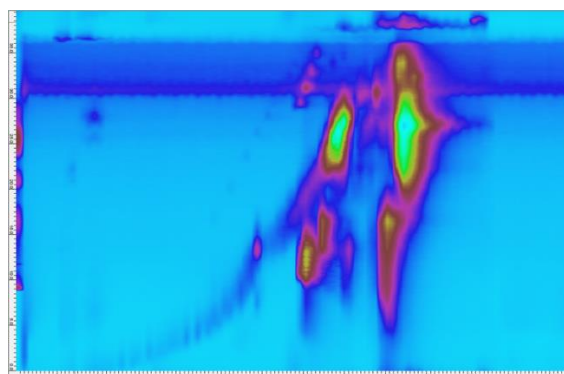


Figure 2: Different families of additives separated in automotive lubricants

This method allowed the separation, identification, and quantification of the main additives present in marine and automotive lubricants.

Metabolomic study of the Archaea *Sulfolobus acidocaldarius*

Lidia Montero

Archaea was defined as the third domain of life. Although it shares some attributes with bacteria and eukaryotes, it presents unique features that differ in this domain. In this sense, one of the most relevant characteristics of Archaea is its capacity for living in extreme temperature and acidic conditions. This ability could be very interesting for specific industrial processes. The aim of this project is the use of the thermoacidophilic Archeon *Sulfolobus acidocaldarius* (*Saci*), which can live under very extreme environments, which became *Saci* a good candidate for biomass conversion in industrial processes, for example for by- and waste-products like glycerol and CO₂. The metabolomic study of Archaea and, therefore of *Saci*, is of special interest since they present unique or modified metabolism pathways, in particular, the ones related to the central carbohydrate metabolism. For example, the Embden-Meyerhof-Parnas (EMP) and the Entner-Doudroff (ED) pathways are modified concerning the bacterial pathways. In these metabolic routes, the D-glucose degradation via phosphorylation is modified. Therefore, the analysis of phosphorylated sugars is crucial to understand the mechanism of *Saci* when growing under different conditions such as on glycerol or CO₂. However, the analysis of phosphorylated sugars is challenging due to negative interaction with stainless steel tubings giving tailing peaks and low sensitivity. For this purpose, an LC-QTOF MS method is developed applying HILIC as a separation mode. The method was optimized using a mix of 9 phosphorylated sugars and one internal standard. Different HILIC columns were tested, but the optimal separation was obtained using the iHILIC(P)-Classic column (Figure 1).

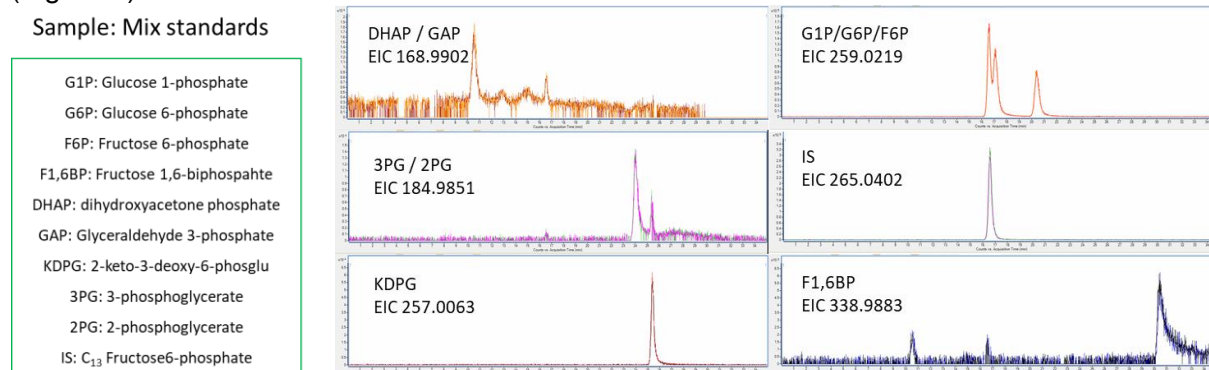


Figure 1: Separation of the 10 phosphorylated sugars using the iHILIC(P)-classic column

This method was employed for the analysis of other different metabolites involved in the pathway, like amino acids giving very good separation (Figure 2). Therefore, this method is promising for the analysis of the *Saci* metabolome analysis.

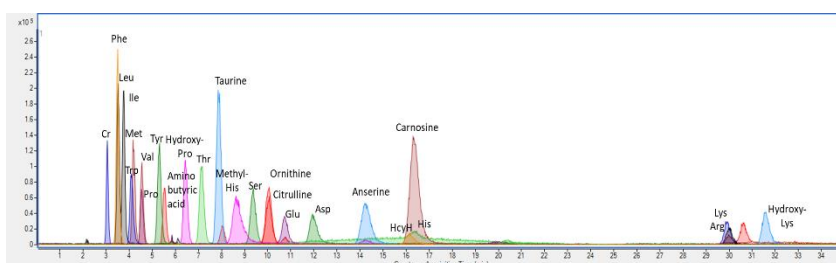


Figure 2: Separation of a mix of amino acids

Collaborative Project – Project Partner: Prof. B. Siebers and Prof. M. Kaiser (DUE, Essen, Germany)

Funded by: BMBF

Thermal and mass spectral analysis of pharmaceutical compounds

Maha Alhasbani, Florian Uteschil

Thermal analysis (TG, DTG, and DTA) was used to study the thermal behavior of Captopril (Figure 1), Pipamperone, Amlodipine, Metoprolol, and Piracetam in raw materials and pills. At the same time, mass spectroscopy, which has been coupled to the thermogravimetry using Fused silica as a transfer line and APPI as a source, was performed. Changes in mass, humidity, type of reaction, and melting were studied, and the spectral study was conducted by identifying positive ions for each drug (Figure 2). In the end, the two studies were compared through the stages of decomposition and the location of ions by comparing the thermal study with time and the study of the spectral mass by finding the ion current extraction that charts the intensity of the selective signal over time.

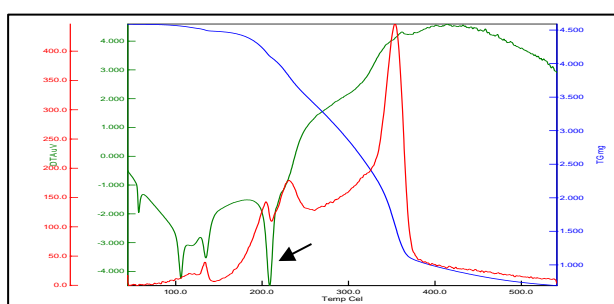


Figure 1: The TG, DTG, and DTA curves of the captopril with a heating rate of 10°C/min at time 51 minutes. The arrow in the DTA curve shows the melting point.

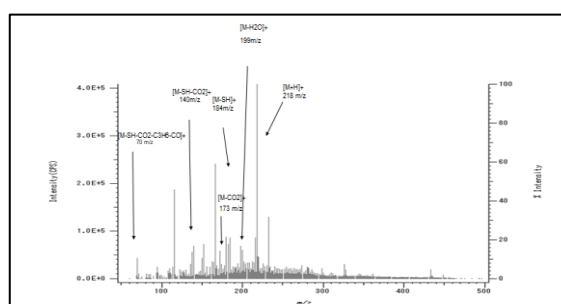


Figure 2: Captopril Ion $M+H=218.0$ m/z and the Fragments that are detected by studying the TIC, EIC, and m/z

All the studied compounds are sensitive to heat, as the first thermal transformation process is mostly indicative of dehydration, and then the greatest dissociation occurs in one or several stages. The extracted data from the thermal study allow us to know many physical properties such as the fingerprint feature that is semi-fixed to the compound and is known from the DTA curve. Whereas the extracted data from the mass spectrometry study allow the interpretation of thermal decompositions that occur at different stages in the drug samples.

For each drug, the decomposition stages, loss of mass, moisture, melting points, and the endothermic and exothermic peaks were studied also the ion and the fragments. Besides the ions, the fragments that were detected from the molecular ion for each drug were 5 for Captopril, 5 for Pipamperone, 4 for Amlodipine, 3 for Metoprolol, and 2 for Piracetam.

This coupling proved its high ability once again to qualitatively identify the pharmaceutical compounds by determining the physical properties of each compound, finding the ions of each drug with its fragments, find some of the components included in the composition of the drug, and Interpretation of thermolysis in stages of drug dissociation.

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

Coupling of thermogravimetry with an Orbitrap-MS

Maha Alhasbani, Florian Uteschil

A new coupling has been developed between the thermogravimetry (TG) and the high-resolution orbitrap (Figure 1). It was done by using a transfer line from Ceramic beads and fused silica (that can use it until 350 °C) to the APPI source which is fixed to the Orbitrap with capillary transfer line and APPI body to allow the coupling of TG to the Orbitrap (Figure 2). The make - up gas flow is Nitrogen gas that is connected by using a T-junction to the APPI body.



Figure 1: Coupling between the Thermogravimetry to the Orbitrap.



Figure 2: APPI source with its Body which is fixed to the orbitrap.

The toluene has been used to determine the parameters to have the highest signal for it. The parameters that were adjusted were Capillary Voltage, Tube lens Voltage, and Skimmer Voltage. After that, adjust the temperature to work at a high temperature for not getting any contamination and to have high ionization. The temperature 250 °C can use it as the highest temperature for the APPI interface, APPI body, transfer line, and Capillary in the Orbitrap to get the sampling in the transfer line to the Orbitrap by the fore vacuum. The first measurement in this coupling was to analyze coffee samples and to identify the caffeine signal. After doing the measurement three times, the caffeine signal (194.0798 m/z) was found three times at high resolution and with high repetition. Several signals were obtained that refer to the compounds included in the coffee grounds. Further work is trying to find differences between the coffee types in the features and m/z signals.

Orbitrap mass spectrometer can achieve very high resolution in a fraction of a second so This coupling is a sensitive technique to improve the separation power to analyze the complex samples and determine the feature list for it.

Comparative study of chromatographic methods for the analysis of carbohydrates in biological samples

Martin Meyer

Assessment of carbohydrate moieties in biological samples confronts scientists with a wide range of different analysis methods. The study aimed to compare different approaches of chromatographic separation, each coupled to mass spectrometry, to evaluate the most appropriate method for the analysis of the carbohydrate fraction of biological samples, such as exopolysaccharides from archaeal biofilms, in terms of separation performance and sensitivity.

Two liquid chromatographic methods, classical reversed-phase liquid chromatography (RP-LC) and hydrophilic interaction liquid chromatography (HILIC), a hybrid chromatographic method, the supercritical liquid chromatography (SFC) and gas chromatographic separation (GC) were compared, each coupled to a triple quadrupole mass spectrometer (TQ-MS). Initially, chromatographic methods were developed and optimized regarding the separation performance for 17 commercially available monomeric compounds naturally occurring in a wide range of biological samples. For RP-LC and GC, prior derivatization with 1-phenyl-3-methyl-5-pyrazolone (PMP) and N,O-Bis(trimethylsilyl)trifluoroacetamide (BSTFA), respectively, is necessary. Subsequently, methods for three operating modes of TQ-MS, full scan, single ion monitoring (SIM), as well as multiple reaction monitoring (MRM), were developed and optimized concerning the highest possible sensitivity in terms of detection and quantification limits (LOD and LOQ) for the different substances. RP-LC and GC coupled to MS showed the highest separation power with 15 and 14 separable monosaccharides (chromatographic or by mass), respectively, being superior to HILIC (11 separated monosaccharides) and SFC (6 separated monosaccharides). Regarding the sensitivity, the study revealed that the LOD is a lot lowered using single ion monitoring or multiple reaction monitoring methods. All in all, RP-LC coupled to mass spectrometry in MRM mode showed the lowest LODs between 1 and 39 µg/L.

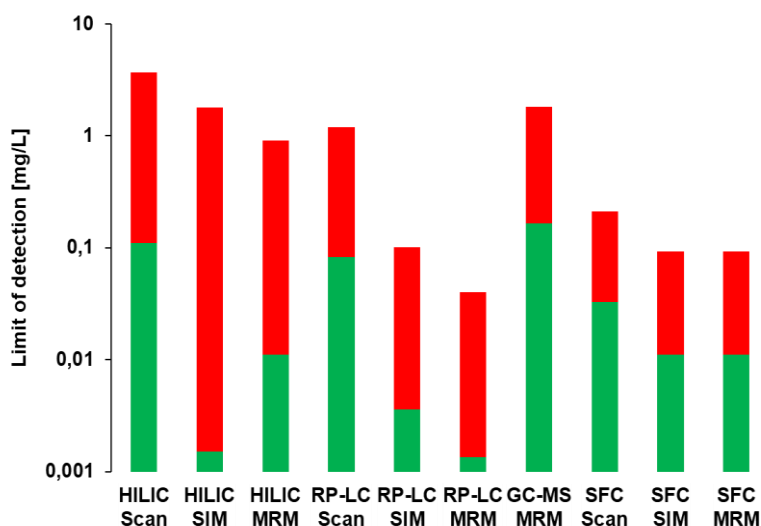


Figure: Lowest (green) and highest (red) limit of detection for different methods

Collaborative Project – Project Partner: Prof. Dr. B. Siebers, Dr. J. Wingender (University of Duisburg-Essen)

Funded by: DFG Project number: 393406057

Analysis of the monomeric composition of exopolysaccharides from archaeal biofilms

Martin Meyer

Microorganisms, such as archaea, favor life in a biofilm rather than the planktonic form of life. A biofilm is defined as a community of microorganisms embedded in a self-produced matrix of hydrated extracellular polymeric substances, mainly polysaccharides (PS), proteins, and DNA. The polysaccharides form a three-dimensional network, which provides stability of the biofilm and mediates the adhesion to surfaces. Analysis of the monomeric composition of polysaccharides requires sample preparation by hydrolysis of the PS and subsequent chromatographic separation and identification by mass spectrometry (MS). As shown in a previous comparative study, reversed-phase liquid chromatography with initial derivatization of the monomeric carbohydrates coupled to mass spectrometry in multiple reaction monitoring mode is best suited for the determination of the composition of the unknown exopolysaccharides regarding separation performance and sensitivity.

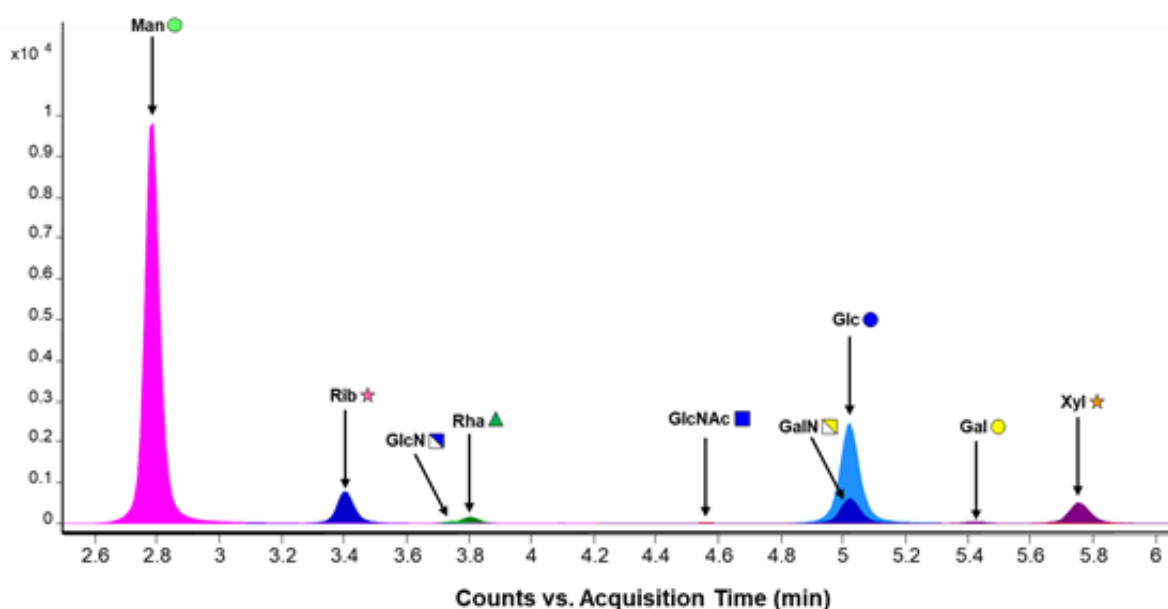


Figure: MRM chromatogram of a real biofilm EPS extract from *Sulfolobus acidocaldarius*.

Therefore, the monomer composition of polysaccharides from archaeal biofilms cultivated on varying substrates concerning the carbon source in the medium was determined by this method. It has been shown that the use of glucose as a carbon source in the nutrient medium causes a significant increase in the total concentration of carbohydrates and promotes the formation of polysaccharides as stabilizing elements of biofilms, compared to the absence of a carbon source or higher polymerized saccharides. Furthermore, the choice of the culture medium influences the monomeric composition of the exopolysaccharides in the molar proportions of the compounds present. Additionally, it could be demonstrated by enzymatic processing of the biofilm extracts and subsequent analysis that the monomeric species found originate from free extracellular polysaccharides and not from co-isolated glycoproteins, which can be a critical source of interference in the analysis of carbohydrate hydrolysates from biological samples.

Collaborative Project – Project Partner: Prof. Dr. B. Siebers, Dr. J. Wingender (University of Duisburg-Essen)

Funded by: DFG Project number: 393406057

Origin of Life – Drill core

Yildiz Danisan

In the foreground of the investigations in 2020 were the analyses of a drill core. The borehole was drilled at Wehr in the Eifel (R 373522.00 m E; H 5587551.00 m N). The borehole has a total depth of more than 1000 m, in the depth range 950-968 m a core of approximately 7 cm diameter was obtained. This spans exactly the depth range in which the CO₂ phase transition to the supercritical state occurs (304.13 K (30.98°C) and 7.375 MPa (73.75 bar). In the depth range of the extracted drill core, the temperature is in the range of 30°C and the hydrostatic pressure is around 95 bar, and CO₂ changes between liquid and supercritical phase in case of expected temperature fluctuations. The rock of the drill core is assigned to the Devonian and consists of an alternation of clay, silt, and sandstones, which have a natural porosity and additionally have an open fissure system. The porosity as well as the fissure system offer natural pathways for hydrothermal solutions, which are to be expected in the volcanic area of the Eifel. These hydrothermal solutions provide the entire material inventory necessary for the formation of precursor compounds for organic life. In the fissures, idiomorphic calcite crystals have been deposited, which have bubble-like inclusions of the solution from which they were deposited. The surrounding rock was also penetrated by the solution and impregnated with its contents. Both, the calcite and the surrounding rock are examined for the occurrence of aldehydes and other organic compounds that can serve as precursors for organic life.

The analytical investigations are aimed at finding possible precursor compounds for organic life in the inclusions in the hydrothermal calcite crystals and the pore space in the surrounding rock. Initially, the focus was on aldehydes. To obtain analytically reproducible results from the very small sample quantities and, if necessary, low concentrations, intensive cleaning of all equipment must be carried out throughout the entire investigation. For this reason, they were post-cleaned after thorough pre-cleaning in an evaporation apparatus using HNO₃. The cleaning success was verified by measurements of the equipment and the process blank. Octanal, Nonanal (see Figures 1 and 2), Decanal, trans-2-Decenal, and Undecanal (verified by standards) were found in the calcite.

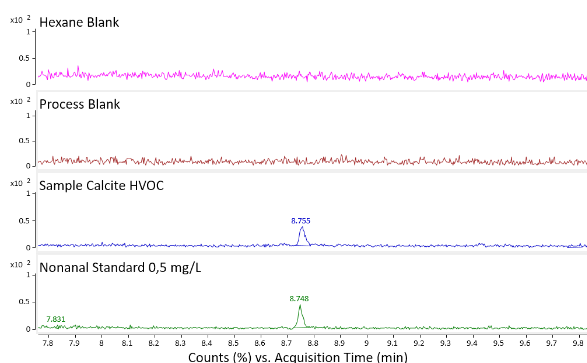


Figure 1: Extracted Ion Chromatograms (EICs) of hexane blank, process blank, calcite sample and nonanal standard.

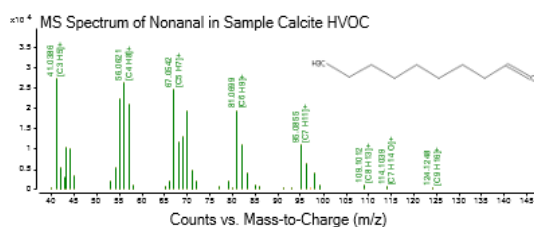


Figure 2: Mass spectrum of nonanal out of calcite crystals.

Further aldehydes were identified, but still, have to be verified by standards. All measurements were carried out three times to verify the results. The method used was Accurate Mass Q-TOF GC/MS (Agilent 7890B GC with Rxi-5MS column and Agilent 7250 MS in full scan mode).

Analysis of free fatty acids by GC-APCI-MS and GCxGC-NCI-MS

Paul Görs, Sven W. Meckelmann

Quantitative targeted analysis of free fatty acids is still challenging and sensitive as well as robust methods are needed to understand biological systems. An elegant way for the analysis of free fatty acids is the derivatization with pentafluorobenzylbromid (PFB) followed by gas chromatographic separation. The derivatization also allows the ionization of the fatty acids by negative chemical ionization (NCI), or electron capture atmospheric pressure ionization (APCI). Due to the ionizability of the PFB-derivates by using these very selective ionization modes, the noise levels are lower compared to other techniques such as ESI or EI. This results in a higher selectivity and sensitivity of the method.

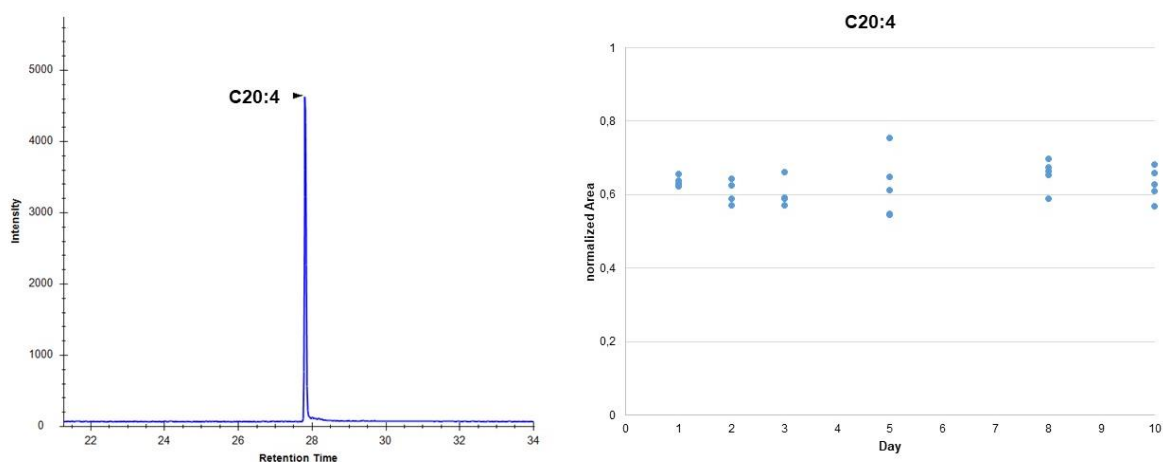


Figure: Left: Example SIM chromatogram for the [M-PFB]-Ion of arachidonic acid. Right: Longtime measurement to determine the stability of the PFB-derivatized fatty acids. The figure is showing the normalized area plotted against the time. The samples were stored at room temperature and measured over ten days.

Currently, we are optimizing a GCxGC-NCI-MS and a GC-APCI-MS method for the later application to Archaea samples in cooperation with the research group of Prof. Dr. B. Siebers. The first results show that LODs of less than 50 nM (~2 fmol on column) for the PFB-derivatized fatty acids for both methods can be expected. Moreover, the derivatized analytes are stable for several days at room temperature, which is a big advantage during sample preparation and analysis. Furthermore, both methods will be characterized according to the EMA-guidelines for bioanalytical method validation.

Analysis of herbal liqueurs by Liquid Chromatography Coupled with Ion Mobility Quadrupole Time-of-Flight Mass Spectrometry

Sven W. Meckelmann, Lidia Montero

Herbal liqueurs are a diverse group of alcoholic beverages with a long tradition that dates back to the Benedictines during the middle age. Applying their exceptional knowledge about the harvested and use of therapeutic herbs, the Benedictines flavored wines with their medicinal plants with a curative purpose. Today they are commonly drunken before or after a meal because of their stimulating effect on the appetite and to aid in digestion. These effects are related to the herbal plants and species selected as ingredients in the recipe of the herbal liqueur. Usually, they are plants that present a rich content in biological compounds correlated to potential effects on human health, in particular, those that have shown a large antioxidant capacity such as phenolic compounds.

We analyzed eight different herbal liqueurs by LC-IM-QTOF-MS(/MS) to characterize the phenolic compounds. The method used an all-ion fragmentation generating full scan data containing the information of the precursor ions as well as fragment data. This allowed the identification of compounds based on MS/MS in a non-target approach without a precursor selection and discrimination of low abundant ions.

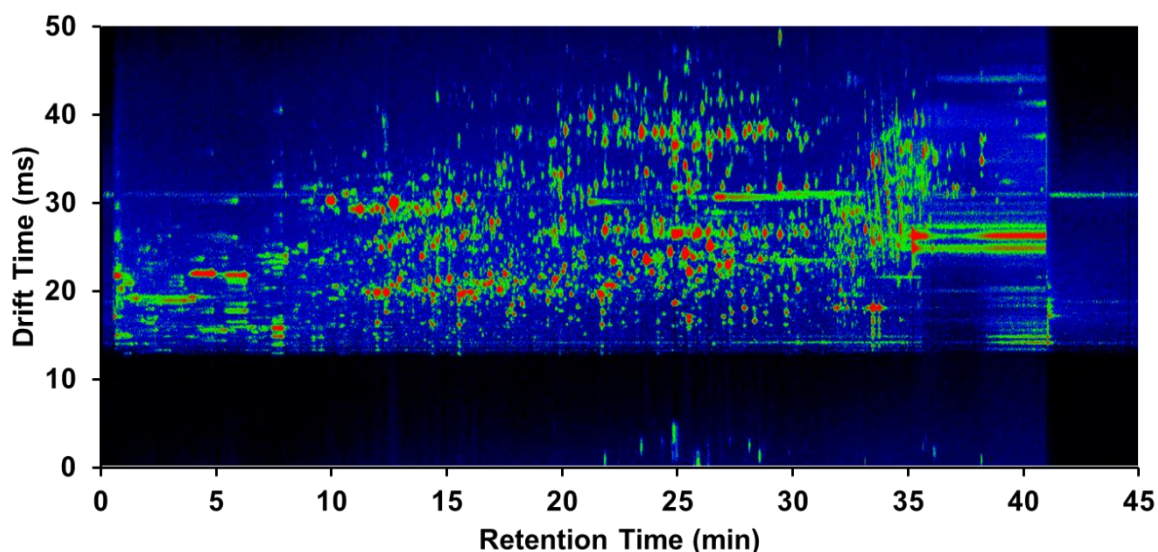


Figure: Heat map of a herbal liqueur sample analyzed by LC-IM-QTOF-MS(/MS) using an Infinity 1290 LC system coupled to an Agilent 6560 drift tube IM QTOF MS equipped with a Kinetex C18 column (100 x 2.1 mm; 1.7 μ m). Separation was carried out using a linear gradient with water, and acetonitrile, both acidified with 0.1% formic acid.

The data provides a fingerprint of over 3,000 detected compounds of which 171 phenolic compounds were tentatively identified. Identification of most of the phenolic compounds present in these samples supports the possible biological effects attributed to these beverages related to the antioxidant activity.

Improving a data analysis workflow for untargeted lipidomics

Kristina Rentmeister, Sven W. Meckelmann

Untargeted analysis workflows usually include a software-assisted search for possible compounds in the data, named feature analysis. This is a critical step in the progress since only compounds that are detected in feature analysis can be identified later on. Especially low abundance substances, which tend to be the ones holding the essential information in lipidomics, may be difficult for the software to detect. Additionally, high background and noisy peaks may lead to the detection of a large number of features that do not belong to real compounds. This makes it harder to filter important information and increases the risk of false identification. We studied different feature analysis settings as well as different ways of data pretreatment that are promising to improve feature analysis for liquid chromatography ion mobility time of flight mass spectrometry (LC-IM-QTOF-MS) data.

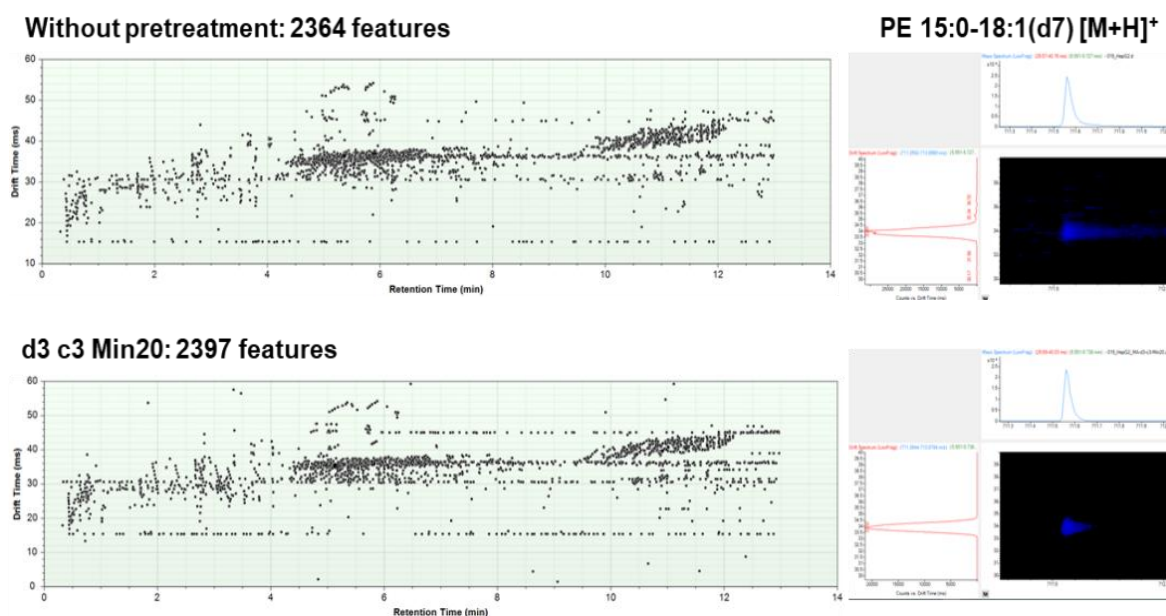


Figure: Left: Feature analysis of lipid extracts of HepG2 cells measured by LC-IM-QTOF-MS without pretreatment (top), and smoothing in the drift and chromatography dimension (bottom); Right: PE 15:0-18:1(d7) as an example for the effect of the data treatment on an individual signal.

The figure shows all detected features plotted with their drift time against their retention time. Without data pretreatment 2364 were detected. Using a simple moving average smoothing over three data points in drift dimension as well as in the chromatographic dimension a similar number of features compared to the untreated data was detected. However, the quality of the detected features has improved due to less noisy peaks that are easier to be detected by the feature analysis. The quality improvement of the signals can be seen when looking at individual lipids. Using data treatment before feature analysis can lower the background and noise over the peak, which can increase the quality of feature detection.

Development of a fast-switching dual (ESI/APCI) ionization source for liquid chromatography-mass spectrometry

Dominik Brecht, Florian Uteschil

The demand for high throughput methods for LC-MS is a growing market in analytical chemistry. Therefore, the group of professor Schmitz is working on solutions to increase the sample throughput in chromatographic analyses hyphenated with a mass spectrometer. Special attention lies in the development of ion sources for mass spectrometry. In this example, an ion source should be created which is capable to ionize the analyte molecules with electrospray ionization (ESI) or atmospheric pressure chemical ionization (APCI). Our first attempt to realize such a source is to combine the ESI and the APCI probe in one ion source housing with two entrances for the effluent of the HPLCs. The high sample throughput is realized by connecting two UHPLCs with a six-port switching valve that switches between the two UHPLCs and the two probes of the ion source. This new ion source shall reduce the delay time of a mass spectrometer to increase the efficiency of mass spectrometric analyses.

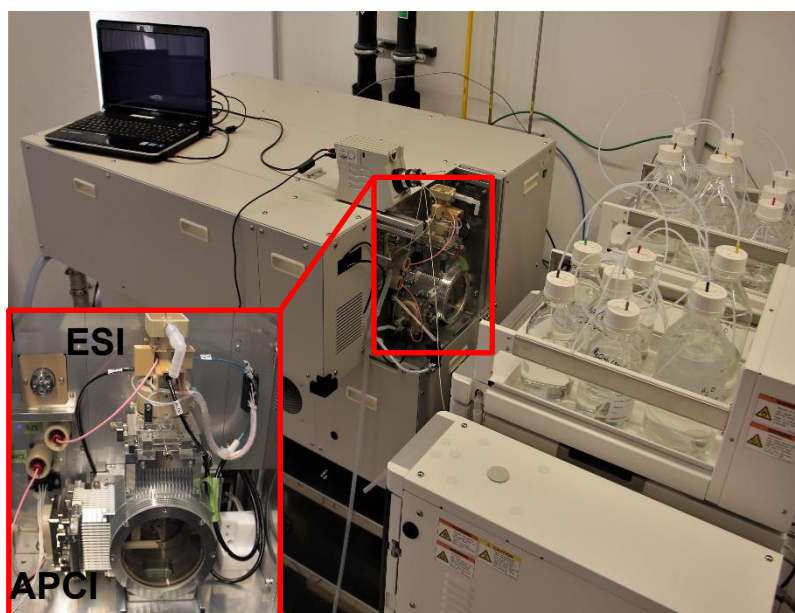


Figure: Photography of the device coupling for fast switching between ESI and APCI with a magnification of the developed dual ion source in the red box

The photo, which is shown with the illustration, shows our solution for reducing the idle time of a mass spectrometer. Starting from the right, two UHPLCs from Hitachi High Technologies were connected to the newly developed dual ion source via a six-port valve. The red box shows a magnification of the ion source. The ESI stands vertically on the ion source body and the APCI horizontally. Now two completely different LC-methods can run on the respective UHPLC. If the analytes of one UHPLC are to be analyzed, the UHPLC is

switched via the six-port valve to the probe just required. This is either the ESI or the APCI. Meanwhile, the eluate of the other UHPLC is led into the waste. If an analyte of this UHPLC is eluted, it is possible to switch to the UHPLC and ionize the analyte by one of the two ionization modes. A final experiment was performed by injecting testosterone on one UHPLC and vitamin D₃ on the other UHPLC, each with a concentration of 100 ppb. Both UHPLCs injected one sample every minute so that 50 samples could be analyzed within 75 min (1.5 min per sample). The repeatability of the peak areas was 1.5% for testosterone (ESI) and 3.8% for vitamin D₃ (APCI). The UHPLC₂-ESI/APCI-MS/MS thus shows promising results in the high-throughput range.

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

Funded by: Hitachi High-Tech Corporation, Tokyo, Japan, Evonik Industries AG, Essen, Germany

Development of a low-temperature plasma ionization source for liquid chromatography-mass spectrometry

Dominik Brecht, Florian Uteschil

The term LTP is the abbreviation for low-temperature plasma which can be explained to its ambient temperature compared to the inductively coupled plasma as it is used in ICP. The LTP is based on a discharge in the presence of noble gases (e.g. Helium, Argon) or environmental gases like nitrogen, oxygen, or air. This LTP is a non-equilibrium which is usually ignited in a dielectric barrier discharge (DBD) by a sine wave voltage function or by high voltage pulses at defined pulse widths and frequencies. In DBD at least one electrode is covered by a dielectric (glass, quartz, ceramic) to prevent the discharge from arcing. There are many applications in the industry for the LTP – for example surface modification of polymers or medical applications like sterilization of bacterial grow media or wounds. Therefore it is obvious that the LTP is generating diverse ion chemistry which can also be used as an ion source for mass spectrometry.

The figure shows the chromatograms of an analysis of LC Multi Residue Pesticide Standard 6 in red and black a blank. The analysis was performed with an LTP, which was operated with argon as the discharge gas. The chromatogram shows a good ion yield and after the analysis, it was found that all pesticides contained in the standard were

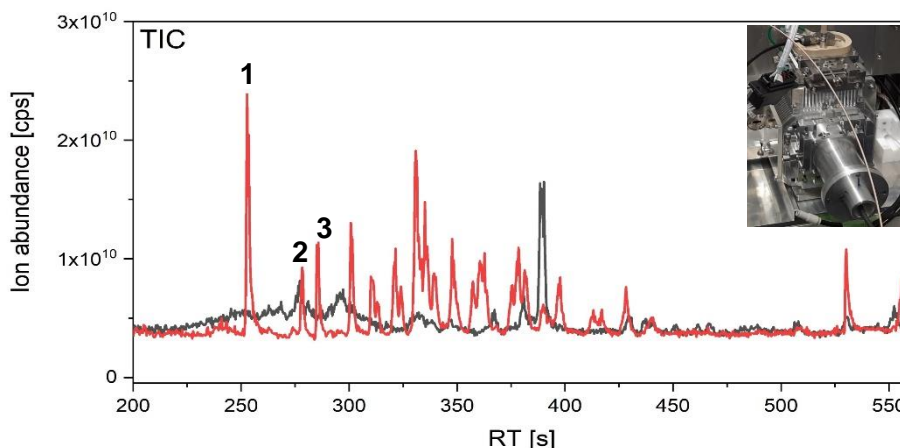


Figure: Analysis of the LC-Multi Residue Pesticide Standard 6 from Restek GmbH with the newly developed UHPLC-LTP-MS/MS coupling with a concentration of 100 ppb. The chromatogram in red describes the analysis of the standard, the chromatogram in black an analysed blank. The chromatographic method was taken from the Restek website. The presented photo shows the LTP ion source. 1: fuberidazole; 2: ethirimol; 3: nuarimol

ionized and detected at a low concentration of 100 ppb. It is also noticeable that there were no breakdowns in the analysis of the standard as well as in the blank in the total ion chromatogram (TIC). As an example, the first three peaks were named with 1: fuberidazole, 2: ethirimol, and 3: nuarimol. The substances mentioned here are all no longer approved in Germany, which makes them of interest for control, as they are serious nerve toxins that can harm humans. Therefore it is necessary to develop better and better methods that could detect even the smallest amounts of the pesticides and the Argon-LTP-Ionization seems to be a valuable contribution. APCI).

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

Funded by: Hitachi High-Tech Corporation, Tokyo, Japan, Evonik Industries AG, Essen, Germany

Application of a Novel Low-Temperature Plasma Ion Source for the Detection of 13 Drugs of Abuse in an LC-LTP-QqQ-MS Coupling

Simon Schastok, Florian Uteschil

The choice of an optimal ion source for a specific task is a critical step that has to be made for any mass spectrometry technique. Especially if liquid chromatography is required before ionization additional interferences and as such subsequently sensitivity losses (because of high effluent concentrations) have to be considered. Because of these reasons we are working on a novel ion source based on a Low-Temperature Plasma (LTP) with a broad field of application, high sensitivity, and low maintenance aspect.

The use of LTP for analytical purposes, as seen in Figure 1, is still relatively new. There exist only a few publications regarding possible applications for ionization of analytes in real-life sample matrices. To demonstrate the versatility and sensitivity that can be achieved by our novel LTP ion source we analyzed 13 Drugs of Abuse (DoA) in water and applied the developed method successfully to human urine. The analysis of DoA is a never-ending story in terms of intoxications, drug trafficking as well as drug-induced acts of violence and sexual assaults.

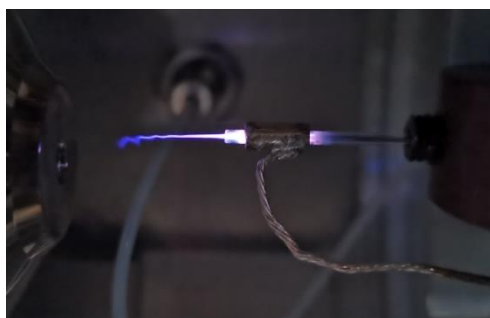


Figure 2: Active Low-Temperature Plasma in front of the MS inlet.

The LC-LTP-QqQ-MS method development for the quantification of 13 DoA was initially applied to an aqueous, matrix-free multistandard with great success. The separation was performed on a 50 mm endcapped C18 column with water and acetonitrile as the mobile phase. The optimization of the timed Multiple Reaction Monitoring (tMRM) resulted in Limits of Detection/Limits of Quantification (LOD/LOQ) as low as 0,1 ppb/0,5 ppb for MDMA “Ecstasy”, 1 ppb/5 ppb for Methamphetamine “Crystal Meth” and 0,05 ppb/0,5 ppb for Carisoprodol to name three examples.

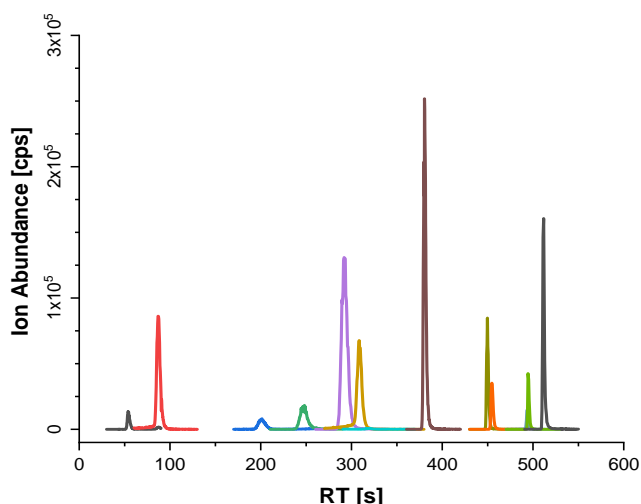


Figure 3: Recovery of all 13 Analytes in human urine with good sensitivity

As seen in Figure 2 the application of the developed method resulted in defined peaks for all 13 DoA in spiked and prepared human urine. Additional work for the application on a matrix containing samples in the future will give us more information about the applicability, robustness, LOD/LOQ, etc.

Collaborative Project – Project Partner: Y. Terui and K. Maruoka (Hitachi High-Tech, Mito, Japan)

Funded by: Hitachi High-Tech (Tokyo, Japan)

Monitoring of defective Silicone-gel Breast Implants by determination of cyclic volatile methylsiloxanes in human whole blood

Janosch Barthelmes

Silicone-gel breast implants (SBI) were introduced to the market in the early 1960s and still, after more than half a century, a sensitive and safe method for the detection of defects in the devices is lacking. This fact gained public interest in a series of events like the Dow Corning scandal in the 1980s and the more recent PIP scandal. In 2010 it became public knowledge, that the SBI manufacturers “Poly Implant Prothèse” (PIP) and “Rofil Medical Nederland B.V” for nearly two decades had used industrial-grade silicone in their medical devices affecting hundreds of thousands of patients worldwide and five thousand in Germany.

PIP and Rofil implants were associated with increased rupture-rates compared to rates up to 10% ten years after implantation in SBI within specification by other manufacturers. These numbers exemplify the need for diagnostic methods as implant-rupture may cause a variety of symptoms including, but not limited to, chronic pain and inflammatory reactions, and is indicative for the explantation of the affected device. Today the monitoring of the functional state of SBI is performed by mama sonography (SONO) to a sensitivity of 25-75%, depending on the operator, and specificity of regularly less than 50%. Magnetic resonance imaging (MRI) may be used as an alternative method and gives sensitivity and specificity of >95% but presents non-circumventable challenges to the healthcare system due to its high cost and need for specialized equipment. In a preceding project, our group was able to define cyclic volatile methylsiloxane blood levels as significant thresholds for the diagnosis of ruptured SBI with a sensitivity of 77% and a specificity of 92%. Following a Multiple Headspace Injection (MHI) approach we now aim for the establishment of a robust method that could be implemented in clinical routine as a more significant and only minimally more invasive alternative for the established SONO that would be more cost-effective than the MRI.

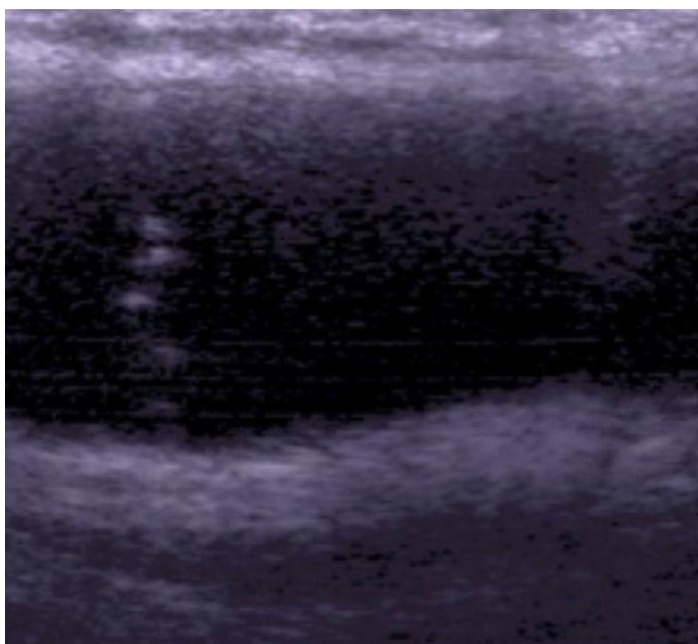


Figure: SONO stepladder sign of defective Silicone-gel Breast Implant provided by DR. P. RUSCH of Essen University Hospital.

Collaborative Project – Project Partner: Dr. P Rusch (Essen University Hospital)

Funded by: Essen University Medicine Foundation

Doctoral Theses accomplished 2020

Dr. Niklas Danne-Rasche (external Ph.D. student)

Development of a nanoLC-MS system for global lipidomics

In the context of this thesis, an advanced nano-flow liquid chromatography (nLC) – nanoelectrospray (NSI) – mass spectrometry (MS) system was developed for a global (i.e. not lipid class- or species restricted) lipidomics approach.

To grant broad range analyses of different lipid classes and species, the loading- and sample preparation procedures were particularly optimized. A direct sample injection with the resuspension mixture of BuOH:IPA:H₂O 8:23:69 + 5 mM phosphoric acid (8Bu+) thereby proved to be suitable for global lipidomics experiments. In this regard, the addition of phosphoric acid to the samples strongly enhanced the general detectability of lipids with terminal phosphate groups, which were found to be hardly analyzable under standard reversed-phase LC conditions. The robustness of the nLC-MS method was then evaluated based on repetitive analyses of a yeast extract that was spiked with standards. Over a measuring period of two days, high retention time stabilities were achieved for all analyzed lipids. The bulk of phospholipids could be stably detected with relative standard deviations below 10%, while the MS-response was less stable for late eluting very hydrophobic lipids. Using normalization approaches, these deviations could nevertheless be reduced with structurally- or retention time-related standards.



A direct sensitivity comparison to a corresponding narrow-bore HPLC platform revealed an increase of 2-3 orders of magnitude for the MS response by application of the nLC system that conformed with an increase of up to two orders of magnitude for the linear dynamic range. Sub-femtomol traces of individual lipids (< nM concentrations) could thus be detected with the nLC-MS platform in both positive and negative mode analyses. To permit a thorough comparison of the lipidome coverage, a semi-autonomous workflow was developed that allowed accurate identification of individual (molecular) lipid species. The presumably simple yeast (*Saccharomyces cerevisiae*) lipidome was then selected as a model for the in-deep evaluation of the lipidome coverage. The direct comparison of the yeast phospholipidome to the corresponding narrow-bore HPLC revealed a more than three-fold increase in lipid identifications on molecular species-level when identical sample concentrations were comparatively analyzed with both LC systems.

All in all, 935 lipid species, with each comprising multiple molecular species isomers, were identified across 30 analyzed lipid classes from 4 lipid categories in yeast. Even though this thesis uncovered more endogenous yeast lipids than any reference study, a detailed analysis of isomeric signals further indicates that also novel lipid classes, such as headgroup-methylated PS variants, and oxidized lipids can be found in natural yeast lipid extracts. Overall, this thesis shows that the insights into the complexity of a lipidome can be strongly deepened by using an nLC-MS system for global lipidomics experiments.

Dr. Amela Bronja

Origin of life in deep-reaching disturbance zones: Analysis of liquid inclusions and simulation experiments of a high-pressure phase equilibrium system

In this thesis different analytical techniques for the investigation of the theory about the origin of life in deep-reaching tectonic faults were applied. Therefore, two main focuses were set. The first one was the analysis of the fluid inclusions of at least 3,2 Ga old quartz minerals from Western Australia. The other focus was the analysis of products from simulation experiments under early earth conditions in a high-pressure apparatus.

In the first part of this work, quartz minerals were analyzed with comprehensive two-dimensional gas chromatography coupled to a quadrupole mass spectrometry (GCxGC-MS). To avoid bringing in contaminations and to release the content of the fluid inclusions, an extended sample preparation procedure was necessary. The comparison of the analyzed spots with the databases NIST and Wiley offers three substance classes. The first category consists of halogenated alcohols, alkanes, and alkenes. Furthermore, non-halogenated branched alcohols were found. A homolog series of the aldehydes heptanal to hexadecanal, which were identified with standards, belong to the third substance category. For the liquid chromatographic analysis (LC-QTOF-MS) of the quartz sample initially, a method for data reducing and alignment was developed. With the analyzed exact masses and the generated formulas, it was possible to search systematically for prebiotic molecules. The feature with m/z 163,0858 and the formula $C_7H_9N_5$ stands out because it corresponds to the purine N^6, N^6 -Dimethyladenine. By adding ion mobility mass spectrometry (LC-IM-QTOF-MS) as third separation dimension N^6, N^6 -Dimethyladenine was identified. The comparison with the analytical standard shows a match of the retention time, the drift time in the drift tube, and the exact mass. The substance-specific CCS value, which was calculated with the drift time, was with a value of $129,3 \text{ \AA}^2$ identical. Consequently, it was shown, that the Western Australian quartzes encapsulated a variety of prebiotic compounds, which were effectively protected against degradation.



In the second part of this work, different simulation experiments under early earth conditions were performed. Therefore, a vesicular peptide system was generated with 12 amino acids and stearic acid/ octadecylamine vesicles in the high-pressure apparatus. The system was exposed to cyclic pressure variations under CO_2 -atmosphere for 7 days. After analysis with LC-QTOF-MS based on the exact masses, it was searched for peptide combinations, which have condensate exclusively in the presence of vesicles. The detected peptide combinations reached up to an octapeptide and had amphiphilic character. They received a selection benefit due to integration into the vesicle membrane and the accompanying protection against hydrolysis. Whereas the vesicles experienced a stabilizing effect and their permeability was increased. This means that the vesicular peptide system exhibits symbiotic properties. Another simulation experiment, in which guanine, cytosine, d-ribose, and Na_2HPO_4 were exposed to early earth conditions was searched for reaction products via LC-QTOF-MS. The condensation of guanosine and cytidine, but also ribose phosphate was observed.

Master Theses accomplished 2020

Ashrafal Alam

Ultra-fast analysis of pesticides with Capillary gas chromatography Triple Quadrupole Mass Spectrometry

Rezaul Karim Chowdhury

Evaluation of APPI and APLI for use in GC-API-MS: Review

Kendra Majewski

Miniaturising the micronucleus test in a multimode plate reader for passive dosing of PAH mixtures

Bachelor Theses accomplished 2020

Zaid Awad

Analysis and identification of metabolites in biological samples using GC-qTOF-MS

Hannes Schlottmann

Study of an atmospheric pressure photoionization ion source for GC-MS

Maximilian Specht

Optimization and application of dielectrically hindered discharge ionization in coupling with LC-MS

Kübra Temel

Analysis of the metabolome of *Pseudomonas aeruginosa* in the biofilm model at different growth parameters using thermodesorption GC-MS

Jasmin Maria Turkowski

Analysis of fatty acids from biological samples using GC-QqQ-MS

Scientific Publications 2020

Original Paper / Peer-reviewed

J. F. Ayala-Cabrera, C. Lipok, J. Li, E. Moyano, O. J. Schmitz, F. J. Santos **Ionic Liquid Stationary Phase for Improving Comprehensive Two-dimensional Gas Chromatographic Separation of Polychlorinated Naphthalenes**, accepted in Journal of Chromatography A

J. F. Ayala-Cabrera, C. Lipok, E. Moyano, O. J. Schmitz, F. J. Santos **Atmospheric Pressure Ionization for Gas Chromatography-High Resolution Mass Spectrometry Determination of Polychlorinated Naphthalenes**, Chemosphere (2021) 263:127963-127973

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P. Rusch, A. V. Hirner, O. Schmitz, R. Kimmig, O. Hoffmann, M. Diel **Zinc distribution within breast cancer tissue of different intrinsic subtypes**, Archives of Gynecology and Obstetrics (2020) doi.org/10.1007/s00404-020-05789-8

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J. Li, C. Rumancev, H. V. Lutze, T. C. Schmidt, A. Rosenhahn, O. J. Schmitz, **Effect of ozone stress on the intracellular metabolites from *Cobetia marina***, Analytical and Bioanalytical Chemistry (2020) doi.org/10.1007/s00216-020-02810-6

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D. Brecht, F. Uteschil, O. J. Schmitz **Development of a fast-switching dual (ESI/APCI) ionization source for liquid chromatography mass spectrometry**, Rapid Communication in Mass Spectrometry (2020) 34:e8845

T. Koehler, I. Ackermann, D. Brecht, F. Uteschil, J. Wingender, U. Telgheder, O. J. Schmitz **Analysis of volatile metabolites from *in vitro* biofilms of *Pseudomonas aeruginosa* with thin-film microextraction by thermal desorption gas chromatography-mass spectrometry**, Analytical and Bioanalytical Chemistry (2020) doi.org/10.1007/s00216-020-02529-4

Y. Chen, L. Montero, J. Luo, J. Li, O. J. Schmitz **Application of the new at-column dilution (ACD) modulator for the two-dimensional RPxHILIC analysis of *Buddleja davidii***, Analytical and Bioanalytical Chemistry (2020) 412:1483–1495

B. Peng, D. Kopczynski, B. S. Pratt, C. S. Ejsing, M. Hermansson, D. Schwudke, S. W. Meckelmann, O. J. Schmitz, B. MacLean, O. Borst, N. Hoffmann, R. Ahrends **LipidCreator: A workbench to probe the lipidomic landscape**, Nature Communications (2020) 11:2057-2070

Q. A. Ngo, D. T. Hoang, T. Duc, H. A. Duong, O. J. Schmitz, H. V. Pham **Characterization of volatile components from Ethyl acetate extract of *Stixis suaveolens* (Roxb.) by comprehensive two-dimensional gas chromatography hyphenated with a time-of-flight mass spectrometer**, Vietnam Journal of Chemistry (2020) 58:261-266

Misc. Publications

M. Vogel, W. Engewald, K. Dettmer-Wilde, O. J. Schmitz, M. Sperling, C. G. Huber, C. Regl, T. Berger, S. Piendl, D. Belder, F.-M. Matysik **Trendbericht Analytische Chemie II: Trenntechniken und Elektroanalytik** Nachrichten aus der Chemie 68 (10), 48-53

L. Mahdi, O. J. Schmitz **Metabolome Studies of Herbal Medicine Using High Performance Liquid Chromatography Ion-Mobility Mass Spectrometry** The Column 16/5 (2020) 2-7

Poster Presentations

M. Meyer, L. Kuschmierz, B. Siebers, J. Wingender, O. J. Schmitz, **Comparative study of chromatographic methods for the analysis of exopolysaccharides from archaeal biofilms**, biofilms 9 conference, Karlsruhe, Germany, September 2020

L. Kuschmierz, M. Meyer, B. Meyer, S.-V. Albers, C. Bräsen, J. Wingender, O. J. Schmitz, B. Siebers, **Archaeal biofilms: Composition of extracellular polymeric substances, exopolysaccharide synthesis and secretion in *Sulfolobus acidocaldarius***, biofilms 9 conference, Karlsruhe, Germany, September 2020

K. Rentmeister, O. J. Schmitz, S. W. Meckelmann, **Evaluation of Lipid Data Analysis Strategies of LC-IM-qTOF-MS Data**

C. Lipok, F. Uterschil, O. J. Schmitz, **Development of a new GC-APCI ion source**, 30th Ph.D. seminar of the Working Group Separation Science of the Section for Analytical Chemistry of the GDCh, Hohenroda, Germany, January 2020

Invited Lectures / Oral Presentations

Prof. Oliver J. Schmitz

The power of IM-MS and the benefit of multiplexing 6th

International Ion-Mobility Spectroscopy Meeting, Essen, Germany, February 2020 (in presence)

To the limits of feasibility:
2D-LC-ACD-HRdm-IM-qTOF-MS
KEYNOTE SPEAKER

SelectScience
Virtual Analytical
Summit 2020
March 21-April 2, 2020

Prof. Dr. Oliver J. Schmitz,
University of Duisburg-Essen



To the limits of feasibility: 2D-LC-ACD-HRdm-IM-qTOF-MS

SelectScience Virtual Analytical Summit 2020, March 2020 (digital)

Reduction of the elution power of the transfer solution to optimize a 2D-LC

Praxistag HPLC, May 2020 (digital)

Analysis of complex samples with LCxLC, LC-IMS or μ LC+LC-IMS coupled to qTOF-MS: Who is the winner?

analytica Munich conference, October 2020 (digital)

Dr. Florian Uteschil

Thermogravimetry atmospheric pressure photoionization mass spectrometry(TG-APPI-MS): Development and Applications

53rd German Society on Mass Spectrometry, Münster, Germany, March 2020 (in presence)

Timo Köhler

Bacterial lung infections: How thermodesorption GC-MS can help to develop early detection

30th Ph.D. seminar of the Working Group Separation Science of the Section for Analytical Chemistry of the GDCh, Hohenroda, Germany, January 2020 (in presence)

How bacterial pneumonia and cystic fibrosis fit together: A metabolomic approach for the analysis of mVOCs from Pseudomonas aeruginosa biofilms

Agilent Webinar Series: Clinical Research (GC/MS & LC/MS for metabolome analysis), June 2020 (digital)

Dominik Brecht

Development of a dual ESI-APCI ionization source for LC-MS/MS analysis

30th Ph.D. seminar of the Working Group Separation Science of the Section for Analytical Chemistry of the GDCh, Hohenroda, Germany, January 2020 (in presence)

Miscellaneous

Conference Organization

Prof. Oliver J. Schmitz, in partnership with Agilent Technologies, organized the 6th International Ion Mobility Spectroscopy meeting at the University of Duisburg-Essen. Many fascinating lectures on ion mobility – mass spectrometry from all areas of analytical chemistry took place on the 1st day. On the 2nd day, 4 workshops were held to discuss the standardization of analytical methods in the field of lipidomics, the use and benefits of IM-MS in the native protein analysis, in-source fragmentation, multiplexing, and high-resolution demultiplexing, and the best practice to calculate CCS values. Thanks to all participants and Agilent without whom this important meeting for the Ion Mobility-Mass Spectrometry community would not be possible.



Prof. Oliver J. Schmitz (together with Yildiz Danisan and Martin Meyer), organization and celebration of the 30th Ph.D. seminar of the

Working Group "Separation Science" of the Section for Analytical Chemistry of the GDCh in Hohenroda. Many thanks to Yildiz Danisan and Martin Meyer for organizing this very successful and inspiring conference with 175 participants, 26 Ph.D. lectures, 16 posters, 2 tutorials, and industrial talks. To celebrate this anniversary accordingly, we started the conference the day before. Peter Schoenmakers gave a great keynote speech and after a party with musical support from well-known separation technicians from the industry, the next morning we visited a neighboring mine. Nevertheless, in 2020 my group has, for the fifth and last time, organized the Ph.D. seminar of the Working Group Separation Science of the Section for Analytical Chemistry of the GDCh in Hohenroda.

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I wish the working group of Prof. Heiko Hayen, who will now organize the Ph.D. seminar in Hohenroda over the next few years, every success, and I am sure that this event will continue to be a highlight in the calendar of events for analytical chemists in Germany, Austria, and Switzerland.



Editorial Tasks by Prof. Oliver J. Schmitz

- 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

Institute Colloquium

(in cooperation with the research group of Prof. Torsten Schmidt)

Prof. Marja Lamoree, VU Amsterdam, The Netherlands, Effect-Directed Analysis: Adding another dimension to toxicant identification, 20.01.2020

Dr. Thomas Eichmann, Uni-Graz, Austria, Explorative Lipidomics, 03.02.2020

And in the summer semester, Corona had us firmly in its grip and no more attendance events were possible.

TRC-Forum

Therefore I decided to found the TRC-Forum in the winter semester, where, in cooperation with Agilent, two internationally recognized analysts are invited to give a digital lecture on 6 dates per semester.

SLIM and the use of traveling waves for IMS

Traveling waves (TW) generated by applying appropriate potentials to arrays of electrodes on two parallel surfaces in a gas at low pressure

- Traveling waves drive ion motion
- Separate electrodes used for generation of TW and confining RF field

Guard electrode (DC)

Segmented TW electrode arrays (5)

Approximate region of ion confinement

SLIM (6,5) electrode arrangement

Hamid et al., Analytical Chemistry, 87, 11301 (2015)
Hamid et al., Analytical Chemistry, 88, 8949 (2016)
Deng et al., Analytical Chemistry, 89, 4628 (2017)

Zoom meeting grid showing participants: Dick Smith, Oliver Schmitz, Kevin Pagel, Erin Baker, Christian Neuß, Ursula Tegheder.

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 and to ensure that this can run smoothly, I would like to ask you to register in my secretariat (email: 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.

Excellent speakers have already agreed to support this event for next year.

You can view 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).

To attract Asian speakers as well, their presentation times have been moved to the morning. Speakers from the US and Canada will give their lectures in the late afternoon.

Date [CET]	1st talk (45 min)	1st Speaker	2nd talk (15 min)	2nd Speaker
3rd Nov 2020 5 pm	New Paths for Ion Mobility- Mass Spectrometry based upon Structures for Lossless Ion Manipulations	Richard D. Smith Pacific Northwest National Laboratory, USA	Increasing Identification Confidence in Metabolomic, Lipidomic & Exposomic Analyses Using Multidimensional Measurements	Erin Baker North Carolina State University, USA
24th Nov 2020 10 am	Recent Advances in Lipidomic Analysis using Flow field-flow fractionation and nanoflow UHPLC-ESI-MS/MS	Myeong Hee Moon Yonsei University, Seoul (Korea)	Fourier transform infrared (FTIR) spectroscopy for lipid quantification and sample quality control in omics workflows	Michelle Hill QIMR Berghofer (Australia)
15th Dec 2020 10 am	Multi-dimensional liquid chromatography-mass spectrometry method development to improve the metabolome coverage	Guowang Xu Dalian Institute of Chemical Physics, China	Modulator – a Key Element for Performance in 2D-LC	Stephan Buckenmaier Agilent Technologies
19th Jan 2021 5 pm	Droplet Microfluidics as a Tool for Chemical Sensing and High-throughput Screening	Robert Kennedy University of Michigan, USA	Cell Analysis at Agilent: Providing new insights into cell function, cell therapy, and disease	James Hynes Agilent Technologies
26th Jan 2021 5 pm	Adventures in multidimensional space	Tadeusz Gorecki University of Waterloo, Canada	Evolving Flow Modulation GCxGC from Experts to Everyone	James D. McCurry, Ph.D. Agilent Technologies
2nd Feb 2021 5 pm	High-dimensional molecular phenomics in systems, synthetic, and chemical biology	John McLean Vanderbilt University (USA)	Recent developments in high-resolution ion mobility measurement	John Fjeldsted Agilent Technologies

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 (Prof. Dr. O. J. Schmitz, and Dr. S. Meckelmann)

Seminar Modern analytical methods for systems medicine (Prof. Dr. O. J. Schmitz, and 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 (Prof. Dr. O. J. Schmitz, and Dr. S. Meckelmann)

Seminar Modern analytical methods for systems medicine (Prof. Dr. O. J. Schmitz, and Dr. S. Meckelmann)

Exercise Environmental Chemistry: Soil and Waste (in English, Dr. M. Sulkowski)

Lecture Environmental Chemistry: Pollutants (in English, Dr. M. Sulkowski)

Tutorial Environmental Chemistry: Pollutants (in English, Dr. M. Sulkowski)

Magisterium

Lecture Environmental Chemistry: Soil (in German, Dr. M. Sulkowski)

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

Research practical courses

Teaching and Research Center for Separation

Course 3: One- and two-dimensional gas chromatography (in German, Prof. Dr. O. J. Schmitz)

TRC-Forum

(in English, well-known scientists around the world will give a digital lecture about their research, open for everyone)

University of Duisburg-Essen

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Applied Analytical Chemistry
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45141 Essen, Germany

www.uni-due.de/aac

2020

