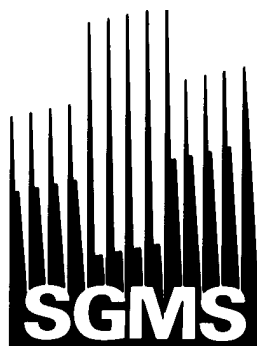


Swiss group for mass spectrometry
Schweizerische Gruppe für Massenspektrometrie



Groupe suisse de spectrométrie de masse
Gruppo svizzero di spettrometria di massa

Newsletter

Rigi Meeting 2002

and

General Assembly 2002

Dorint Hotel Blüemlisalp, Beatenberg

November 14 and 15, 2002

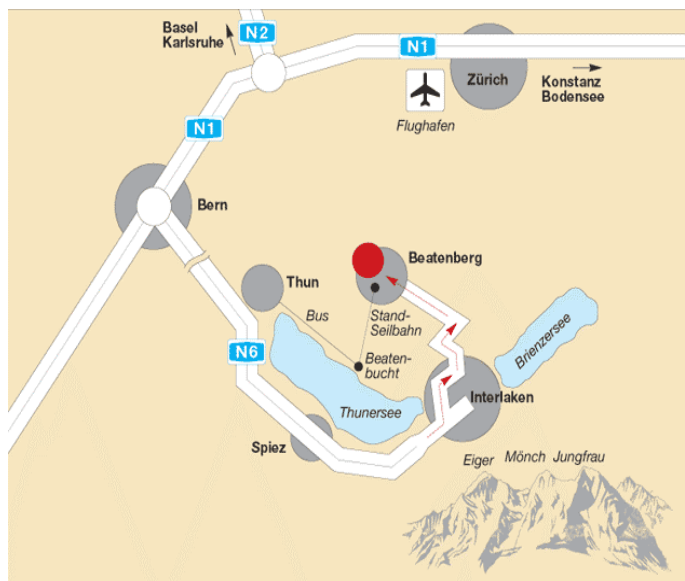
In this Newsletter:

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Travel information

Please note that the Beatenbucht-Beatenberg mountain railway is not running. The railway is under revision during this period of time.

By car: Take Highway no. 6 from Berne to Thun, then no. 8 direction Interlaken. Right before reaching Interlaken follow direction Unterseen/**Beatenberg** at the first possible off ramp. At the roundabout still follow **Beatenberg**. You will reach Beatenberg. Don't be afraid of having missed the Dorint Hotel Blüemlisalp. Beatenberg is quite a stretched mountain village and our



destination is located at the very far end. Please use the indicated parking lots behind the Hotel (free of charge).

By train:

Geneva , Lausanne and Fribourg take **IC711** leaving **Geneva at 06:30** platform 4, **Lausanne 07:06** platform 1 and **Fribourg at 07:51** platform 3 arriving in Berne at 08:13.

Then see Berne.

Basel take **IC861** leaving **Basel at 07:04** platform 9 arriving in Berne at 08:11.

Then see Berne

Schaffhausen take D 2555 leaving Schaffhausen at 06:07 platform 1. Then see Zurich.

Zurich take **IC908** leaving **Zürich at 07:04** platform 18 arriving in Berne at 08:13. Please stay in the train. It will continue to Interlaken West.

Berne take **IC908** leaving **Berne at 08:26** platform 7 arriving in Interlaken West at 09:14.

Interlaken take **Bus 107** leaving **in front of the main station at 09:25**. The bus will arrive at 09:53 in front of the Hotel Dorint Blüemlisalp.

Dear SGMS Member,

After 6 years of heading the SGMS Committee, it is time for me to resign and to leave the SGMS in other hands. In order to avoid complacency or comfortable habits, new people need to join the Committee and bring new ideas to its organization. This is why I think that a new President has to be elected and I am sure that it will move the SGMS one step forward.

Before leaving, I would like to warmly thank all the members of the last three Committees who have worked with me and done their very best to keep the SGMS running. We have managed this twenty year old Society taking into account its scientific excellence, its strong tradition, its friendly atmosphere but also looking to the future, enrolling the SGMS in the international scientific network through its connection to the Web and its registration as a member of the International Mass Spectrometry Society.

Being President of the SGMS has been an enjoyable task not only from a scientific viewpoint but also - on a more personal level. It gave me the opportunity to meet brilliant scientists and friendly people and I will hold many good souvenirs of this experience.

I wish all success to the new Committee and to the new President, and all the best to the SGMS.

Laurent Fay

November 14, 2002

10:00 - 10:15 Welcome***MALDI and Proteomics*****Chair: Hansjörg Walter****10:15 - 11:00 Markus Stoeckli, Novartis Pharama AG, Basel, CH**

MALDI MS imaging of biological tissue: a powerful tool in the drug discovery process.

11:00 - 11:20 Martin Hornberger, Millipore Corporation, Danvers MA, USA

Complexity reduction of biological samples prior to in-gel digestion and high resolution proteomics analysis.

11:20 - 11:40 Rachel L. Martin, Shimadzu Biotech, Manchester, UK

Enhanced structural characterization of protein post-translational modifications using a MALDI QIT TOF MS.

11:40 - 12:00 Uwe Rapp, Bruker Daltonik GmbH, Bremen, GER

An investigation of MALDI TOF/TOF technology and its applications.

12:15 - 13h30 Lunch***SGMS 20th Birthday Special Session*****Chair: Marc Suter****13:30 –14h15 Michael S. Story, ThermoFinnigan, San José, USA**

The development of quadrupole field mass spectrometers.

14:15 - 15:00 General Assembly**15:00 - 19:00 20th Birthday Special Event**

**Somewhere in the region...
...with a nice view!**

19:30 - Bar Magic Buffet Dinner

November 15, 2002

| | |
|----------------------------------------------|---------------------------------|
| <i>Contaminants and Drug Analysis</i> | Chair: Andreas Staempfli |
|----------------------------------------------|---------------------------------|

- 08:30 - 09:15 Hans H. Richnow, Environmental Research Centre
Leipzig-Halle Ltd., Leipzig, GER**
IRM-GC-MS techniques to characterise sources and sinks of organic contaminants in groundwater.
- 09:15 - 9:35 Zdenek Zencak, University of Basel, CH**
Dichloromethane as reagent gas for the selective detection of polychlorinated n-alkanes by negative ion chemical ionization.
- 9:35 - 9:55 Frederic Grisel, Waters S.A., Guyancourt, F**
Development of a mass spectra library with ESI and in-source CID for the screening of toxicants in biological samples.
- 9:55 - 10:15 Stephan Kölliker, University of Basel, CH**
Dancing molecules - ion trap MSⁿ structure elucidation of unknown designer drugs.
- 10:15 - 10:45 Coffee Break**

| | |
|-----------------------------------------------|---------------------------|
| <i>Metabolism and Natural Products</i> | Chair: Laurent Fay |
|-----------------------------------------------|---------------------------|

- 10:45 - 11:30 Oliver Fiehn, Max Planck Institute of Molecular Plant
Physiology, Potsdam, GER**
Can we cover the metabolome only by means of mass spectrometry?
- 11:30 - 11:50 Jean-Luc Wolfender, Institute de Pharmacognosie et
Phytochimie, University of Lausanne, CH**
On-line structural investigation of natural products by LC/MS/MS: the need for a complementary LC/NMR approach.
- 11:50 - 12:10 Michael Affolter, Nestlé Research Centre, Vers-chez-les-Blanc,
Lausanne, CH**
Identification of non-volatile flavor compounds by hydrophilic interaction liquid chromatography electrospray ionization mass spectrometry (HILIC-ESI-MS).
- 12:10 - 12:30 Manuel Tzouros, Institute of Organic Chemistry,
University of Zürich, CH**
Is HPLC-tandem mass spectrometry a suitable method for the characterization of new acylpolyamine derivatives?
- 12:30 - 12:40 Closing Remarks**
- 13:00 - Lunch (voluntary)**

MALDI MS Imaging of Biological Tissue: A Powerful Tool in the Drug Discovery Process

Markus Stoeckli

Analytical and Imaging Sciences, Novartis Pharama AG, Basel

The detailed analysis of biological tissues for their molecular contents is a key element in the search for cures for diseases. A wide variety of techniques is available for this challenging task, but there is a continuous need for tools that enable the collection of large amounts of data with higher spatial resolution in a short time.

Expression profiling by mass spectrometry is a powerful technique that can quickly provide information on a wide range of molecular contents in tissues, but its spatial resolution is only as good as the tissue portion used for the experiment. The goal of our work was to identify molecular entities in tissues and to localize them within small, defined cell populations.

A method is presented for direct spatial analysis of biological tissue sections for their molecular distribution. The technique takes advantage of the very sensitive matrix-assisted laser desorption/ionization mass spectrometry technology and employs a commercial instrument with modifications only to a few components and the software. With this setup, hundreds of molecular images can be generated simultaneously and within just a few minutes. The current features are a spatial resolution of 50 μm and a sensitivity in the attomol range.

In this presentation, the basic principle of this technology is demonstrated, covering the complete process from tissue preparation to image analysis. Improvements developed in our lab will be shown, which allow fast data acquisition and processing. The potential of this method for the drug development process is shown in examples of protein and drug imaging.

Reference

Stoeckli et al., A new technology for the analysis of protein expression in mammalian tissues. Nat. Med., 2001 7(4), 493-496

Complexity Reduction of Biological Samples Prior to In Gel Digestion and High Resolution Proteomics Analysis

Martin Hornberger, Sara Gutierrez**, Malcolm G. Pluskal*, Mary Lopez*, Rebecca M. Doyle*, Alla Bogdanova*, Myra Robinson*, and Aldo M. Pitt**.**

**** Proteome Systems, Woburn, MA. ** Millipore Corporation, Life Sciences Division, Danvers, MA. USA. Phone (+1) 978 762-5243***

E-mail: aldo_pitt@millipore.com

Current Proteomics techniques such as two dimensional gel electrophoresis, tryptic digestion, and mass spectrometry require comprehensive sample preparation for optimal results. The analysis of complex samples, such as plasma or serum, is frequently hindered by the presence of high abundance proteins such as, albumin or immunoglobulin. As a result, sample complexity reduction to lower the level of these abundant proteins is rapidly becoming an essential first step of any high throughput analysis approach. Subsequent in gel digestion and protein identification requires extensive sample preparation at each part of the process. This poster describes two Montage™ Proteomics kits that specifically solves these sample preparation issues: albumin depletion and in gel digestion. The Albumin Deplete Kit provides a convenient and efficient process for removal of abundant proteins from plasma or serum, whereas the In-Gel Digest Kit has optimized 96-well sample purification using the MultiScreen™ filter plate and also offers the option of ZipTip® C18 based microscale sample purification and concentration. A sensitivity of 250 fmole with successful protein identification and coverage was routinely achieved. The procedures and results were found to be convenient, sensitive, and reproducible for both defined and unknown protein mixtures such as serum and cell lysates. These advances should further accelerate the automation and throughput needed to meet the continuously expanding sample numbers in Proteomics requiring identification and characterization.

Enhanced Structural Characterization of Protein Post Translational Modifications Using a MALDI QIT TOF MS.

Rachel L Martin, Emmanuel Raptakis and Kathryn A Jackson.

***Shimadzu Biotech, Wharfside, Trafford Wharf Road,
Manchester, M17 1GP, UK.***

MALDI TOF MS has become widely accepted in the field of protein determination. High sensitivity, high resolution and mass accuracy combined with rapid automated analysis for high throughput are all vital factors in this area, the union of which provides simple, rapid protein identification. Peptide mass fingerprints may be generated for first pass protein assignment by database searching. The confidence in protein identification can be improved by the use of seamless post source decay (sPSD). The use of a curved field reflectron significantly increases the speed and sensitivity of the PSD analysis by enabling the acquisition of a fully focussed PSD spectrum in a single analysis.

However, it has become apparent that this approach does not provide a universal solution to proteomics problems as it relies on the protein being present in a database. In addition, the presence of post translational modifications somewhat complicate the determination of protein structure. In order to decipher both the final sequence and functionality of a protein the nature, abundance and positioning of these modifications must be elucidated. The variety of post translational modifications necessitates an analytical methodology that allows both the detection and precise structural determination of these important adaptations to protein sequence. A new generation of MALDI MS instrument equipped with a quadrupole ion trap and reflectron TOF analyser, has been shown to provide unprecedented levels of structural information for protein characterization through MSⁿ analysis.

The MALDI QIT TOF MS spectra shown display high mass accuracy and resolution regardless of mode of operation (MSⁿ) and the sensitivity necessary to analyse low abundance digested proteins from 2D gels. We will present data displaying the ability of the instrument to provide structural information on post translational modifications and other relevant biological molecules, for example carbohydrates, the characterization of which is key to understanding biological pathways.

AN INVESTIGATION OF MALDI TOF/TOF TECHNOLOGY AND ITS APPLICATIONS

Uwe Rapp, Anja Resemann and Detlev Suckau

Bruker Daltonik GmbH, Bremen, Germany

Email: ur@bdal.de and dsu@bdal.de

The use of MALDI-TOF instruments is primarily for the determination of molecular weights of individual components, but also of complex mixtures. The peptide mass fingerprint spectrum (PMF) represents a one dimensional characterization of the protein via the different molecular masses of the peptides generated during digestion. For the identification of a protein the PMF is not always specific enough, resulting with data bank search machines in low scoring factors. An increase in scoring or specificity requires a second dimension which is typically the MS/MS technique, whereby for peptides sequence information is generated. The sequence information or a significant sequence tag, obviously, results in a very high specificity. A high or extremely high scoring can be expected, making the identification of a protein in many cases more reliable than using the PMF spectrum.

We have recently developed the "LIFT" technique, where a complete MS/MS spectrum is recorded from every laser shot overcoming the well known deficiencies of PSD. Thus, the acquisition time for an MS/MS spectrum is now in the range of 10 – 30 seconds, as is required for a normal MS spectrum. Furthermore, the sample consumption is reduced compared to PSD resulting in a larger number of MS/MS spectra which can be obtained using one individual preparation on the target plate, only.

During the lecture we explain the LIFT method as a TOF/TOF technology and show some characteristic results of protein digests, also from silver stained 2D gels.

We will also present some data showing the use of high energy CID as additional tool for peptide sequencing. The benefits of the TOF/TOF technology together with CID and sophisticated data evaluation in the context of protein identification will be summarized.

The Development of Quadrupole Field Mass Spectrometers

M. S. Story

ThermoFinnigan, San José, USA

While the principles were thoroughly published in the early 50's, widespread availability of mass spectrometers utilizing these principles was not given until 20 years later. Linear and three dimensional quadrupole (ion trap) mass spectrometers represent the overwhelming majority of instruments operating in laboratories today.

As with any technology, there needed to be a driving force for the commercial development. Individuals and companies often do initiate this development, but without a significant market need to direct the technical development to a unique solution, there is most often failure. The success of quadrupole and ion trap mass spectrometry has relied on the environmental and biotechnology markets to provide the problems and support for academic, industrial, and commercial use and development.

This will be a retrospective description of these technical developments and the inter-play of instrumentation development, academia, and market needs.

IRM-GC-MS techniques to characterise sources and sinks of organic contaminants in ground water

***Hans H. Richnow
UFZ Environmental Research Centre Leipzig Halle Ltd.
Permoserstr. 15, 04318 Leipzig, Germany***

In the past decade, stable isotope chemistry has received increasing attention in environmental science. The stable isotope signature of organic substances yields useful information to decipher source, distribution, and fate of organic substances in the ground water. The isotopic composition (D/H, $^{13}\text{C}/^{12}\text{C}$, $^{15}\text{N}/^{14}\text{N}$, $^{37}\text{Cl}/^{35}\text{Cl}$) of organic contaminant can be used as fingerprints to trace their origin (Smallwood et al., 2002; Drenzek et al., 2002) which may have some potential in forensic approaches with respect to separate pollution sources. Isotope fractionation processes can be used to characterise *in situ* biodegradation.

Monitoring of ground water contamination has gained importance in the context of risk assessment, plume management strategies, and in the evaluation of remediation measures, in particular where natural attenuation concepts are applied. Thus, innovative approaches are needed to monitor processes governing the concentration of contaminants in the aquifer. A decrease of pollutants concentration in a contamination plume could have many reasons like dilution, sorption or biological degradation, but only the latter leads to sustainable contaminant reduction. Thus, the assessment and quantification of *in situ* biodegradation is essential to evaluate the risk of contaminated aquifers and is essential to prove the success of monitored natural attenuation (MNA) or any other remedy.

To characterise *in situ* biodegradation, a concept based on the isotope fractionation of organic contaminants during biodegradation had been developed (Richnow and Meckenstock, 1999; Meckenstock et al., 1999; Richnow et al., 2002). Biodegradation of pollutants such as aromatic hydrocarbons and chlorinated ethenes leads to an enrichment of ^{13}C and ^2H in the residual fraction (Meckenstock et al., 1999; Hunkeler et al., 1999; Bloom et al., 2000; Ward et al., 2000; Morasch et al., 2001). This fractionation process can be described by the Rayleigh-Equation. The relation

between concentration and isotopic composition of a compound is described by the kinetic isotope fractionation factor (α). In laboratory degradation experiments with batch cultures, the isotope fractionation factors have been determined for some typical BTEX, mineral oil and chlorinated groundwater contaminants. These factors were applied to quantify the biodegradation in several field studies and to evaluate the validity of the isotope fractionation concept.

Various test sites with distinct geochemical and hydrological characteristics were examined for isotopic fractionation to assess the *in-situ* biodegradation. Laboratory derived isotope fractionation factors were applied to calculate the extent of biodegradation (Vieth et al., 2002). Test site comprises variety of contaminants, such as (i) tar oils (BTEX and naphthalene), (ii) landfill leachate with BTEX, mineral oils (diesel fuel) and (iii) chlorinated solvents. Isotope fractionation may be well used to evaluate the biodegradation in contaminated aquifers independent of other concentration diminishing processes such as sorption and dilution. In the context of Natural Attenuation, this concept has a large potential to improve ground water monitoring and risk assessment strategies.

Modern IRM-GC-MS systems can be used in routine analysis and enable the exploitation of the large potential of isotope chemistry in ground water research. This paper discusses various aspects of IRM-GC-MS approaches in ground water analysis chemistry from a technical and scientific perspective.

References

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- Drenzek NJ, Tarr CH, Eglinto TI, Heraty LJ, Sturchio NC, Shinner VJ Reedy CM (2002) Org.Geochem. 33, 437-444.
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Dichloromethane as Reagent Gas for the selective Detection of Polychlorinated n-Alkanes by Negative Ion Chemical Ionization

Zdenek Zencak and Michael Oehme

Organic Analytical Chemistry, University of Basel, Switzerland

The presence of thousands of congeners in technical of polychlorinated n-alkanes (PCAs) make both the chromatographic separation and the mass spectrometric quantification of these compounds very demanding.

Nowadays, the detection method of choice for PCAs is electron capture negative ion chemical ionization mass spectrometry (NICI-MS). Depending on the degree of chlorination, the position of the chlorine atoms at the carbon chain and on the sample amount, the relative abundances of the three most abundant ions $[M-HCl]^-$, $[M-Cl]^-$ and $[M+Cl]^-$ vary strongly [1]. Consequently, response factors of different congeners vary by a factor of 15 making an accurate quantification of PCAs impossible, since most single congeners are not available as reference standards.

The use of dichloromethane/methane mixtures as reagent gas for NICI has been already reported for other chlorinated compounds such as chlordanes [2]. Its application to PCAs allowed to enhance the formation of chlorine adducts and to suppress fragmentation. The response factors of single congeners differed by only a factor of two or less. This allowed a more precise quantification of different congeners present in the technical mixtures. This ionization method proved to be linear showing detection limits of single congeners similar or lower than those of conventional NICI (1-2 ng technical PCA mixture). Additionally, other polychlorinated compounds, such as PCBs, chlordanes, toxaphenes, etc. showed lower response factors, when ionized with this technique than under NICI conditions.

[1] G.T. Tomy, *et al.*, *Chemosphere* **1998**, 37, 1395.

[2] E.A. Stemmler and R.A. Hites, *Anal. Chem.* **1985**, 57, 684.

Development of a Mass Spectra Library with ESI and in source CID for the Screening of Toxicants in Biological Samples.

***Frederic Grisel
Waters S.A., rue Jacques Monod, Rond-Point des Sangliers, F-78280
Guyancourt, France***

Identification of drugs and toxicants in biological fluids can be achieved using different analytical techniques such as the well known and widely used immunoassays techniques as well as chromatographic techniques such as GC in combination with MS detection (EI and/or CI) and LC in combination with UV detection (Photodiode array). Although these techniques can cover most of the analytical needs, the number of compounds and related metabolites that have to be determined is becoming more and more important.

The difficulty is that some molecules do not exhibit a strong UV absorbance, while some others are very active and used at extremely low concentration, making the determination very difficult. Also, many substances are thermolabile and cannot be analyzed by GC without a derivatization step.

LC in combination with ESI/MS and PDA-UV detection provides a rapid means of determining those types of compound, and can now be considered a good complementary technique to GC/MS and LC/UV.

Working in collaboration with an hospital toxicology laboratory (Pr. Lhermitte and Luc Humbert, hospital of Lille, France), we have developed an LC/MS method for the screening of molecules of toxicological interest. For the separation, we have modified a pre-existing method, changing the phosphate buffer to a formate buffer. The determination of the compounds is achieved by searching a mass spectra library. The library was built using in source CID, using six different cone voltages in both positive and negative electrospray. After data acquisition, all spectra are checked, so that only the

relevant spectra are entered into the library. This library counts now more than 1200 spectra, corresponding to more than 250 molecules and metabolites. After running samples, the library search is done either manually or automatically. The retention time can use used as a filter for the library search.

We will present some real life application examples of using that screening method.

Dancing Molecules. Ion Trap MSⁿ ***Structure Elucidation of Unknown Designer Drugs***

Stephan Kölliker, Michael Oehme

Org. Analyt. Chemistry, University of Basel, CH-4057 Basel

First synthesized around 1900 by Köllisch et. al. at Merck, the compound *N*-methyl-3,4-methylenedioxyamphetamine (MDMA) has attracted considerable attention during the past fifteen years. Used as an aid for overcoming personal barriers and misused as stimulant the compound has found a widespread acceptance among young people in the urban dance culture.

Due to the classification of MDMA as *class 1 compound* (along with Heroin) and the restricted availability of precursor chemicals a substantial percentage of *Ecstasy* pills does contain compounds other than MDMA. Usually these substitutes do not induce the state of openness, inner peace and empathy known from pure MDMA¹. Therefore many people try to reach the state longed for by taking additional pills, sniffing cocaine, smoking marijuana, or drinking alcohol. This misuse leads to increasing problems in our society.

More than 200 psychoactive compounds containing the phenethylamine / amphetamine substructure are described in the literature. The analysis of close MDMA analogues with GC-EI mass spectrometry often leads to virtually identical mass spectra². The use of NMR for structure elucidation of unknown compounds is rather time-consuming and – in case of an emergency – impossible.

HPLC coupled with ion trap MSⁿ mass spectrometry offers the needed sensitivity and selectivity for rapid structure elucidation³ of new *designer*

¹ Adamson, S. (ed.): *Through the Gateway of the Heart*, Four Trees Publications, San Francisco **1985**

² Borth, S.; Hänsel, W.; Rösner, P.; Junge, T.: *For. Sci. Int.* **2000**, *114*, 139

³ Berger, U.; Kölliker, S.; Oehme, M.: *Chimia* **1999**, *53*, 492

drugs, their metabolites and their reaction byproducts. Low nanogram amounts are sufficient for multiple MS experiments. The drawback of the relatively new technique (1996) is the lack of generally applicable fragmentation rules.

A yet unpublished structure elucidation scheme for rapid and unequivocal structure elucidation of *Designer Drugs* from the phenethylamine / amphetamine class will be presented. Method development will be shown in detail and with special emphasis on labeling experiments. Possible rearrangement reactions appearing inside the ion trap⁴ will be discussed as well. In addition anecdotal information about the effect of certain new compounds will be given.

⁴ Kölliker, S. Oehme, M., Merz, L.: *Rapid Comm. Mass Spectrom.* **2001**, *15*, 2117

Can we cover the metabolome only by means of mass spectrometry?

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Analogous to the transcriptome and the proteome, an organism's metabolome is defined as the complete set of its metabolites present in a certain tissue under defined conditions. Plant metabolomes are comprised by thousands of individual compounds. Is it possible to identify and quantitate all metabolites in a biological system by means of mass spectrometry?

Currently, the answer is a clear 'no'. However, in the context of functional genomics, there is the need to analyse as detailed as possible the response of an organism to genetic, environmental or developmental perturbation. We have therefore started to analyse parts of the metabolome in an unbiased way by combining GC-TOF with mass spectral deconvolution, and RP and HILIC-ion trap-MS³ at positive and negative ESI for assessing the relative abundance of all detectable peaks, with currently some 1,000 peaks to be found in a plant sample. This strategy leads to a high number of unidentified compounds, and *de novo* identification is an essential part of truly metabolomic approaches. Using the example of a novel amino-callose found in cucurbit phloem we demonstrate how ion trap mass spectrometry alone may be misleading in structural elucidation, and that accurate mass MS is required by necessity. We compared the use of GC-Quadrupole MS (!), QTOF and FT-MS for that purpose, and concluded that without the additional help of 2D μ NMR, metabolites cannot be elucidated, even with the help of software like MassFrontier or databases like KEGG and Beilstein. After *de*

novo identification of several metabolites we later found to be already published, we concluded that it would be a great help to have a comprehensive biological LC/MS library, despite the fact that standardisation between different instruments is hardly possible.

As a biological application example, the comparison of a silent SuSy antisense potato line and its corresponding Desirée cultivar is shown. Using the peak areas of identified and unidentified compounds, we normalized each individual plant sample to the total metabolome content. Metabolic distances as well as shifts in biochemical networks could be computed. Network generation was performed by correlation analysis and 3D visualization. By investigating these networks, novel hypotheses on hexose transformations and sugar alcohol metabolism could be generated.

On-line structural investigation of natural products by LC/MS/MS: the need for a complementary LC/NMR approach

J-L. Wolfender and K. Hostettmann

***Institut de Pharmacognosie et Phytochimie, Université de Lausanne,
BEP, CH-1015 Lausanne, Switzerland***

Plants represent an extraordinary reservoir of novel molecules and there is currently a resurgence of interest in the vegetable kingdom as a possible source of new lead compounds for introduction into therapeutical screening programs. Plant constituents of interest are usually isolated following a bioactivity guided fractionation procedure. In order to render this approach more rapid and efficient, the dereplication of crude plant extracts with LC-hyphenated techniques represents a strategic element to avoid finding known constituents and to target the isolation of new bioactive compounds. Spectroscopic information can be obtained on-line, directly from crude plant extracts, with hyphenated techniques such as high performance liquid chromatography (HPLC) coupled to UV photodiode array detection (LC-DAD/UV), to mass spectrometry (LC/MS) and to nuclear magnetic resonance (LC/NMR) [1,2].

For the on-line identification of natural products, often LC/MS or LC/MS/MS alone are not sufficient and LC/NMR bring invaluable complementary information. The potential of such a complementary approach will be demonstrated for the detail on-line identification of new oxidised forms of hyperforin in St-John's Wort (*Hypericum perforatum*). The use of combined LC/UV/MS and LC/NMR approach will also be shown for the study of unstable compounds or for the screening of novel bioactive molecules.

LC/NMR and LC/MS are powerful tools for solving phytochemical problems. In combination with LC-bioassays they allow a rapid estimation of the interest of a given compound in a complex extract. These techniques do not replace

the activity-guided fractionation of the extracts, but provide a strategic complement to standard isolation procedures: furthermore they permit the recording of the spectroscopic data of labile constituents which could not be recorded by other means.

- 1.** Hostettmann et al. (2002) *Pharm. Biol.* 39: 18-32, **2.** Wolfender J.-L. (2001) *Phytochem. Anal.* 12: 2-22

***Identification of Non-Volatile Flavor Compounds by
Hydrophilic Interaction Liquid Chromatography
Electrospray Ionization Mass Spectrometry (HILIC-ESI-MS)***

Hedwig Schlichtherle-Cerny, Michael Affolter, Christoph Cerny

***Nestlé Research Centre Vers-chez-les-Blanc, P.O. Box 44, 1000 Lausanne
26, Switzerland***

Reversed phase high performance liquid chromatography coupled to electrospray ionization mass spectrometry (RP-HPLC-ESI-MS) has nowadays become a standard separation and identification method. However, small hydrophilic molecules, such as free amino acids, sugars, and polar di- and tripeptides are not retained by RP-HPLC and require either derivatization to increase their hydrophobicity or complementary chromatographic methods, such as ion exchange chromatography. Hydrophilic interaction liquid chromatography coupled to electrospray ionization mass spectrometry (HILIC-ESI-MS) has been proposed for separation of polar components, such as cephalosporin C or vancomycin. In the present study this technique was applied for the separation and identification of non-volatile flavor compounds from complex food matrices. HILIC-ESI-MS, tandem MS, and MS³ in positive and negative ionization modes allowed the successful separation and identification of taste-active hydrophilic peptides and glycoconjugates, free amino acids, and organic acids without prior derivatization.

Is HPLC-Tandem Mass Spectrometry a Suitable Method for the Characterization of New Acylpolyamine Derivatives?

Manuel Tzouros, Nikolay Manov, Sergiy Chesnov, Laurent Bigler, Stefan Bienz, and Manfred Hesse

***Organisch-chemisches Institut der Universität Zürich
Winterthurerstrasse 190, CH-8057 Zürich***

Recently, as many as 33 acylpolyamines with 11 different masses were detected in the complex mixture of *Agelenopsis aperta* (Agelenidae) spider venom [1]. With the aim of proving their structures, 12 of these spider toxins were synthesized on solid-phase and investigated by HPLC-APCI-MS/MS [2]. The CID spectra of the synthetic references were compared with those obtained from natural spider venom and supported the structures and assignments of seven of the previously found toxins. In addition, the comparison allowed the identification of an additional five minor polyamine derivatives that are coeluting with other components of the venom. Furthermore, the MS/MS study of isomerically pure polyamine toxins revealed an unexpected fragmentation pattern for these compounds, which can be relevant for the characterization of further polyamine derivatives

[1] S. Chesnov, L. Bigler, M. Hesse, *Helv. Chim. Acta* **2001**, 84, 2178.

[2] N. Manov, M. Tzouros, S. Chesnov, L. Bigler, S. Bienz, *Helv. Chim. Acta* **2002**, 85, 0000.

"Rigi"-Meeting 2002: This years participants

| | | |
|-----------|---------------|----------------------------------|
| Beat | Aebi | IRM, Bern |
| Michael | Affolter | Nestlé Research Centre, Lausanne |
| Louis | Allemann | F. Hoffmann-la-Roche Ltd, Basel |
| Walter | Amrein | ETH Zurich |
| Manfred | Bergmann | Varian, Zug |
| Laurent | Bigler | University of Zurich |
| Norbert | Bild | University of Zurich |
| Serge | Bilger | Shimadzu, Reinach |
| Joachim | Blanz | Syngenta AG, Basel |
| Gerard | Bondoux | Waters France |
| Hans | Brandenberger | Rigi Kaltbad |
| René | Burkhard | Syngenta AG, Basel |
| Heribert | Dollt | F. Hoffmann-la-Roche Ltd, Basel |
| Jens | Donath | Lonza AG, Visp |
| Laurent | Fay | Nestlé Research Centre, Lausanne |
| Winfried | Fiedler | Cilag AG, Schaffhausen |
| Oliver | Fiehn | MPI Potsdam |
| Joaquim | Figueiredo | Syngenta AG, Basel |
| Peter | Fischlewitz | F. Hoffmann-la-Roche Ltd, Basel |
| Joel | Fricker | Waters |
| Ernst | Gassmann | Syngenta AG, Basel |
| Tino | Gäumann | EPFL Ecublens |
| Hans | Gfeller | Givaudan, Dübendorf |
| Patrick | Graf | Novartis Pharma, Basel |
| Frederic | Grisel | Waters, France |
| Christian | Guenat | Novartis Pharma, Basel |

| | | |
|------------|-------------|----------------------------------|
| Jörg | Hau | Nestlé Research Centre, Lausanne |
| C.W. | Heizmann | Uni Zurich |
| Harald | Hertle | Micromass, Frauenfeld |
| Matthias | Herzog | Applera Europe, Rotkreuz |
| Johannes | Hewel | University of Bern |
| Peter | Hirter | Solvias, Basel |
| Martin | Hornberger | Millipore, Molsheim, France |
| Klaus | Kaiser | Spectronex |
| Werner | Kloeti | Université Genève |
| René | Knecht | Novartis Pharma, Basel |
| Richard | Knochenmuss | Novartis Pharma, Basel |
| Stephan | Koenig | Applera Europe, Rotkreuz |
| Martin | Kohler | EMPA, Dübendorf |
| Stephan | Kölliker | Universität Basel |
| Fabian | Kuhn | Universität Basel |
| Jürgen | Kühnol | Novartis Pharma, Basel |
| Thomas | Läubli | Brechbuehler, Schliesen |
| Grid | Laue | Syngenta AG, Basel |
| Gabriela | Laufenberg | Inst Pharma, Marburg |
| Walter | Lehmann | MS-Service, Weggis |
| Jürg | Leu | Macherey-Nagel, Oensingen |
| Rachel | Martin | Kratos, manchester |
| Hanspeter | Moser | Novartis Pharma, Basel |
| Stephan | Müller | F. Hoffmann-la-Roche Ltd, Basel |
| Paul | Nägeli | Labo Cantonal, Zurich |
| Jörg | Niebel | Advion Ltd, Wachenheim |
| Jean-Marie | Oberson | Nestlé Research Centre, Lausanne |
| Michael | Oehme | Universität Basel |

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|-----------|-----------------|------------------------------------------------|
| Peter | Oggenfuss | Syngenta AG, Basel |
| Gerd | Paulus | Shimadzu, Reinach |
| Marion | Petrzika-Kitzka | Syngenta AG, Basel |
| Urs | Ranalter | F. Hoffmann-la-Roche Ltd, Basel |
| Uwe | Rapp | Bruker Daltronix, Bremen |
| Vittorio | Raverdino | Agilent, Meyrin |
| Hans | Richnow | Environ. Res. Center Leipzig Halle AG, Leipzig |
| Sonja | Riediker | Nestlé Research Centre, Lausanne |
| Fabrizio | Sabini | Micromass, Frauenfeld |
| Stephan | Sack | Syngenta AG, Basel |
| Gisbert | Schäfer | Applera Europe, Rotkreuz |
| Martin | Schär | HTA, Burgdorf |
| Kurt | Schellenberg | Novartis Pharma, Basel |
| Patrick | Schindler | Novartis Pharma, Basel |
| Urs | Schlunegger | Stettlen |
| Joachim | Schmid | Givaudan, Dübendorf |
| Stephan | Schürch | University of Bern |
| Andreas | Staempfli | F. Hoffmann-la-Roche Ltd, Basel |
| Daniel | Stahl | Lausanne |
| Markus | Stöckli | Novartis Pharma, Basel |
| Brigitte | Stofer | Applera Europe, Rotkreuz |
| Siegfried | Stolz | F. Hoffmann-la-Roche Ltd, Basel |
| Mike | Story | Thermo Finnigan, San Jose |
| Marc | Suter | EAWAG, Dübendorf |
| Raphael | Tabacchi | Uni Neuchatel |
| Jan | Tromp | University of Bern, |
| Michael | Tzouros | University of Zurich |
| J.J. | Veith | University of Darmstadt |

| | | |
|-----------|-----------|------------------------------|
| Walther | Vetter | Arlesheim |
| Hansjörg | Walther | Solvias, Basel |
| Annemarie | Weibel | MS-Wil, Wil |
| Peter | Weibel | MS-Wil, Wil |
| André | Wetter | Bruker Daltronics, Fällanden |
| Urs | Widmer | Bruker Daltronix |
| Urs | Wirth | Novartis Pharma, Basel |
| Jean-Luc | Wolfender | IPP BEP UNIL |
| Hartmut | Wuester | Applied Biosystems, Rotkreuz |
| Joseph | Youssefi | Firmenich, Genève. |
| Zdeneck | Zencak | Universität Basel |

General Assembly 2002

The committee would like to thank Laurent Fay for its precious work he did on behalf of the SGMS. He did a great job and we regret very much that we loose such a motivated and overall friendly person. The entire committee wishes to Laurent Fay a bright future and all the best for his forcoming industrial and academic career.

Due to the fact that Laurent Fay has decided to retire from the position of President of the SGMS but also to leave the committee of the SGMS, the committee announces the following nominations to the general assembly:

For President:

Dr. Andreas A. Staempfli, F. Hoffmann-La Roche Ltd, Basel

As New Member of the Committee:

Dr. Jean-Luc Wolfender, Institute de Pharmacognosie et Phytochimie,
Université de Lausanne, BEP, CH-1015 Lausanne, Switzerland

If there are other nominations/proposals: Please address them directly to:

Dr. Laurent Fay, Nestlé Research Center, Vers-chez-les-Blanc,
CH-1000 Lausanne 26, Fon +41-21-785 8609 Fax +41-21-785-8925

Swiss group for mass spectrometry
Schweizerische Gruppe für Massenspektrometrie



Groupe suisse de spectrométrie de masse
Gruppo svizzero di spettrometria di massa

Please join us for the

General Assembly of the SGMS 2002

Thursday, November 14, 2002

1415 h

Dorint Hotel Blüemlisalp, Beatenberg

Agenda

1. Nomination of the scrutineers.
2. Approval of the minutes of the 2001 general assembly.
3. Presidents report and its approval.
4. Treasurer's report.
5. Auditor's report and approval of treasurer's and auditor's report.
6. Decision on the 2003 membership fee.
7. Admission of new members.
8. Election of the President and the SGMS committee.
9. News from the NSCG - HJ. Walther.
10. News form ESMS - R.Tabachi.
11. Individual proposals.
12. Miscellaneous

Individual proposals must be **sent by (e)- mail before October 31, 2002 to the president:** Dr. Laurent B. Fay, Nestlé Research Center, Vers-Chez-les-Blanc, CH-1000 Lausanne 26

for the committee
Andreas A. Staempfli



MEMBERSHIP APPLICATION

Name: _____

First Name: _____

Title: _____

Prof. Address :

Phone: _____ **Fax:** _____

E-Mail: _____

Instruments : _____

Fields of activities: _____

Are you already member of the New Swiss Chemical Society (NSCG)? _____

wishes to become member of the SGMS:

Date: _____

Signature:

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