

Novel Strategies to Guide Sample Preparation for Compound-Specific Isotope Analysis

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Abstract

Numerous research fields, from forensic to environmental sciences, benefit from information about the variation of stable isotope abundances (e.g., by measuring δ^{13} C as the ratio of 13 C and 12 C) in (bio)chemical substances. In compound-specific isotope analysis (CSIA), the isotopic signature of a compound can be measured with high precision using an isotope ratio mass spectrometer (IRMS) hyphenated to gas- or liquid chromatography (GC- and LC-IRMS). During the isotope measurement using the IRMS, the compound of interest is combusted into a universal analyte, in the case of carbon measurements to CO₂. The structural information gets lost during this process, which makes CSIA prone to matrix interferences in case the separation power provided by GC/LC is insufficient. For many real-world applications, large amounts of matrix compounds are co-enriched during the extraction of the sample and, thus, must be removed using further purification steps to guarantee accurate CSIA. While there are many purification techniques available, like molecularly imprinted solid phase extraction (MISPE) or the most commonly used one, reversed-phase high-performance liquid chromatography (RP HPLC), optimizing matrix removal during the respective purification is still one of the greatest challenges of CSIA sample preparation. For optimal and efficient purification using RP HPLC, for example, simultaneous online monitoring and quantification of both the target analyte and the matrix is highly valuable. Still, no commercially available detector can quantify the entirety of the matrix online during an RP HPLC purification. Hence, the overarching goal of this dissertation was to expand the applicability of CSIA by investigating the effectiveness of strategies to optimize the matrix removal during the purification of sample extracts prior to GC-IRMS isotope analysis, with a specific focus on developing a novel detection technique for the online quantification of the sample matrix during RP HPLC purification.

The first part of the thesis investigated the influence of the anionic character of the environmental matrix natural organic matter (NOM) on non-specific sorption of NOM during MISPE to increase the understanding of processes governing non-specific binding of the sample matrix. To this end, acidic functional groups of NOM were methylated to significantly reduce the charge density of NOM and, thus, the electrostatic repulsion of dissolved and sorbed NOM compounds. The study successfully shows the reduction of the charge density of NOM by a factor of 3.4 using a trimethylsilyl diazomethane (TMSD) based selective methylation of NOM carboxy groups. Breakthrough curves revealed that 30% more methylated NOM compared to untreated NOM remained on the MIP after a washing procedure using dichloromethane (DCM). This implies stronger MIP-methylated NOM interactions, which are most likely caused by the smaller charge density of the methylated

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NOM and the consequently smaller electrostatic repulsion between NOM molecules. The presented findings prove the importance of NOM's anionic character for the sorption on MIPs and provide a knowledge base for future research on non-specific binding of the sample matrix NOM during MISPE.

The second and major part of the thesis addressed the challenge of developing a detection technique that can quantify matrix components online during RP HPLC. For this purpose, this thesis investigated the suitability of quartz crystal microbalance (QCM) using two different strategies: (i) QCM liquid sensing and (ii) QCM dry mass sensing. First, a suitable coating must be found to quantify matrix components in the liquid phase using QCM liquid sensing. The second chapter thus investigated for the first time a grafting approach for a hypercrosslinked divinylbenzene (DVB)-based copolymer using ethylene glycol dimethacrylate (EGDMA) as a hydrophilic modifier on a QCM sensor, characterized the sensor coating, and evaluated the interaction of the coating with humic acids. The study demonstrates the successful grafting of a DVB-EGDMA co-polymer onto the QCM sensor using radical polymerization. A laterally heterogeneous polymer layer with a thickness of 200-300 nm inside the dynamic range of QCM measurements was further achieved. While humic acids did sorb onto the grafted copolymer during sorption experiments, leading to a high frequency decrease of 18-20 Hz in comparison to other studies, this number is still too low for matrix online monitoring. Future research can build upon this study's grafting and characterization procedure to optimize and explore other co-polymers further.

The third chapter explored the feasibility of coupling a commercial HPLC with a microfluidic spray-dryer and a QCM using a flow splitter for online monitoring of organic matrix components during RP HPLC gradient purification. To this end, a measuring, calibration, and data processing strategy was developed, and the system was characterized in terms of lower and upper quantification limits and accuracy. Validation of NOM in an environmental sample against offline total organic carbon analysis confirmed the approach's feasibility with an absolute recovery of $103\pm10\%$. A correlation ($R^2 \ge 95$) between the amount of matrix quantified by QCM dry mass sensing during an HPLC clean-up of a brown rice extract and matrix effects measured during the subsequent GC-MS analysis of the investigated pesticides was found. This suggests that QCM dry mass sensing can be a valuable tool to the analyst where HPLC clean-up is routinely performed and can thus benefit many analytical fields.

The fourth chapter investigated the limitations and enhancement of HPLC purification on C_{18} and C_8 phases for single- and multiple-targets using QCM dry mass sensing. Further, the benefit of such an optimized HPLC purification for isotope analysis of polar micropollutants typically present in environmental samples was examined. Strong isotopic shifts of up to 3.3% towards the isotopic signature of NOM were observed for samples with a NOM-to-analyte ratio ≥ 10 . Thanks to QCM sensing, optimization of matrix removal of up to 97 for early and 99.8% for late-eluting compounds was possible. The efficiency of HPLC purification deteriorated when aiming for simultaneous purification of two or three compounds, leading to up to 2.5% less NOM removal. Our results suggest that one optimized HPLC purification can be achieved through systematic screening of 3 to 5 different gradients, thereby shifting the boundaries of accurate carbon-CSIA by up to two orders of magnitude toward lower micropollutant concentrations.

Overall, the results of this work emphasize the importance (i) of suitable detection techniques for the specific requirements of analytical tasks and (ii) of optimized, highly selective, and automated purification techniques for sample clean-up to use the full potential of CSIA. Specifically, QCM dry mass sensing proved to be successful in online quantifying of the entirety of the extracted sample matrix during RP HPLC purification, thus tremendously increasing the percentage of NOM that can be removed in one clean-up step. QCM dry mass sensing paves the way to efficiently develop optimized purification strategies for various purification problems using a large range of liquid chromatographic solid phase materials and modes. Using optimized chromatographic purification in combination with selective extraction procedures that were recently developed will, in the future, help to expand the applicability of CSIA to compounds present in real-world samples in the low to middle ng/L range, enabling thus insights into environmental and biological processes and forensic cases that are presently not accessible. Furthermore, the possibility of online detection of both the target and the matrix during RP HPLC is a big step towards a fully automated method development and optimization of CSIA sample preparation.

Zusammenfassung

Zahlreiche Forschungsbereiche, von der Forensik bis zu den Umweltwissenschaften, profitieren von Informationen über die Variation stabiler Isotopenhäufigkeiten (z.B. durch Messung von δ^{13} C als Verhältnis von ¹³C und ¹²C) in (bio)chemischen Stoffen. Bei der substanzspezifischen Isotopenanalyse (engl. compoundspecific isotope analysis, CSIA) kann die Isotopensignatur einer Verbindung mithilfe eines Isotopenverhältnis-Massenspektrometers (engl. isotope ratio mass spectrometry, IRMS) verbunden mit Gas- oder Flüssigkeitschromatographie (engl. gas- or liquid chromatography, GC- und LC-IRMS) mit hoher Präzision gemessen werden. Bei der Isotopenmessung mit dem IRMS wird die Zielverbindung zu einem universellen Analyten verbrannt, bei Kohlenstoffmessungen zu CO₂. Die Strukturinformation geht bei diesem Prozess verloren, was CSIA anfällig für Matrixinterferenzen macht, falls die Trennleistung der GC/LC nicht ausreicht. Bei vielen Realanwendungen werden bei der Extraktion der Probe große Mengen an Matrixverbindungen angereichert und müssen daher durch weitere Aufreinigungsschritte entfernt werden, um eine genaue CSIA zu gewährleisten. Auch wenn viele Aufreinigungstechniken zur Verfügung stehen, wie beispielsweise die molekular geprägte Festphasenextraktion (engl. molecularly imprinted solid phase extraction, MISPE) oder die am häufigsten verwendete Methode, die Umkehrphasen-Hochleistungsflüssigkeitschromatographie (engl. reversed-phase high-performance liquid chromatography, RP HPLC), ist die Optimierung der Matrixentfernung während der jeweiligen Aufreinigung immer noch eine der größten Herausforderungen der CSIA-Probenvorbereitung. Für eine optimale und effiziente Aufreinigung beispielsweise mittels RP-HPLC ist die gleichzeitige Online-Überwachung und Quantifizierung sowohl des Zielanalyten als auch der Probenmatrix von großem Wert. Dennoch kann kein kommerziell erhältlicher Detektor die gesamte Matrix während einer RP-HPLC-Reinigung online quantifizieren. Daher bestand das übergeordnete Ziel dieser Dissertation darin, den Anwendungsbereich von CSIA zu erweitern, indem die Wirksamkeit von Strategien zur Optimierung der Matrixentfernung während der Aufreinigung von Probenextrakten vor GC-IRMS-Isotopenmessungen untersucht wurde. Ein besonderer Schwerpunkt lag dabei auf der Entwicklung einer neuartigen Messtechnik zur Online-Quantifizierung der Probenmatrix während RP-HPLC Probenaufreinigung.

Der erste Teil der Arbeit untersuchte den Einfluss des anionischen Charakters der natürlichen organischen Materie (engl. *natural organic matter*, NOM) auf die unspezifische Sorption von NOM während MISPE, um das Verständnis der Prozesse zu verbessern, die die unspezifische Bindung der Probenmatrix steuern. Zu diesem Zweck wurden saure funktionelle Gruppen von NOM methyliert, um die Ladungsdichte von NOM und

damit die elektrostatische Abstoßung gelöster und sorbierter NOM-Verbindungen deutlich zu reduzieren. Die Studie zeigt erfolgreich die Reduzierung der Ladungsdichte von NOM um den Faktor 3,4 mithilfe einer auf Trimethylsilyldiazomethan (engl. *trimethylsilyl diazomethane*, TMSD) basierenden selektiven Methylierung von NOM-Carboxygruppen. Durchbruchskurven zeigten, dass nach einem Waschvorgang mit Dichlormethan (DCM) 30% mehr methyliertes NOM im Vergleich zu unbehandeltem NOM auf dem MIP verblieben. Dies lässt auf stärkere Wechselwirkungen zwischen MIP und methyliertem NOM schließen, welche höchstwahrscheinlich durch die geringere Ladungsdichte des methylierten NOM-Werursacht werden und der daraus resultierenden geringeren elektrostatischen Abstoßung zwischen NOM-Molekülen. Die präsentierten Ergebnisse belegen die Bedeutung des anionischen Charakters von NOM für die Sorption an MIPs und bieten eine Wissensbasis für zukünftige Forschungen zur unspezifischen Bindung der Probenmatrix NOM während MISPE.

Der Hauptteil der Arbeit befasste sich mit der Herausforderung, eine Detektionstechnik zu entwickeln, mit der Matrixkomponenten online während RP-HPLC quantifiziert werden können. Zu diesem Zweck untersuchte diese Arbeit die Eignung der Quarzkristall-Mikrowaage (engl. quartz crystal microbalance, QCM) mit zwei verschiedenen Strategien: (i) QCM Messungen in Flüssigkeiten (engl. QCM liquid sensing, Flüssigkeiten-QCM) und (ii) QCM Messung von Trockenmassen (engl. QCM dry mass sensing, Trockenmassen-QCM). Zunächst muss eine geeignete Beschichtung gefunden werden, um Matrixkomponenten in der flüssigen Phase mithilfe der Flüssigkeiten-QCM zu quantifizieren. Das zweite Kapitel untersuchte daher erstmals eine Methode, ein hypervernetztes Divinylbenzol (engl. divinylbenzene, DVB)-basiertes Copolymer unter Verwendung von Ethylenglykoldimethacrylat (engl. ethylene glycol dimethacrylate, EGDMA) als hydrophilem Modifikator auf einem QCM-Sensor zu synthetisieren, die Sensorbeschichtung zu charakterisieren und die Wechselwirkung der Beschichtung mit Huminsäuren zu quantifizieren. Die Studie demonstriert das erfolgreiche Synthetisieren eines DVB-EGDMA-Copolymers auf den QCM-Sensor mittels radikalischer Polymerisation. Die Polymerschicht war lateral heterogen mit einer Dicke von 200-300 nm, womit sie innerhalb des dynamischen Bereichs von QCM-Messungen liegt. Auch wenn Huminsäuren während der Sorptionsexperimente an das Copolymer sorbierten, was im Vergleich zu anderen Studien zu einer starken Frequenzabnahme von 18–20 Hz führte, ist diese Zahl für Online-Quantifizierung von Matrix Substanzen immer noch zu niedrig. Zukünftige Forschung kann auf dem in dieser Studie präsentierten Synthese- und Charakterisierungsverfahren aufbauen, um andere Copolymere zu synthetisieren, weiter zu optimieren und zu erforschen.

Das dritte Kapitel untersuchte die Machbarkeit der Kopplung einer kommerziellen HPLC mit einem mikrofluidischen Sprühtrockner und einer QCM unter Verwendung eines Flusssplitters zur Online-Überwachung organischer Matrixkomponenten während RP-HPLC-Gradientenaufreinigung. Zu diesem Zweck wurde eine Mess-, Kalibrierungs- und Datenverarbeitungsstrategie entwickelt und das System hinsichtlich unterer und oberer Quantifizierungsgrenzen und Genauigkeit charakterisiert. Die Validierung von NOM in einer Umweltprobe gegen eine Offline-Analyse des gesamten organischen Kohlenstoffs bestätigte die Machbarkeit des Ansatzes mit einer absoluten Rückgewinnung von 103 \pm 10%. Eine Korrelation (R² \geq 95) zwischen der Matrixmenge, die durch Trockenmassen-QCM während einer HPLC-Reinigung eines Braunreisextrakts quantifiziert wurde, und Matrixeffekten, die während der anschließenden GC-MS-Analyse von Pestiziden im Extrakt gemessen wurden, wurde identifiziert. Dies deutet darauf hin, dass Trockenmassen-QCM ein wertvolles Werkzeug für den Analytiker sein kann überall wo eine HPLC-Aufreinigung routinemäßig durchgeführt wird, und daher vielen analytischen Bereichen zugutekommen kann.

Das vierte Kapitel untersuchte die Limitierungen und Möglichkeiten der HPLC-Aufreinigung mit Hilfe von C₁₈- und C₈-Phasen für Einzel- und Mehrfachanalytprobleme mithilfe Trockenmassen-QCM. Darüber hinaus wurde der Nutzen einer solchen optimierten HPLC-Aufreinigung für die Isotopenanalyse polarer Mikroschadstoffe untersucht, die typischerweise in Umweltproben vorkommen. Für Proben mit einem NOM-zu-Analyt-Verhältnis von ≥ 10 wurden starke Isotopenverschiebungen von bis zu 3.3 ‰ in Richtung der Isotopensignatur von NOM beobachtet. Dank QCM war eine Optimierung der Matrixentfernung auf bis zu 97% für früh und 99,8% für spät eluierende Verbindungen möglich. Die Effizienz der HPLC-Aufreinigung verschlechterte sich, wenn zwei oder drei Verbindungen gleichzeitig aufgereinigt werden sollten, was zu einer um bis zu 2,5% geringeren Entfernung von NOM führte. Unsere Ergebnisse legen nahe, dass eine optimierte HPLC-Aufreinigung durch systematisches Screening von 3 bis 5 verschiedenen Gradienten erreicht werden kann, wodurch die Grenzen einer genauen Kohlenstoff-CSIA um bis zu zwei Größenordnungen hin zu niedrigeren Mikroschadstoffkonzentrationen verschoben werden kann.

Insgesamt unterstreichen die Ergebnisse dieser Arbeit die Bedeutung (i) geeigneter Nachweistechniken für die spezifischen Anforderungen analytischer Aufgaben und (ii) optimierter, hochselektiver und automatisierter Aufreinigungstechniken für die Probenaufreinigung, um das volle Potenzial von CSIA auszuschöpfen. Insbesondere erwies sich Trockenmassen-QCM als erfolgreich bei der Online-Quantifizierung der gesamten extrahierten Probenmatrix während der RP-HPLC-Aufreinigung und erhöhte so enorm den Prozentsatz an NOM, der in einem Reinigungsschritt entfernt werden kann. Trockenmassen-QCM ebnet den Weg zur effizienten Entwicklung optimierter Aufreinigungsstrategien für verschiedene Aufreinigungsprobleme unter Verwendung einer Vielzahl von Festphasenmaterialien und -modi für die Flüssigchromatographie. Die Verwendung einer optimierten wird in Zukunft dazu beitragen, das Anwendungsspektrum von CSIA auf Verbindungen zu erweitern, die in realen Proben im niedrigen bis mittleren ng/L-Bereich vorhanden sind, und so Einblicke in Umwelt- und biologische Prozesse und forensische Fälle zu ermöglichen, die noch nicht zugänglich waren. Darüber hinaus ist die Möglichkeit der Online-Quantifizierung sowohl des Zielanalyts als auch der Probenmatrix während RP-HPLC ein großer Schritt hin zu einer vollautomatischen Methodenentwicklung und -optimierung zur Vorbereitung von CSIA.

List of Publications

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- Christopher Wabnitz, Wei Chen, Martin Elsner, and Rani Bakkour. Quartz Crystal Microbalance as Holistic Detector for Quantifying Complex Organic Matrices During Liquid Chromatography: 2. Compound Specific Isotope Analysis. *Analytical Chemistry* 2024, *96*, 7436–7443.
- Rani Bakkour and Christopher Wabnitz, and David Glöckler. Lack of selectivity in sample preparation

 An achilles heel of compound-specific isotope analysis for environmental micropollutants. *Trends in Analytical Chemistry* 2024, 180, 117908.

Co-author contributions beyond the scope of this doctoral thesis:

- David Glöckler, Christopher Wabnitz, Martin Elsner, Rani Bakkour. Avoiding Interferences in Advance: Cyclodextrin Polymers to Enhance Selectivity in Extraction of Organic Micropollutants for Carbon Isotope Analysis. *Analytical Chemistry* 2023, 95 (20), 7839-7848. DOI: 10.1021/acs.analchem.2c05465
- Gabriel Sigmund, Stephanie Castan, Christopher Wabnitz, Rani Bakkour, Thorsten Hüffer, Thilo Hofmann and Martin Elsner. NO₂ and natural organic matter affect both soot aggregation behavior and sorption of S-metolachlor. *Environmental science*. Processes & impacts 2019, 21, 1729-1735. DOI: 10.1039/c9em00354

Student Research Supervised During This Work

The following student reports contain data contributing to the research presented in this dissertation. I have supervised all internships and theses.

Research internships:

- 1. David Kostadinov (2020), Towards the Synthesis of Molecularly Imprinted Polymers with a Grafting Approach for Sample Preparation in Automated Solid Phase Extraction.
- 2. Wei Chen (2021), Improvement of Molecularly Imprinted Polymer Solid Phase Extraction for Environmental Organic Pollutants by Derivatizing Natural Organic Matter.
- Malte Kubisz (2022), Matrix Effect of Pesticides on Gas Chromatography Mass Spectrometry caused by Natural Rice and Natural Organic Matter Matrices.
- Carmen Pedri (2022), Possibilities and Limitations of GC and HPLC Sample Purification for GC/C/IRMS Measurements.

Master's thesis:

- Aoife Canavan (2021), Quartz Crystal Microbalance as a Tool for Online Monitoring of Natural Organic Matter during Clean-Up of Organic Extracts.
- Wei Chen (2022), The Application of Online Matrix Monitoring during HPLC Purification Using Dry Mass Sensing on a Quartz Crystal Microbalance.

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1 General Introduction

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1.1 Compound-Specific Isotope Analysis

Numerous research fields, from forensic to environmental sciences, benefit from information about the variation of stable isotope abundances (e.g. by measuring δ^{13} C as the ratio of 13 C and 12 C) in (bio)chemical substances.^{1–10} These isotopic variations can have different origins: (i) Different processes or raw materials in the synthesis of the compounds or (ii) transformation processes that act on these chemicals, including chemical reactions, biological processes, or phase transfer. (i) In case of a different synthesis, the relative abundance of isotopes can provide information like a fingerprint that can distinguish a different provenance of otherwise identical chemicals.^{11–15} (ii) In contrast, isotope ratios change during transformation processes. These changes over time are like a footprint left by reaction-specific kinetic isotope effects that give insight into the path by which the compounds are transformed.^{16–20} Measuring the isotopic signature of a compound with high precision requires Isotope Ratio Mass Spectrometry (IRMS).^{21–24} The ability to distinguish different sources of the same compound makes IRMS unique; the information gained is challenging to acquire from concentration measurements or other techniques.

To achieve high trueness with IRMS, isotopic values must be measured relative to a reference standard. Further, it is necessary to combust the compound of interest into a universal analyte, in the case of carbon measurements to CO_2 .^{6,21–23} The downside is, however, that the structural information gets lost during this process, and thus, only bulk measurements are possible. Coupling gas chromatography (GC) with IRMS revolutionized the field in the late 70s/ early 80s by providing the separation power to move from bulk isotope analysis to compound-specific isotope analysis (CSIA).^{21–23} Later, other chromatographic techniques were hyphenated with IRMS, such as liquid chromatography (LC) in 1991.²⁵ The ability to separate compounds and measure compound-specific isotope ratios opened various applications with different timescales that would not have been accessible otherwise. Paleo-/ geochemists use CSIA to reconstruct paleoclimate profiles by measuring variations in δ^{13} C of biomarkers, like plant waxes preserved in fossils.^{8,26,27} In doping analysis, GC-IRMS is used as a confirmation procedure to prove exogenous administration of endogenous anabolic androgenic steroids by utilizing depleted δ^{13} C values in synthesized steroids.^{28,29} In environmental sciences, CSIA helps to identify the source and the fate of micropollutants, their degradation products, and pathways by measuring isotope fractionation.^{3,30–33} In food analysis, CSIA can be used for authentication purposes.^{9,34–36}

1.2 Analytical Challenges of Real-World Applications of CSIA

Despite these enormous advances, the separation power provided by GC is insufficient for many real-world applications to separate the target analyte and other components present in the sample, known as the sample matrix. An incomplete separation can lead, however, to biased isotope values since (i) the IRMS is not able to distinguish between CO_2 from the analyte and from the sample matrix with the same retention time and

(ii) since the isotope ratio varies over the chromatographic peak due to vapor pressure isotope effects.^{2,21,37–41} Consequently, correction techniques used in conventional mass spectrometry to account for adverse effects of matrix compounds using, for example, curve fitting to restore overlapped peaks,⁴¹ internal standards,^{42–45} analyte protectants,^{46,47} or matrix-matched calibration,^{42,45,48} can not be used in CSIA. To guarantee accurate CSIA, there is thus no substitute for complete baseline separation during GC. Bakkour et al.⁴⁹ and Glöckler et al.⁵⁰ observed for a typical water sample containing environmental micropollutants isotopic shifts in carbon CSIA due to incomplete baseline separation during GC. These isotope shifts occurred as soon as there was ten times more carbon from matrix substances than from the target analyte in the sample extract that was injected into GC-IRMS. Consequently, samples containing higher amounts of matrix often necessitate further purification measures.

On the one hand, such measures can involve increasing chromatographic resolution using longer columns⁵¹ or hyphenated multi-dimensional chromatography instead of one-dimensional chromatography.^{34,52–55} On the other hand, suitable sample preparation is often crucial to get rid of matrix components before injecting the sample into the GC-IRMS.^{2,3,5,50,56} In contrast to its importance, however, sample preparation in CSIA is pursued on a case-by-case basis rather than systematically and is still underdeveloped. Consequently, the applicability of CSIA is limited by matrix interferences in real-world samples and the lack of suitable sample preparation strategies to remove them.

1.2.1 Case Study 1: Limited Field-Applicability of CSIA for Non-Volatile Compounds

In few applications, limitations by matrix interferences are as prominent as in extracts from soil and water samples. Here, CSIA in environmental contaminant chemistry, therefore, serves to show how these limitations affect the real-world applicability of CSIA and which analytical challenges need to be overcome. For this purpose, more than 600 publications from isotope analysis in environmental chemistry (see Table A.1) have been evaluated by grouping them into classes of compounds and plotting them according to their air-water partitioning, using Henry's law constant, and octanol-water partitioning as a proxy for their distribution in different environmental compartments (see Figure 1.1). The publications in every group are classified as work on new methods to measure a given compound with isotope analysis (method, grey circles), as a study on the lab scale (lab, green circles), or as a field study using real-world samples (field, black circles).

It becomes apparent from Figure 1 that most of the work on CSIA in environmental contaminant chemistry was published on volatile organic compounds present in the air-water or air-water-soil compartment such as BTEX (e.g., benzene) or volatile chlorinated aliphatics (e.g., trichloroethene). There is, however, not just a difference in the total number of papers published on volatile compounds (i.e., volatile chlorinated aliphatics: 266) and non-volatile compounds present in the water or soil compartment (i.e., pesticides: 57), but also a difference in the ratio of studies on method development (grey) and laboratory studies (green) in comparison



Figure 1.1 Number of published papers of different compound classes in the environmental sciences subdivided into publications on method development (grey), laboratory studies (green), and field studies (black). The size of each bubble correlates to the amount of papers published. Compound classes with fewer than 15 publications are enlarged by factor 6 for better visibility (bubbles in frames). BTEX: aromatic hydrocarbons benzene, toluene, ethylbenzene, and xylene, PCB: polychlorinated biphenyl, PCDD: polychlorinated dibenzodioxins, PAH: polycyclic aromatic hydrocarbon, HCH: hexachlorocyclohexane. Source: Kuntze et al.⁵⁷ and Web of Science. Publications were considered till 04.10.2023. All publications together with their classification are listed in Table A.1.

to field studies (black). While there is nearly an equal number of publications on method development and laboratory studies in comparison to field studies available for volatile compounds (ratio (lab+method)/field: fuel oxygenates: 1.7, volatile chlorinated aliphatics: 1.7, BTEX: 1.2), field studies are scarce for non-volatile compounds (ratio: pesticides: 6.1, pharmaceuticals: 4.5). There are two main reasons for this predominance of field studies on volatile compounds: (i) The contaminant concentration in the field relative to the matrix concentration and (ii) available sample preparation strategies to separate the contaminant from the sample matrix.

(i) Many of these volatile compounds were ubiquitously used as solvents in the past and, therefore, correspond to priority pollutants at contaminated sites, where they occur at concentrations ranging from mg/L to even g/L.^{58–61} The sample matrix, namely natural organic matter (NOM), is present in environmental water samples in the low mg/L range and thus in lower or equal concentrations than the volatile contaminants. In contrast, pesticides and pharmaceuticals usually occur at a ng/L to µg/L range and thus at 10³ to 10⁶ lower concentrations than NOM.⁶² (ii) Separating volatile compounds from other matrix components is straightforward using the Purge and Trap (P&T) technique. In P&T, volatile compounds are purged from the sample by a gas stream and then concentrated in a trap, while matrix interferences are left behind.^{2,63,64} To measure non-volatile compounds using GC-IRMS, they are extracted from the environmental sample using, for example, solidphase extraction (SPE).^{50,65,66} Their low natural abundance, in combination with the method detection limits (MQL) of carbon CSIA on GC-IRMS (≥ 0.8 nmol C on column), make the extraction of several liters of water necessary.^{2,37,62,67,68} High amounts of NOM are potentially co-extracted and must be removed using further purification steps.^{50,69}

1.2.2 Case Study 2: Tediousness of Sample Preparation for Non-Volatile Compounds

In the recent two decades, sample preparation strategies were developed to purify extracts containing high amounts of matrix in several fields of CSIA. Various purification techniques are utilized in these strategies, ranging from liquid-liquid extraction (LLE)^{26, 28, 70, 71} to several types of chromatography, including size-exclusion,⁷² silica gel,^{73,74} ion-exchange chromatography,⁷⁰ or the most commonly used reversed-phase (RP) high-performance liquid chromatography (HPLC).^{28,66,68,75-79} Frequently, the high amount of matrix co-extracted during the sample extraction (see Figure 1.2, light blue) in combination with the heterogeneity of the sample matrix — NOM consists, for example, of thousands of different organic compounds⁸⁰ — renders the separation of the target analyte and matrix interferences challenging using only one purification step (see purification steps in brown colors in Figure 1.2). In doping analysis, eight steps, including two HPLC clean-up steps, are used to extract steroids from urine, to purify the extract, derivatize the steroids, and accurately measure them using GC-IRMS.²⁸ The required time to process one sample for the final isotope measurement using this eight-step procedure can be up to two days, which shows how time- and labor-intensive the sample preparation



Figure 1.2 Comparison of the number and the type of sample preparation steps used in established sample preparation techniques in the environmental sciences (pesticides, 1H-benzotriazole, chlorinated solvents), food science (amino acids), geosciences (*n*-alkanes), and doping analysis (steroids). Sampling steps are not included. The concentration of the target analyte in the sample is reported on the right side of the diagram. Abbreviations: SPE: solid phase extraction, LLE: liquid-liquid extraction, IAC: immunoaffinity chromatography, Derivat.: Derivatization reaction, HPLC: preparative HPLC, MISPE: molecularly imprinted solid phase extraction, IEC: ion-exchange chromatography, ult. extr.: ultrasonic extraction, urea reac.: urea reaction, ASE: accelerated solvent extraction, saponif.: saponification, LC: liquid chromatography, Ag pip.: Ag⁺ impregnated silica pipette, LC past.: LC on a pasteur pipette, Soxhlet: Soxhlet extraction, Headspace: headspace extraction, P&T-GC-IRMS: Purge and Trap coupled to GC-IRMS.

of non-volatile compounds for CSIA can be.^{28,81} On the contrary, the sample purification of volatile compounds using P&T hyphenated to GC-IRMS is a fast, wholly automated one-step process (see Figure 1.2, chlorinated solvents (water)).^{2,60,63,64} Furthermore, it is not only the sample preparation that is time-consuming but also the development of a tailor-made multi-step solution as used in doping analysis.

To reduce the time of both sample preparation and method development and enable field measurements of non-volatile compounds present in the sample matrix in low concentrations, optimized, highly selective purification steps are warranted to reduce the overall number of purification steps. In recent years, efforts have been put into optimizing the selectivity of each sample preparation step. For instance, Glöckler et al.⁵⁰ optimized the initial extraction of aquatic micropollutants. Using cyclodextrin polymers as selective SPE sorbent instead of commercially available sorbents (i.e., Oasis HLB), it was possible to reduce the amount of co-extracted NOM by a factor of 7.5, which reduced GC-IRMS backgrounds significantly.^{50,82,83} Other works investigated new selective materials to enhance the selectivity of purification steps of the sample extract, using, for example, molecularly imprinted polymers (MIPs)^{49,56} or immunoaffinity sorbents.⁸¹ Using these optimized procedures, it was possible to extend the applicability of CSIA to micropollutants in the environment present in the high ng/L to low µg/L range. To enable CSIA of real-world samples for compounds present at even lower concentrations (low to mid ng/L range) or present in samples containing higher amounts of the matrix (i.e., wastewater, food, biological samples), additional optimization approaches of sample purification for CSIA are outlined in the following chapters.

1.3 Strategies to Optimize Matrix Removal During CSIA Sample Preparation

1.3.1 Influence of Charge on Non-Specific Sorption of Matrix During MISPE

One strategy to optimize the selectivity of CSIA sample preparation and thus reduce the number of steps needed to purify the sample for accurate isotope measurements is to use a highly selective sorbent like MIPs. MIPs possess specific recognition sites that can extract target molecules in a very selective way.^{84–90} These recognition sites are tailored to the analyte of choice during the synthesis, where a three-dimensional polymer network is created around them or a similar molecule. In this way, a cavity that has complementary shape, size, and chemical binding sites to the analyte is produced.^{88–92} While MIPs are frequently used in, for example, chromatographic separation,^{93–95} as (bio)sensors,^{96–98} or in drug delivery,^{99–101} only recently they have been utilized in CSIA sample preparation for the first time.^{49,56} Bakkour et al.^{49,56} developed successful sample preparation strategies for CSIA for three classes of compounds involving MIPs, namely benzotriazoles, triazines, and glyphosate, demonstrated their purification power with significantly reduced backgrounds in GC-IRMS chromatograms and matrix to analyte ratios before and after the purification, and outlined strategies to

assess and circumvent challenges of MIPs for CSIA regarding potential isotope fractionation or the inherent low capacity of MIPs.

Even though MIPs are a powerful purification tool, they potentially co-extract matrix components due to non-specific binding of matrix components on the MIP polymer.^{102,103} Assessing and reducing this non-specific binding is crucial to maximize matrix removal during MIP purification steps for CSIA. While there is much literature available on reducing non-specific binding by optimizing the MIP synthesis, including functional monomers, reaction conditions, and treatments to block the accessibility of functional groups on the MIP surface or optimizing molecularly imprinted solid phase extraction (MISPE) procedures, to date the underlaying processes that govern the non-specific sorption of the matrix are not studied systematically but rather on a case by case basis.^{90,91,104–107} Despite its importance for the sorption of matrices,^{80,108,109} little is known, for example, about the role of charge on non-specific binding of the sample matrix during molecularly imprinted solid phase extraction (MISPE). However, improving our understanding of these underlying mechanisms has the potential to help reduce non-specific binding in the future and thus significantly increase matrix removal during MISPE before CSIA.

1.3.2 Improving Chromatographic Purification by Monitoring both the Target and the Matrix

While MIPs are a promising novel strategy to remove matrix components selectively during CSIA sample preparation, the most often used strategy for this purpose is RP HPLC.^{28,66,68,75–79} RP HPLC is a versatile and powerful purification technique suitable for a wide range of analytes.^{110–113} While the RP HPLC purification is fully automated, the method development of the purification of analytes present in organic extracts is often tedious and challenging. This is the case since there is no straightforward way to monitor and quantify the sample matrix online during RP HPLC. Monitoring both the target analytes and the sample matrix online is, however, necessary to optimize their respective separation during the HPLC purification optimally and efficiently and to thus use the full potential of the purification power of RP HPLC for CSIA sample preparation. For the online monitoring of organic target analytes, detectors commonly hyphenated with HPLC, like UV-Visible spectrometry (UV/Vis), fluorescence spectrometry, or MS, can be used. In contrast, these detectors can not be used for the online quantification of the sample matrix. UV/Vis, fluorescence, or MS can only measure certain fractions of the matrix that are either chromophoric, fluorescent, or ionizable.^{114,115} Other detectors that are considered to be semi-universal, like (i) the total organic carbon (TOC) analyzer, (ii) the charged aerosol detector (CAD), or (iii) the evaporative light-scattering detector (ELSD), have other shortcomings: (i) The TOC analyzer can only measure the carbon content of compounds that are soluble in water.^{114,115} (ii) + (iii) The ELSD and the CAD detector can measure all non-volatile compounds but show inter-compound response differences (ELSD: deviations higher than 50%, CAD: up to 11%), thus prohibiting the quantification of the sample matrix during RP HPLC.^{116–118} There is thus a need for a novel detection technique that can be coupled to RP HPLC and can quantify the entirety of the sample matrix online during chromatographic purification in a robust way. Such a detector would enable the optimization of the separation of the target analyte and the sample matrix during the HPLC purification and, thus, improve the selectivity of the respective purification step.

1.3.3 Strategies for Quantifying Complex Organic Matrices During Liquid Chromatography using Quartz Crystal Microbalance

Quartz Crystal Microbalance: Theoretical Background

The most straightforward way to measure the mass of the matrix online during a chromatographic run is by using a detector that can measure mass directly and does not rely on other principles such as absorption or ionization, which can vary from compound to compound. Since the mass measurement should be at the same time as sensitive as possible, the quartz crystal microbalance (QCM) holds potential as a promising detector with its sub-nanogram resolution.^{119,120} The QCM is a resonator consisting of a quartz crystal, which can be excited electrically to resonate acoustically due to its piezoelectric nature.^{119,120} For QCM measurements, AT-cut crystals that vibrate in the thickness-shear mode are used.^{119,120} When the acoustic wave produced by the excited crystal is in resonance, the deformation is a standing wave with the crystal surface at the antinodes.^{119,120} This standing wave can be described using Eq. 1.1.

$$f_{\rm r} = \frac{c_{\rm q}}{\lambda} = \frac{c_{\rm q}}{2d} \tag{1.1}$$

Here, f_r is the resonance frequency of the vibrating crystal, c_q is the speed of sound in quartz, and λ the wavelength of the sound.¹²⁰ Since λ is two times the crystal thickness d, f_n is inversely proportional to the crystal thickness. If mass is deposited on the sensor crystal in the form of a rigid film — a very thin film where the acoustic wave propagates through without energy loss —, the acoustic thickness increases and can now be described by Eq. 1.2, where d_q is the original thickness of the quartz crystal and d_f the film thickness.¹²⁰

$$f_{\rm r} = \frac{c_{\rm q}}{2d} = \frac{c_{\rm q}}{2(d_{\rm q} + d_{\rm f})} \tag{1.2}$$

From this equation, one can derive the Sauerbrey equation (see Eq. 1.3, see Johannsmann et al.¹²⁰ for the exact mathematical steps), which can be used to calculate the deposited mass on the sensor crystal.¹²¹

$$\Delta m = -\frac{A\sqrt{\rho_{\rm q}\mu_{\rm q}}}{2f_0^2}\frac{\Delta f}{n} \tag{1.3}$$

Here, the mass change Δm is calculated using the active area of the sensor crystal (A), the density (ρ_q), the fundamental frequency (f₀, e.g., 5 MHz) and the shear modulus (μ_q) of the quartz crystal, Δf , which is the

resonance frequency change, and the overtone order (odd) of the standing wave n. All constants (ρ_q , f_0 , μ_q) can be summarized using the mass sensitivity coefficient C (see Eq. 1.4), which is 17.7 ng/(cm²Hz) for 5 MHz quartz crystals and 4.42 ng/(cm²Hz) for 10 MHz quartz crystals.¹²⁰

$$\frac{\Delta m}{A} = -C\frac{\Delta f}{n} \tag{1.4}$$

Since shear waves decay rapidly in gas and liquid media and since, for the Sauerbrey equation, the deposited mass layer must be rigid, and the deposited mass small in comparison to the mass of the sensor, next to the frequency, the overall energy loss is usually measured.^{119,120} Information about the energy loss can be gained from measuring the dissipation (D), which is the sum of all energy losses, or the bandwidth of the resonance (Γ), which is proportional to the dissipation (see Eq. 1.5).¹²⁰

$$\Delta\Gamma = \frac{f_0}{2}\Delta D \tag{1.5}$$

The Sauerbrey equation can only be used to measure mass changes if the shift in the bandwidth is much smaller than the frequency change (see Eq. 1.6).^{119,120}

$$|\Delta\Gamma| << |\Delta f| \tag{1.6}$$

If Eq. 1.6 is not valid, viscoelastic modelling can be used, which necessitates the measurement of several overtones.^{119,120,122}

Quartz Crystal Microbalance: Different Interfaces for Different Measurements

Depending on the exact interface used, different parameters for the energy loss are measured, and information is gained to interpret the QCM measurement. There are three different ways to perform QCM measurements to get a resonance frequency and an output parameter for the energy loss, namely using (i) an oscillator circuit, (ii) impedance analysis, or (iii) the ring-down method. In this thesis, a QCM with resistance measurement (QCM-R) based on (i) and a QCM with dissipation monitoring (QCM-D) based on (iii) are used. One requirement for all measurement approaches is that the quartz crystal is coated with electrodes made frequently of gold. (i) A simplified model (Butterworth-van Dyke electrical model) of the oscillator circuit can be seen in Figure 1.3a, where R_m is a resistor, C_m a capacitor, L_m an inductor, C₀ the parasitic capacitance, AMP an amplifier, and R_L a load resistor. For a more detailed illustration of the oscillator circuit, see Arnau et al.¹²³ For sensing applications, a frequency counter must be added to the oscillator circuit. While this technique is the cheapest of the three, it has several disadvantages: The bandwidth can only be measured indirectly using the motional resistance, which prevents an absolute quantification of energy losses and allows only the acquisition of relative data. Further, it is not well suited for liquid sensing since only one harmonic is measured, and thus, data interpretation is severely



Figure 1.3 (a) QCM-R: Simplified oscillator circuit model, where R_m is a resistor, C_m a capacitor, L_m an inductor, C_0 the parasitic capacitance, AMP an amplifier, and R_L a load resistor. In this thesis, a QCM-R is used for dry-mass sensing. (b) QCM-I: Frequency and bandwidth are determined using the resonator's electrical impedance, which is acquired by measuring different frequencies near resonance. (c) QCM-D: Ring-down method, where the frequency and the dissipation are determined by intermittently switching the driving voltage on and off using the decay of the oscillation and the generated voltage during the decay. In this thesis, a QCM-D is used for liquid sensing. The scheme is adapted from Ref.^{119,120}

limited. In contrast, due to its superior measurement stability, the oscillating circuit approach is the method of choice for gravimetric sensing in air on one overtone.^{120,124} (ii) In the impedance analysis, the frequency and the bandwidth are determined using the resonator's electrical impedance, which is acquired by measuring different frequencies near resonance (see Figure 1.3b).¹²³ Impedance analysis is especially suited for complex experimental setups since measurement interferences can be identified using the impedance curve.¹²⁰ (iii) In the ring-down method, the frequency and the bandwidth are determined by intermittently switching the driving voltage on and off. The oscillation of the quartz crystal decays while the driving voltage is off (see Figure 1.3c), and another voltage is generated due to the piezoelectric nature of the quartz crystal, which can be measured and transferred into the frequency and the dissipation, which is equivalent to the bandwidth.^{119,125} In this way, several overtones can be measured quickly, enabling viscoelastic modeling and thus the measurement and interpretation of complex samples in vacuum, air and liquid media.^{120,125}

Using these different measurement techniques, the QCM has been used in the last decades for various applications, including the sensing of small molecules, proteins, bacteria, or lipids in both gas and liquid phases, the investigation of the formation or deposition of membranes, polymer films, and other composites like MOFs, and the behavior of films under different conditions.^{122,126–130} Two different strategies could enable the QCM to monitor matrix compounds online during the RP HPLC purification of an organic extract prior to GC-IRMS. Firstly, a part of the HPLC eluate could be passed over the QCM sensor coated with a polymer, on which the matrix can sorb to. Secondly, a rigid film could be produced by spraying a part of the HPLC eluate onto the QCM sensor and immediately evaporating the solvents using a gas stream to enable dry-mass sensing in the gas phase. Both strategies could enable the quantification of matrix substances in the HPLC eluate at each time point of the measurement. They, including potential challenges, research gaps, and ways to overcome them, are discussed in detail in the following sections of this chapter.

Strategy 1: Liquid Sensing Using a Polymer Coated QCM Sensor

The first strategy is based on QCM liquid sensing, which is one of the most frequently used techniques to study interactions between compounds in a liquid phase and materials coated on the QCM sensor.^{122,126–130} Here, the QCM crystal is fully immersed in a liquid media, which is passed over it. The sorption of different types of analytes onto the QCM crystal, or most of the time onto a crystal coating, can be measured using the frequency change during the sorption process. Thus, the concentration of analyte in a solution can be determined. Different QCM sensor coatings are produced and studied for each analyte to observe the interactions during the sorption procedure. For NOM, a variety of model coatings were already investigated, including silica,¹³¹ polystyrene,¹³¹ aluminum oxide,^{131–135} iron oxide,¹³¹ hydroxyapatite,¹³¹ poly(vinylidene) fluoride,¹³⁶ positively charged polyelectrolyte layer,^{137–142} and self-assembled monolayers.^{143,144} Even if many insights were gained using these model sorbents regarding the sorption behavior of NOM, they can not be used

for the quantification of the entirety of NOM during liquid chromatography, since (i) only certain fractions of NOM sorb onto these coatings (i.e., charged fractions)^{131–135} and since (ii) the capacity of the different coatings is minimal.^{131,134,136,143} To use liquid sensing for real-time quantification of matrices like NOM during an HPLC purification of a formerly extracted sample, a new sensor coating that can extract all NOM compounds present in the sample extract and has a higher capacity than available coatings must be developed. For this purpose, it is ideal to coat the sorbent used during the original extraction of the water sample on the QCM crystal. For the extraction of environmental water samples, frequently polystyrene-divinylbenzene (PS-DVB)-based polymers modified with a hydrophilic monomer are used.^{69,145–148} Since these types of polymers are often hyper crosslinked and possess, therefore, a high capacity,¹⁴⁹ it seems ideal to coat a QCM sensor with a PS-DVB-based polymer modified with a hydrophilic monomer. Such a coated sensor could be used to quantify NOM in the liquid phase.

Strategy 2: QCM Dry Mass Sensing

The second strategy is based on QCM dry mass sensing, where the analyte-containing solution is sprayed onto the QCM sensor. During this process, the solvent evaporates, and the non-volatile matrix substances remain on the sensor. Their dry weight can be determined using the frequency change measured with the QCM.^{150–153} While liquid sensing used in strategy 1 is frequently used in the field of QCM for many different studies, QCM dry mass sensing was introduced by Schulz and King in the 70s¹⁵⁰ but, however, only recently developed further and applied. In the last decade, microfluidic sprays were optimized to make dry mass sensing possible by Müller et al.¹⁵¹ and Kartanas et al..¹⁵² This development, together with technical advancement on the QCM,¹²⁰ made the first application of dry mass sensing possible. Kartanas et al.¹⁵³ coupled a QCM with the help of a microfluidic spray-dryer with aquatic size-exclusion LC for the separation and detection of proteins. While this system seems to be ideal for online monitoring of matrix compounds during HPLC purification prior to CSIA, several development steps need to be taken, and challenges need to be overcome: First, till now, QCM dry mass sensing has been used only for aquatic LC. For the purification of micropollutants for CSIA, RP gradient HPLC is necessary. Therefore, investigations must be conducted on how organic solvent gradients affect the spraying and measuring process. Secondly, while the system could successfully quantify proteins, it was never used for a mixture as complex as an environmental extract. Hence, the suitability of this measurement approach for such samples needs to be fully validated. Thirdly, a strategy for calibrating, processing, and evaluating the data needs to be developed.

1.4 Objectives and Approach

The overall goal of this work was to develop novel strategies to optimize the selectivity of sample purification for CSIA. This thesis specifically focused on MISPE, a promising purification strategy only recently applied to CSIA, and RP HPLC, the most frequently used purification strategy for CSIA.

Chapter 2, entitled *Influence of the Anionic Character of Natural Organic Matter on Sorption on Molecularly Imprinted Polymers*, investigates the influence of the anionic character of NOM on non-specific sorption of NOM during MISPE. To this end, (i) acidic NOM groups were methylated using trimethylsilyl diazomethane (TMSD), (ii) the change in the charge density of NOM was assessed, and (iii) the different behavior of NOM and methylated NOM determined during MISPE by constructing MIP breakthrough curves.

Chapters 3-5 systematically explore the feasibility of QCM liquid sensing and QCM dry mass sensing for online matrix quantification during RP HPLC, with the ultimate goal of using such a detector to optimize the separation of the target analyte and the sample matrix during the respective purification to improve the selectivity of the RP HPLC purification prior to CSIA. Chapter 3, entitled *Application and Preparation of Hydrophilic-Lipophilic Balance-Type Polymers Grafted on Quartz Crystal Microbalance Sensors*, focuses on developing a procedure to coat a QCM sensor with a hypercrosslinked DVB-based copolymer using ethylene glycol dimethacrylate (EGDMA) as a hydrophilic modifier to enable QCM liquid sensing of NOM. The chemical composition, thickness, and surface coverage of the coating were characterized using Fourier-transform infrared (FTIR), Raman spectroscopy, scanning electron microscopy imaging (SEM), and energy dispersive X-ray mapping (EDX). The interaction of NOM with the novel QCM coating was investigated using flow-based sorption experiments.

Chapters 4 and 5 explore the feasibility of coupling QCM dry mass sensing with RP HPLC for online quantification of organic matrix components during the respective chromatographic gradient purification. To this end, chapter 4, entitled *Quartz Crystal Microbalance as Holistic Detector for Quantifying Complex Organic Matrices During Liquid Chromatography: 1. Coupling, Characterization, and Validation,* lays the technical and fundamental groundwork for the matrix online monitoring using QCM dry mass sensing during RP HPLC. It systematically studies the connection, characterization, calibration, and validation of QCM dry mass sensing with RP HPLC. Moreover, the lower and upper limits of quantification were determined, and the applicability of HPLC purification of pesticides in brown rice for subsequent GC-MS residue analysis was evaluated.

Chapter 5, entitled *Quartz Crystal Microbalance as Holistic Detector for Quantifying Complex Organic Matrices During Liquid Chromatography: 2. Compound Specific Isotope Analysis*, applies QCM dry mass sensing coupled with RP HPLC to CSIA. Here, the limitations and enhancement of HPLC purification using QCM dry mass sensing on C_{18} and C_8 phases for single- and multiple-targets were investigated, and the impact on accurate ${}^{13}C/{}^{12}C$ analysis of polar micropollutants present in environmental water samples explored.

In the concluding chapter 6, the essential discoveries of this study are highlighted to form a comprehensive conclusion. Further, unresolved aspects that beckon further exploration in future research are identified.
2 Influence of the Anionic Character of Natural Organic Matter on Sorption on Molecularly Imprinted Polymers

2.1 Introduction

Organic and inorganic compounds present in real-world samples (i.e., environmental, biological) can prevent the accurate identification and quantification of organic target analytes in trace analysis and have a negative effect on the sensitivity of the detection.^{3, 88, 112, 154, 155} The removal of these organic and inorganic compounds, known as sample matrix, during sample preparation is often considered to be the bottleneck of the analytical process.^{88, 154, 156, 157} To this end, molecularly imprinted polymers (MIPs) are frequently used as tailor-made sorbent materials to selectively extract or purify organic target analytes from the sample matrix. MIPs are customized, synthetically produced materials that show a high recognition of a target analyte due to their antibody mimicking structures.^{84–90} In molecular imprinting, a three-dimensional polymer network is polymerized around a template molecule (i.e., the target analyte) using functional monomers and a cross-linker in the presence of a porogen. After the polymerization, the template is removed, leaving behind a cavity with complementary size, shape, and chemical binding sites to the template molecule, which acts with high selectivity as antibody mimicking recognition site.^{88–92} In non-covalent imprinting, the recognition is driven by molecular interactions like van-der-Waals interactions, pi-pi stacking, ionic interactions, or hydrogen bridges.^{84,90,91} The exact molecular interactions that are determinant for the recognition of a specific MIP impact the whole MIP solid phase extraction (MISPE) procedure: After the sample loading during MISPE, non-specifically bound matrix substances are washed off using a solvent mixture that at the same time cannot disrupt the specific analyte binding.^{84,89,90} Increasing the selectivity of the MIP by, for example, reducing the non-specific binding of matrix compounds on the MIP and increasing their removal during the washing step is one of the current research focuses in the field of molecular imprinting.^{90,91,104–107}

So far, the emphasis on enhancing selectivity by decreasing non-specific binding has been on optimizing the MIP synthesis (i.e., polymerization conditions, the choice of functional monomers, blocking agents) or optimizing MISPE procedure (i.e., washing solvent).^{90,91,104–107} Designing a tailor-made MIP for a specific

target analyte and optimizing its selectivity by screening these different parameters is, however, a time- and labor-intensive procedure.^{89,90,104} Therefore, gaining as much knowledge as possible on the factors governing the sorption of the matrix onto the MIP and desorption processes during the washing step using organic solvents is essential. While there is a lot of information available regarding the optimization of the MIP, the role of the matrix is usually not studied systematically but rather on a case-by-case basis.^{90,91,104–107} Such a systematic study would, however, be beneficial for the understanding of sorption processes of matrices that occur in many different applications, like the environmental matrix natural organic matter (NOM).^{49,56,108,158–160} NOM can be found in natural water or soil, consisting of thousands of different organic compounds with acidic functionalities like humic, fulvic, or hydrophilic acids.^{80,161} The abundance of acids in NOM — especially in the form of carboxylic functional groups — leads to an anionic character due to their dissociation that is responsible for many characteristics of NOM, such as solubility, binding sites, electrostatic attraction/repulsion, and represents a significant factor in its sorption behavior.^{80,108,109,162} Despite its importance for sorption processes, no literature is available on the role of its anionic character on the non-specific sorption on MIPs.

The overall goal of this work is to investigate the influence of the anionic character of NOM — and particularly the role of carboxylic acids — on non-specific sorption of NOM during MISPE. To study this influence, a masking approach using selective methylation of carboxy groups can give unique insights due to the possibility of directly comparing the sorption of NOM and masked NOM with a different charge.^{163,164} To this end, we (i) methylated acidic NOM groups using trimethylsilyl diazomethane (TMSD), (ii) assessed the change in the charge density of NOM, and (iii) determined the different behavior of NOM and methylated NOM during MISPE by constructing breakthrough curves using DCM as washing solvent.

2.2 Experimental

2.2.1 Chemicals and Materials

A list of purchased chemicals, materials, and solvents used in this study is provided in the supporting information section B.1.

2.2.2 Extraction of NOM from River Water

River water samples (Wiesäckerbach, Garching, Germany, latitude 48.269009, longitude 11.667976) were passed through glass microfiber filter membranes (1.2 µm particle retention, 47 mm diameter, Whatman, UK). The filtrate was acidified to pH 3.0 using HCl (32%). NOM was subsequently extracted from the acidified sample under conventional SPE conditions at 5 mL/min using Oasis HLB SPE cartridges (Waters, 500 mg, 12 cc) and an automated SPE system (Smart Prep Extractor, Horizon Technology, USA). The Oasis HLB cartridges were dried overnight under vacuum and eluted using 5 mL of DCM containing 3% methanol. The eluates were

combined, the solvents evaporated, and NOM was reconstituted in methanol. The dissolved NOM was filtrated using a glass microfiber syringe filter (1.2 μ m particle retention, 13 mm diameter, Whatman, UK) and stored at -18 °C.

2.2.3 Molecular Masking of NOM - Methylation Procedure

To methylate NOM carboxy groups, 5 mL methanol were added to 1 mg extracted NOM in a Teflon beaker. 100 μ L of a 2 M TMSD solution in hexane were added to the solution, which was then stirred at room temperature for 1 h. Afterward, TMSD-hexane solution was added in increments of 100 μ L every 30 min until a total volume of 600 μ L was reached. See Figure B.1 for mechanistic details of the methylation reaction. Methanol and hexane were evaporated using a gentle stream of nitrogen at 50 °C, followed by 30 min evaporation at 105 °C to remove potential by-products.

2.2.4 Determination of Methylation Efficiency and Charge Density Change Using Acid-Base Titration

The carboxyl and phenolic content were estimated for the extracted NOM before and after the methylating procedure using acid-base titration according to a procedure used for samples of the International Humic Substances Society.^{165, 166} After organic solvents were removed from (methylated) NOM (3 mgC), 15 mL 0.1 M NaCl solution as background electrolyte was added in a Teflon beaker with 1-2 mL 0.1 M NaOH to reach pH 10. Afterward, the pH was adjusted to 3-3.3 using 0.1 M HCl. The titration was performed at 25 °C, which was maintained using a water bath under a nitrogen gas atmosphere. The titrant (0.1 M NaOH) was added in increments of 15 µL using a Multipipette (E3x, Eppendorf, Germany). The pH (stable for 7s with drift of no more than 0.01 pH units) was recorded after each titrant addition using a pH meter (Lab850, SI Analytics, Germany). The sample was titrated from the initial pH of 3-3.3 to a final pH of 10.5. At each titration point, the ionic strength (I) was calculated using Equation 2.1.

$$I = \frac{1}{2}([Na^+] + [Cl^-] + [OH^-] + [H^+] + \sum_i [Org_i^-])$$
(2.1)

Here, the contribution of ionized functional groups of NOM to the ionic strength, $[Org_i^-]$, was approximated using the assumption that NOM consists of monoprotic acids. $[Org_i^-]$ during the titration can be thus calculated using the electroneutrality Equation 2.2.

$$\sum_{i} [Org_{i}^{-}] = [Na^{+}] - [Cl^{-}] - [OH^{-}] + [H^{+}]$$
(2.2)

I is, therefore, given by Equation 2.3.

$$I = [Na^+] + [H^+]$$
(2.3)

[Na⁺] is the dilution-corrected concentration of the initial NaCl and the added NaOH. [H⁺] was derived from the pH. To this end, the activity for the hydrogen ion (α_{H^+}) was calculated using the Davies Equation¹⁶⁷ with A=0.5, B=0.30 to obtain the activity coefficient for hydrogen ion, γ_H (see Equations 2.4, 2.5, and 2.6).

$$log\gamma_{\rm H^{+}} = -0.5(\frac{\sqrt{I}}{1+\sqrt{I}} + 0.3I)$$
(2.4)

$$pH = -log_{10}\alpha_{\rm H^+} \tag{2.5}$$

$$\alpha_{\mathrm{H}^+} = \gamma_{\mathrm{H}^+}[H^+] \tag{2.6}$$

These calculations were iteratively repeated till [H⁺] change was smaller than 1%. The charge density (Q_{tot} / meq g/C) can then be calculated using the concentration (c_a) and volume (v_a) of strong acid HCl added, the concentration (c_b) and volume (v_b) of strong base NaOH added, the total volume (V_{tot}), and the mass of carbon originating from NOM (m_{NOM}) in the titration cell (see Equation 2.7).

$$Q_{\text{tot}} = \frac{c_b V_b - c_a V_a + ([H^+] - [OH^-]) V_{\text{tot}}}{m_{\text{NOM}}}$$
(2.7)

The carboxyl content can be estimated as the Q_{tot} value at pH 8 and the phenolic value as two times the change of Q_{tot} between pH 8 and pH 10.^{80,166,168}

2.2.5 Impact of Methylation on NOM Retention during MISPE

Cartridges filled with 1 g triazine MIPs (Affinisep) were soaked with methanol from the bottom to guarantee a complete wetting of the MIP surface. The cartridges were sequentially conditioned with two times 5 mL methanol, two times 5 mL methanol/ formic acid (9/1 v/v), and three times 5 mL DCM. To quantify material bleed during MISPE, the cartridges were further washed using three times 5 mL DCM (bleed samples 1-3), one time 10 mL MeOH (bleed sample 4), one time 5 mL methanol/ formic acid (9/1 v/v), 3 times 5 mL DCM, 3 times 5 mL DCM (bleed samples 5-7), one time 10 mL MeOH (bleed sample 8), one time 5 mL methanol/ formic acid (9/1 v/v), and 3 times 5 mL DCM. The 5 mL sample consisting of either (i) 0.5 mgC NOM, (ii) 0.5 mgC NOM that was methylated using the previously described procedure, or (iii) a control, which included no NOM but was subjected to the same reaction conditions used for the NOM methylation, was passed over the MIP (sample 1). The MIP was then washed using 16 times 5 mL DCM (samples 2-17) and one time 10 mL methanol (sample 18). Afterward, the bleed sample eluates and the sample eluates were evaporated to dryness under a gentle stream of N₂ at 30 °C and reconstituted in 16 mL water using an ultrasonic lab homogenizer (UP200St, Hielscher, Germany; 5 min, power = 190 W, puls = 100%, amplitude = 100%). The organic carbon



Figure 2.1 Titration data for NOM (gray) and methylated NOM (blue). The charge density is shown on the y-axis. All carboxyl groups are titrated at pH 8 (black dashed line), and all phenolic groups between pH 8 and 10 (difference between gray and black dashed line).

content was then determined in the reconstituted sample using a TOC analyzer (TOC-L, Shimadzu, Japan) equipped with a combustion catalytic oxidation reactor (680 °C) and a non-dispersive infrared detector.

2.3 Results and Discussion

2.3.1 Methylation Efficiency and Change in Charge Density

We assessed the change in charge density as a result of the methylation of NOM acidic groups and the overall efficiency and selectivity of the methylation of NOM carboxy groups using an acid-base titration. To this end, we assumed that the only two classes of proton-binding sites are phenolic and carboxylic hydroxy groups.^{80, 166, 168} We titrated extracted NOM (gray) and, after the extraction methylated NOM (blue) from an initial pH of 3-3.3 to a final pH of 10.5 using 0.1 M NaOH, measured the pH after each 15 μ L increment, and plotted the pH against the calculated charge density Q_{tot} (see Figure 2.1). All carboxyl groups are titrated at pH 8 (black dashed line), and all phenolic groups between pH 8 and 10 (gray and black dashed line).

We determined a carboxyl content in the extracted NOM (gray) of 12.1 meq/gC and a phenolic content of 4.7 meq/gC. These values are in the range of values found by the international humic substance society for other organic matter samples.^{165,166} We observed a significant shift of the NOM titration curve to lower Q_{tot} values for the methylated NOM curve (blue). While the carboxyl content dropped from 12.1 meq/gC for NOM to 0 meq/gC for methylated NOM, the phenolic content (NOM: 4.7 meq/gC, methylated NOM: 5 meq/gC) stayed constant within our results' uncertainty of 0.4% according to triplicate measurements (see Figure B.2). This shows that the overall lower Q_{tot} values originate exclusively from changes in the carboxyl content. These results prove the



Figure 2.2 Breakthrough curves of NOM (gray) and methylated NOM (blue) on MISPE. After sample loading (green dashed line), the MIP is washed with 80 mL DCM in 5 mL increments, followed by a 10 mL methanol elution step (black dashed line). The percentage of DOC in each breakthrough fraction (bars, left y-axis) and the total breakthrough (dots, right y-axis) are shown.

success of the charge density reduction by methylating all carboxy groups present in the sample. They further confirm the selectivity of the used methylation procedure: Diazomethane methylates only carboxylic and acidic phenolic hydroxy groups; it does not react with weakly acidic phenolic or alcoholic groups.^{163,169–171} The presented methylating procedure can thus significantly change the acidity and charge of NOM in a controlled manner.

2.3.2 Impact of Methylation on NOM Retention during MISPE

After the NOM carboxy groups were successfully methylated and the charge density significantly reduced, we investigated how NOM (gray) and methylated NOM (blue) retention behavior differs during MISPE. MISPE breakthrough curves (see Figure 2.2) were determined by washing the MIP after sample loading (green dashed line) with 80 mL DCM in 5 mL increments followed by a 10 mL methanol elution step (black dashed line); organic carbon present in the breakthrough was quantified using TOC analysis. In the case of the methylated NOM breakthrough curve, the control was used to subtract contaminations present in the sample originating from the methylating procedure (see Figure B.4). A complete mass balance was determined for both breakthrough curves (NOM: $101\pm4\%$, methylated NOM $104\pm4\%$), confirming the suitability of the approach to quantify organic carbon in the breakthrough.

Methylated NOM (blue) shows a stronger retention to the MIP, resulting in 55% methylated NOM remaining after the DCM washing procedure in comparison to only 43% remaining in the case of the untreated NOM (see Figure 2.2 gray square and blue dots before black dashed line). To explain the different sorption behaviors of methylated NOM and NOM, the (i) MIP-NOM interactions and (ii) DCM-NOM interactions play an essential

role. (i) The initial sorption of NOM to the MIP is caused by a variety of intermolecular interactions like hydrogen bridges, van der Waals forces, and ionic interactions.^{49, 56, 80, 108, 109, 158–160, 162, 172} While the MIP has strong hydrogen acceptor and hydrogen donor functions originating from both building blocks methacrylic acid (MAA) and ethylene glycol dimethacrylate (EGDMA) and the possibility to accommodate negative charge with the hydrogen donor function of MAA,^{89, 173–175} for NOM the hydrogen accepting functions in the form of ether and carbonyl groups dominate.^{80, 109, 176, 177} Since the hydrogen accepting function of NOM is not impacted by the methylation, the role of hydrogen bridges for the different behaviour of NOM and methylated NOM should thus be negligible. On the other hand, the more NOM sorbs onto the MIP, the higher the charge density will get on the surface of the MIP and thus the electrostatic repulsion that prevents more NOM to sorb.^{80, 177–180} In contrast, this effect is nearly wholly taken out of the picture by methylating NOM carboxy groups and reducing thus the charge density of NOM by a factor of 3.4, which leads to more methylated NOM sorbing onto the MIP as observed during the breakthrough curves.

(ii) The lower charge density did, however, impact not only the sorption of NOM onto the MIP but also the total desorption and the volume of DCM necessary to wash off all elutable fractions of NOM. During the first 10 mL percolated through the MIP, 1.6 times more NOM breaks through than methylated NOM (compare to Figure 2.2 gray and blue bars). Furthermore, while the elutable fraction of NOM broke through in the first 25 mL, it took nearly double the volume of DCM (45 mL) until the elutable fraction of methylated NOM broke through. This observation can again be explained using the reduced charge density: The higher the charge density, the more readily NOM will desorb and vice versa due to electrostatic repulsion.^{80,177–180} DCM, with its weak hydrogen donor ability, can still interact with NOM's strong hydrogen acceptor functions, but it takes a higher volume to wash off all elutable fractions, and less total methylated NOM can be washed off.¹⁸¹ These results show that methylation of NOM leads to higher non-specific binding of NOM during MISPE due to the change in charge density.

2.4 Conclusion

The current work investigates the influence of NOM's anionic character on NOM's non-specific sorption during MISPE by comparing breakthrough curves of NOM and methylated NOM. We demonstrate that the charge density of NOM can be significantly reduced by a factor of 3.4 by methylating NOM carboxy groups using TMSD. Breakthrough curves revealed that less methylated NOM, compared to untreated NOM, could be washed off the MIP using DCM during a MISPE procedure. This implies stronger MIP-methylated NOM interactions, which are most likely caused by the smaller charge density of the methylated NOM and the consequently smaller electrostatic repulsion between NOM molecules.^{80, 177–180} These results prove the importance of NOM's anionic character for the sorption on MIPs and emphasize the influence of the charge of the sample matrix on non-specific sorption. Manipulating electrostatic repulsion between the MIP and the sample matrix, or compounds

sorbed onto the MIP and the remaining sample matrix, could help in the future to reduce non-specific binding and thus significantly increase matrix removal during MISPE.

3 Application and Preparation of Hydrophilic-Lipophilic Balance-Type Polymers Grafted on Quartz Crystal Microbalance Sensors

3.1 Introduction

Natural organic matter (NOM), which is produced from the decomposition of animal and plant biomass, is a key environmental aquatic component, which represents a very complex mixture of organic compounds like humic acids, fulvic acids, or hydrophilic acids.^{80,161} The adsorption of NOM to surfaces and the sorption of compounds to NOM influence the properties of (i) NOM and the respective (ii) surface or (iii) compound. (i) The adsorption of NOM on surfaces prevents NOM degradation and alters the composition of NOM in solution due to preferential adsorption.^{182–185} (ii) NOM sorption on particle surfaces affects the particle's deposition and coagulation behavior, while the sorption on membranes causes membrane fouling.^{186–190} (iii) Compounds sorbing onto NOM often show altered properties regarding their degradation or transport behavior.^{191–195} Since (i-iii) can have a significant impact on, among others, water quality, water treatment efficiency, or carbon cycling, it is essential to get a comprehensive understanding of NOM sorption processes.^{131,143,185,196,197}

These NOM sorption processes, together with the corresponding adlayer properties and the influence of external factors (i.e., pH, oxidants, ionic strength), are studied using different analytical techniques, including spectroscopic methods, chromatographic methods, batch sorption experiments, titrations, or in situ surface techniques.^{114,144,198–202} Especially the quartz crystal microbalance with dissipation monitoring (QCM-D) as an in situ surface technique led in the recent decade to essential insights into NOM sorption processes.^{131–144} This information can be acquired using the QCM-Ds ability to measure small mass changes on its sensor surface as resonance frequency changes of its oscillating piezoelectric quartz crystal with a sub-nanogram resolution in combination with information on layer viscoelasticity and thickness gained from the dissipation monitoring.^{119,121} For the NOM sorption studies, different model sensor surfaces were used that are either commercially available (i.e., silica, polystyrene, aluminium oxide, iron oxide, hydroxyapatite),^{131–135} can be produced using spin coating (i.e., poly(vinylidene fluoride)),¹³⁶ or can be made in the lab using established procedures (positively charged polyelectrolyte layer, self-assembled monolayers).^{137–144} While it is possible to answer many

important questions regarding NOM sorption behavior using these few sensor coatings, many research questions regarding interactions of NOM and sorbent materials, polymers, or membranes used, for example, during water treatment cannot yet be investigated because of the lack of suitable novel sensor coatings.^{69, 147, 148, 203, 204} Such novel sensor coatings could open up new possibilities to study the interaction of NOM with polymers used as sorbent or membrane materials using the QCM-D.

Thin polymer layers with different compositions, surface properties, and structures can be coated on the QCM using various polymerization techniques.²⁰⁵ Polymer grafting from the QCM substrate is, for example, a controllable, versatile approach that enables the coating of a thin and dense polymer brush layer with high stability.^{205,206} Grafting different polymer chains (i.e., polyvinyl, -acryl, -styrene-based) from the QCM sensor has been achieved in the past using photo, reversible addition-fragmentation chain-transfer (RAFT) or radical polymerization.^{205,207–209} One of the most frequently used polymers as sorbents for environmental applications are polystyrene-divinylbenzene (PS-DVB)-based polymers (commercial products: i.e., Chromabond HR-P, Isolute ENV+, or Lichrolut EN) or (PS-DVB)-based polymers modified with a hydrophilic monomer to get a co-polymer with hydrophilic moieties (commercial products: i.e., Oasis HLB with N-vinylpyrrolidone (NVP) as modifier).^{69,145–148} Establishing a grafting procedure for hypercrosslinked (PS-DVB)-based polar-modified co-polymers would enable the study of interfacial dynamics between NOM and one of the most important sorbent classes and could be used as a model approach for the grafting of other relevant co-polymers on a QCM sensor.

In this work, we report for the first time a grafting approach for a hypercrosslinked DVB-based copolymer using ethylene glycol dimethacrylate (EGDMA) as a hydrophilic modifier on a QCM sensor. (i) We characterized the sensor coating regarding chemical composition using Fourier-transform infrared (FTIR) and Raman spectroscopy. (ii) Further, we assessed the polymer distribution, the thickness, and the chemical composition of the grafted polymer layer using scanning electron microscopy imaging (SEM) and energy dispersive X-ray mapping (EDX). (iii) Lastly, we performed flow-based sorption experiments to evaluate the interaction between humic acids as a proxy for NOM and the polymer coating.

3.2 Experimental

3.2.1 Chemicals and Materials

A list of purchased chemicals and materials and a description of the standard solutions and ultrapure water is provided in the supporting information section C.1.



Figure 3.1 Schematic representation of the modification procedure used to graft a DVB-based copolymer in a two-step process onto a QCM sensor. Step 1: Silanization of the silica coated electrode using γ -MAPS. Step 2: Hypercrosslinking polymerization reaction using DVB, EGDMA, and AIBN as initiator.

3.2.2 Surface Modification of Quartz Crystal Microbalance Sensor

10 MHz QCM sensor crystals (Au coated with SiO₂, Novaetech S.r.l., Italy) were coated with a DVB-based copolymer in a two-step process (see Figure 3.1). The sensor crystals were immersed in the first step, the silanization, in toluene (100 mL) using a tailor-made sensor holder (see Figure C.1). γ -Methacryloxypropyl-trimethoxysilane (γ -MAPS) (5.00 mL, 20.9 mmol) were added, and the solution stirred at 70 °C overnight. Afterward, the sensor crystal was cleaned using acetone (5 mL) and water (5 mL) and then dried at 60 °C. In the second step, the hypercrosslinking of a co-polymer, the silanized crystal in its holder is immersed in toluene (40 mL). DVB (276 mL, 1.94 mmol, 1.0 eq.) and EGDMA (91.3 mL, 0.484 mmol, 0.25 eq.) were added. The polymerization was initiated using 2,2'-Azobis(2-methylpropionitrile) (AIBN) (8.70 mg, 53.0 mmol). The mixture was stirred at 60 °C overnight under an argon atmosphere. The sensor crystal was then again cleaned using acetone (5 mL) and water (5 mL) and water (5 mL) and dried at 60 °C.

3.2.3 Surface Characterization of Quartz Crystal Microbalance Sensor

The chemical composition of the grafted co-polymer was studied using FTIR spectroscopy (FTIR spectrophotometer, Elmer Perkin Frontier, Germany) and Raman spectroscopy (alpha300R Confocal Raman Microscope, WITec GmbH, Germany). The IR spectra were recorded with a resolution of 1 cm⁻¹ in the spectral range of 4000-650 cm⁻¹. The Raman spectra were recorded using 10 mW laser power, an integration time of 1 s, and 50 accumulations. The surface morphology and elemental composition of the coated QCM sensor were investigated using SEM (ZEISS SIGMA VP Field Emission Scanning Electron Microscope, Carl Zeiss Microscopy GmbH, Germany) equipped with an EDX detector (EDS Quantax XFlash 6l60 Detector, Bruker Nano GmbH, Germany).



Figure 3.2 Schematic overview of the setup used for sorption experiments. 1: Water bottle, 2: Peristaltic Pump, 3: Sample injector, 4: QCM

Unit	Exp. 1	Exp. 2
mgC/L	4	5
μL	19	200
	15	6
ngC	77	1000
ngC	1152	6000
μL/min	30	30
	Unit mgC/L µL ngC ngC µL/min	Unit Exp. 1 mgC/L 4 μL 19 15 15 ngC 77 ngC 1152 μL/min 30

Table 3.1 Measurement parameters of sorption experiments 1 and 2.

3.2.4 Preparation of Humic Acid Solutions

A humic acid stock solution was prepared by dissolving 50 mg in water (50 mL). The solution was filtered through glass microfiber filter membranes (1.2 µm particle retention, 47 mm diameter, Whatman, UK) and stored at -4 °C. Organic carbon concentrations were determined using a total organic carbon (TOC) analyzer (TOC-L, Shimadzu, Japan) equipped with a combustion catalytic oxidation reactor (680 °C) and a non-dispersive infrared detector. Humic acid samples were prepared by diluting aliquots of the stock solution.

3.2.5 Sorption Experiments

Figure 3.2 shows a schematic overview of the setup used for sorption experiments. In this setup, degassed water (1) is constantly passed over a QCM (openQCM Q^{-1} , openQCM by Novaetech S.r.l., Italy) (4) using a peristaltic pump (IPC 24, Ismatec, Germany) (2) with a flow rate of 30 µL/min. The instruments were connected using inert tubes (Tygon MHSL 2001, inner diameter: 1.52 mm, wall thickness: 0.85 mm, Ismatec, Germany). Samples were injected using an injection valve (Model 7725i, Rheodyne, USA) (3). The measurement parameters, including injection volume, injected mass of humic acids, and times of injections for experiment 1 and experiment 2, are shown in Table 3.1. The experiments were conducted at room temperature with temperature fluctuations below 1 °C.



Figure 3.3 IR spectrum of a silica QCM sensor (uncoated sensor, black) and a silica QCM sensor coated with a DVB-EGDMA polymer (coated sensor, blue).

3.2.6 Data Evaluation

We defined the resonance frequency shift measured during the sorption experiments as the difference between the average of 250 measured data points before and after the injection of the sample. The resonance frequency shift was corrected using the baseline drift observed before the injection of the sample. The baseline drift was determined using a linear regression of the weighted average of 701 data points within the moving window (adjacent-averaging method). The code used for the data processing is shown in section C.3.

$$\Delta\Gamma = \frac{f_0}{2}\Delta D \tag{3.1}$$

The half-bandwidth at half height of a resonance ($\Delta\Gamma$) is calculated using Eq. 3.1 by dividing the fundamental resonance frequency of the oscillating quartz (f₀ = 10 MHz) by 2 and multiplying it with the measured dissipation change (Δ D).^{119,120}

3.3 Results and Discussion

3.3.1 Chemical Composition of the Grafted DVB-EGDMA Co-Polymer

To evaluate the success of the grafting of a DVB-based copolymer using EGDMA as a hydrophilic modifier on a QCM sensor (Au coated with SiO_2), we analyzed the chemical composition of the coated and the uncoated sensor crystal using FTIR spectroscopy and Raman spectroscopy. The IR spectrum is shown in Figure 3.3 (blue data: coated sensor, black data: uncoated sensor), the Raman spectrum in Figure A.4.1, and the peak

IR Peak	Raman Peak	Peak Assignment ^{210–214}	Monomer Assignment
cm ⁻¹	cm ⁻¹		
-	3106	ν (C-H _{aromatic})	DVB
2918	2928	ν (C-H _{aliphatic})	DVB, EGDMA
2851	-	ν (C-H _{aliphatic})	DVB, EGDMA
1721	1714	$v_{\rm s}({\rm C=O})$	EGDMA
1637	1639	ν (C=C _{aliphatic})	DVB, EGDMA
-	1609	Ring skeletal stretch	DVB
1454	1454	$\delta_a(C-H)$ of $\alpha(C-H_3)$	EGDMA
1408	1406	δ (C-H _{vinyl}), γ (C-H ₂)	DVB, EGDMA
-	1201	$v_{a}(C-O-C)$	EGDMA
-	1013	Ring breathing mode	DVB

Table 3.2 IR and Raman	peak assignment f	or grafted DVB	-EGDMA copolymer.
	a construction of the second s	A	

assignment in Table 3.2. Even if the main part of the fingerprint region in the IR spectrum is overlayed by intense peaks from the silica coating (below 1250 cm⁻¹),²¹⁵ there are several additional signals visible in the IR spectrum of the coated sensor crystal (see Figure 3.3 blue data and Table 3.2) originating from the two polymer building blocks DVB and EGDMA. The peaks around 2900 cm⁻¹ can be assigned to the aliphatic C-H vibration of DVB and EGDMA, while the pronounced peak at 1721 cm⁻¹ likely originates from the C=O stretching vibration of EGDMA. The stretch vibration of the methacrylate C=C double bond can be observed at 1637 cm⁻¹, the deformation vibration of the methyl group of EGDMA at 1454 cm⁻¹, and the deformation of the CH2=CH bond at 1408 cm⁻¹.^{210,211,213} Raman (see Table 3.2), on the other hand, reveals additionally the aromatic C-H vibration at 3106 cm⁻¹, the ring skeletal stretch at 1609 cm⁻¹, the C-O-C stretch at 1201 cm⁻¹, and the ring breathing mode at 1013 cm⁻¹.^{212,214} These additional signals on the spectrum of the coated sensor measured with IR and Raman, two complementary techniques, prove the successful grafting of a DVB/EGDMA copolymer onto the sensor crystal.

3.3.2 Thickness and Surface Morphology of the Grafted DVB-EGDMA Co-Polymer

We assessed the surface morphology, polymer distribution, layer thickness, and chemical composition of the grafted DVB-EGDMA polymer layer using SEM and EDX. SEM images of the top and the side view of the sensor crystal before and after the grafting and EDX imaging of the side view are shown in Figure 3.4. SEM pictures of the top (Figure 3.4, a: uncoated, b: coated) and the side view (Figure 3.4, c: uncoated, d: coated) confirm the successful grafting of a polymer on the sensor crystal. SEM picture of the top view (Figure 3.4b) shows that the grafted polymer film is laterally heterogeneous, consisting of areas with a homogeneously grafted polymer film and regions without any coating. This heterogeneous coverage can potentially lead to energy dissipation during the QCM measurement.¹¹⁹ The side view (Figure 3.4d) also shows that the polymer layer's thickness varies with a maximal thickness of up to 300 nm. This film thickness lies in the optimal range since a few hundred nanometres is the upper limit of the dynamic range in liquid applications where polymer swelling



Figure 3.4 SEM and EDX images of the QCM sensor coated and uncoated with the DVB-EGDMA polymer. The QCM sensor consists of a quartz crystal coated with a 200 nm thick gold coating and a 50 nm thick silicon dioxide layer. SEM images: (a) Top view of QCM sensor, (b) top view of coated QCM sensor, (c) side view of QCM sensor, (d) side view of coated QCM sensor. EDX images for the elements gold (Au, red), carbon (C, green), oxygen (O, dark blue), and silicon (Si, light blue): (e) Side view of QCM sensor, (f) side view of coated QCM sensor.

Table 3.3 Determined values for the frequency change (Δf), the dissipation change (ΔD), and the bandwidth change $\Delta \Gamma$ during sorption experiment 1 and 2.

Experiment	Δf	ΔD	ΔΓ
1	18 ± 2	1.9 ± 0.2	10±1
2	20 ± 2	6.1 ± 0.1	31±1

can occur.^{120,216} A lower thickness is, however, not beneficial since the capacity of the coating is dependent on the thickness. The EDX images visualize the different layers of the sensor crystal and give information about the elemental composition of the grafted film (see Figure 3.4). The quartz crystal (dark and light blue for oxygen and silicon) is coated with a 200 nm thick gold coating (red) and a 50 nm thick silicon dioxide layer. The crystal with the grafted polymer (Figure 3.4f) has an additional layer (approximately 200 nm) that mainly consists of carbon (green) with some oxygen incorporated (dark blue), supporting the findings of FTIR and Raman spectroscopy and confirming the incorporation of both DVB (only green signals for carbon) and EGDMA (green and blue signals for carbon and oxygen) in the grafted polymer.

3.3.3 Interactions Between DVB-EGDMA Co-Polymer and Humic Acids during Flow-Based Sorption Experiments Revealed by QCM-D

After characterizing the successfully grafted DVB-EGDMA co-polymer, we further assessed the interaction between the grafted co-polymer and humic acids. To this end, we carried out two continuous flow experiments: In the first one, we injected 1152 ngC humic acids dissolved in MilliQ distributed over 15 injections, and in the second one, 6000 ngC dissolved humic acids distributed over 6 injections. The resonance frequency shift during these experiments is shown in (Figure 3.5). The measurement results are summarized in Table 3.3. Passing humic acids over the coated QCM sensor led to a significant frequency decrease (experiment 1: 18±2 Hz, experiment 2: 20±2 Hz). Injecting water on a coated sensor and humic acids on an uncoated silica sensor led to no significant frequency shift (see Figure A.4.2), thus demonstrating that the changes in the resonance frequency in experiment 1 and 2 are a result of the interaction between humic acids and the sensor coating. There is no sorption on the uncoated silica sensor since the negatively charged humic acids at neutral pH are electrostatically repulsed from the negatively charged silica surface.²¹⁷ The extent of the frequency decrease due to humic acid sorption on the coated sensor is comparable to numbers reported in the literature for the sorption of humic acids or NOM to different model surfaces (silica: 0 Hz,¹³¹ PS: 0.1-2.4 Hz,¹³¹ aluminium oxide: 3-15 Hz,^{131,134} poly(vinylidene fluoride) blended with SiO2 nanoparticles: 20-35 Hz,¹³⁶ alkylthiol self-assembled monolayer: 4-14 Hz¹⁴³). It has to be noted that we can compare frequency changes and cannot quantify the absolute sorbed mass since the Sauerbrey equation cannot be used for this application. This is the case since one requirement for the Sauerbrey equation is the small load approximation, which is only valid if $\Delta\Gamma$ is much smaller than the frequency change.^{119,120} This approximation does not apply to our measurements since $\Delta\Gamma$ is only by a factor of 2 smaller than the frequency change in experiment 1 and even bigger than the frequency



Figure 3.5 Frequency change (black) during humic acid sorption experiments 1 and 2 on a QCM sensor coated with the DVB-EGDMA copolymer. Water was passed constantly over the sensor with a flow rate of 30 μ L/min. Using an injection valve, humic acid solutions were injected during the flow experiments. The brown bars visualize the time when the humic acid solution is passed over the sensor.

change in experiment 2. The reason for this is that — as the SEM images showed — the surface coating is not homogeneous and not rigid, prohibiting humic acids from being sorbed and distributed evenly across the sensor. Instead of the Sauerbrey equation, which would significantly underestimate the sorbed mass, viscoelastic modeling has to be used. This is, however, not possible using openQCM Q^{-1} since only one overtone can be measured per experimental run, while for viscoelastic modeling, at least two are necessary.^{119–121}

The extent of sorption is not constant among the different injections for both experiments. There is a decline of the frequency decrease visible that leads, in the case of experiment 2, to no significant frequency change after the 4th injection. Together with the observation that the overall frequency decrease in both experiments 1 and 2 are similar — even if in experiment 2 nearly 6 times more humic acids were passed over the sensor — we conclude that the non-linear sorption behavior is a result of reaching the capacity limits for the coated polymer.²¹⁸ Experiment 2 shows further that after the initial sorption, parts of the adsorbed humic acids desorb until an equilibrium, the capacity limit, is reached. This sorption behavior is comparable to the observations of Eita et al.¹³⁴ for the sorption of humic acids on aluminium oxide. However, rinsing the surface with excess water did not lead to any further removal of sorbed humic acids. In a consecutive sorption experiment, we further rinsed the sensor after humic acid sorption equilibrium was reached with three different organic solvents (acetonitrile; $+2\pm 2$ Hz, isopropyl alcohol; -2 ± 1 Hz, methanol; $+2\pm 1$ Hz). These results suggest that the fraction of humic acids sorbing to the grafted DVB-EGDMA co-polymer forms a very stable adlayer.¹³¹

3.4 Conclusion

The current work presents the grafting of a DVB-EGDMA co-polymer onto a QCM sensor using radical polymerization. FTIR and Raman spectroscopy confirmed the successful incorporation of DVB and EGDMA into the polymer. SEM and EDX measurements showed that the polymer is coated laterally heterogeneous on the sensor chip. These techniques further revealed that the polymer layer is 200-300 nm thick and thus inside the dynamic range of QCM measurements.^{120,216} The demonstrated polymerization and characterization strategy can be used as a model to graft other (DVB-based) co-polymers onto QCM sensors. We observed humic acid sorption during two flow experiments, leading to a significant frequency decrease of 18-20 Hz. This decrease is on the higher end compared to frequency changes measured during the sorption of humic acids to other model surfaces — especially considering the lateral heterogeneity of the coating. The stability of the adlayer formation further proves the strong interactions between the DVB-EGDMA co-polymer coating and humic acids — and prohibits, at the same time, regeneration of the sensor with common organic solvents. Future research can build upon our findings and optimize the presented polymerization strategy to enable the coating of a more homogeneous polymer layer to study NOM sorption processes using the QCM.

4 Quartz Crystal Microbalance as Holistic Detector for Quantifying Complex Organic Matrices During Liquid Chromatography: 1. Coupling, Characterization, and Validation

Abstract

Matrix in highly complex samples can cause adverse effects on trace analysis of targeted organic compounds. A suitable separation of target analyte(s) and matrix before the instrumental analysis is often a vital step for which chromatographic clean-up methods remain one of the most frequently used strategies, particularly high-performance liquid chromatography (HPLC). The lack of a simple real-time detection technique that can quantify the entirety of the matrix during this step renders optimization of the clean-up challenging. This paper, along with a companion one, explore the possibilities and limitations of quartz crystal microbalance (QCM) dry mass sensing for quantifying complex organic matrices during gradient HPLC. To this end, this work coupled a QCM and a microfluidic spray-dryer with a commercial HPLC system using a flow splitter and developed a calibration and data processing strategy. The system was characterized in terms of quantification limits, accuracy, and applicability for subsequent pesticide residue analysis in food using gas chromatography-mass spectrometry (GC-MS). Validation of natural organic matter in an environmental sample against offline total organic carbon analysis confirmed the approach's feasibility with an absolute recovery of $103\pm10\%$. We found a correlation ($R^2 \ge 95$) between the amount of matrix quantified by QCM dry mass sensing during an HPLC clean-up of a brown rice extract and matrix effects measured during the subsequent GC-MS analysis of the investigated pesticides. This suggests that QCM dry mass sensing can be a valuable tool to the analyst where HPLC clean-up is routinely performed and can thus benefit many analytical fields.



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4.1 Introduction

A challenge in trace analysis of targeted organic compounds are highly complex samples, such as environmental,^{3,112} biological,^{219,220} or food samples.^{154,157,221} This is the case because abundant organic and inorganic constituents of the complex sample, other than the target analyte(s) and also known as matrix, can have a variety of adverse effects on the analytical mode of detection. These adverse effects include increased detection noise, higher detection limits, obscured peaks, false positive signals/ results, signal suppression (negative matrix effect), or signal enhancement (positive matrix effect).^{154,155} Despite many instrumental developments that improved the overall detection or the separation of the sample matrix and target analytes, e.g., high-resolution mass spectrometry or multi-dimensional hyphenated chromatography, there are still limitations in trace analysis of targeted organic compounds due to the sample matrix.^{154,157,222} A suitable sample preparation before the instrumental analysis is often a vital key to the reduction of matrix-related adverse effects.^{154,156,157}

An efficient separation of the matrix constituents from the target analyte(s) is usually the focus of such sample preparation procedures for which chromatographic clean-up methods remain one of the most often used strategies, particularly high-performance liquid chromatography (HPLC). As a stand-alone purification system or directly coupled to a detector, HPLC cleanup finds many applications mainly due to the wide variety of available column materials and modes (e.g., reversed phase (RP)),^{110,111} as well as the possibility to optimize purification using an unlimited combination of solvents.^{110–112} In addition to the easy automation of the sample clean-up, which increases reliability and accuracy,^{223–225} the possibility to pack columns with highly selective materials^{226,227} makes the sample preparation tunable to any target analyte of interest. Yet, the HPLC method development becomes tedious and challenging when the matrix is a complex mixture that cannot be quantified with straightforward measures. In fact, an optimal and efficient optimization of the HPLC clean-up warrants a simultaneous online quantification of both the target analyte(s) and the interfering matrix.

While there are numerous detectors for organic target analytes (UV-Visible spectrometry (UV/Vis), mass spectrometry (MS)), they cannot be directly used for the online quantification of organic matrices. This is because the matrix composition is often very heterogeneous and complex. Natural organic matter (NOM) consists, for example, of thousands of different compounds with a wide variety of physicochemical properties, while food matrices are a complex mixture of different fatty acids, proteins, carbohydrates, vitamins, and many more compounds.^{80,228} Also, most instruments typically used to quantify analytes can only monitor certain matrix fractions (e.g., chromophoric or ionizable).^{114,115} Semi-universal sensors like the total organic carbon (TOC) analyzer, the charged aerosol detector (CAD), or the evaporative light-scattering detector (ELSD) are limited by their inter-compound response differences (TOC: solubility in H₂O, only carbon content is measured; CAD: up to 11% relative standard deviation for different compounds, ELSD: relative standard deviations higher than 50% are reported),^{115–118} which play an important role if not just one compound but the sample matrix should be quantified. A robust, simple, and inexpensive detection technique capable of quantifying the entirety

of the matrix online during a gradient HPLC purification would help improve the selectivity of the respective separation process in a straightforward approach.

One promising detector that could be used for this purpose is the quartz crystal microbalance (QCM). The QCM measures small mass changes with a sub-nanogram resolution on the surface of its oscillating piezoelectric quartz crystal by measuring changes in the oscillating resonance frequency as a function of deposited mass on its surface.^{119,121} Several studies showed how the QCM can be used to measure the sorption of the matrix NOM directly in a solution or the adsorption of dissolved compounds onto NOM and get thus insights into adsorption, adlayer formation, and interfacial dynamics of this matrix.^{131–144} NOM real-time quantification directly in liquid phase is, however, challenging to achieve due to (i) the limited capacity of available sensor surface coatings,¹³¹ (ii) the dependency of the sorption behavior on the type or fraction of NOM,^{132,143} the pH,^{132,134} and the continuous desorption,¹³⁴ (iii) the often slow deposition rate,¹³¹ (iv) and other known challenges of liquid-based QCM measurements (e.g., viscous damping).^{119,151} The challenges of liquid-based QCM measurements can, however, be overcome using QCM dry mass sensing introduced in the 70s by Schulz et al.¹⁵⁰ Technical advancement on the QCM and substantial optimization measures in the last decade make dry mass sensing seem to be an ideal solution for a robust and inexpensive strategy to monitor and quantify the entire matrix.^{120,151–153} In QCM dry mass sensing, a small fraction of the HPLC column effluent is diverted and nebulized into micron-sized droplets using a microfluidic spray nozzle and sprayed onto the QCM sensor. The nebulized solvent evaporates, while non-volatile components are deposited evenly on the QCM sensor, which can be quantified using the direct correlation between frequency change and mass.^{151–153} Kartanas et al.¹⁵³ showed how this OCM dry-mass sensing could be used in combination with aquatic size-exclusion LC to separate and detect different proteins. It has, however, never been explored for a mixture as complex as an environmental extract or a food matrix. Moreover, the transition from aquatic to RP gradient elution is expected to cause variations in QCM response as a result of changing fluid dynamics and evaporation rates. To this end, comprehensive characterization and validation of such a system is warranted to deal with organic solvents along with the development of a suitable calibration strategy.

The work presented in this and the companion paper²²⁹ has the overall goal of exploring the feasibility of coupling a commercial HPLC with a microfluidic spray-dryer and a QCM for online monitoring of organic matrix components during RP HPLC gradient purification for different mass spectrometry-based applications in environmental and food sciences. Both studies focus on organic matrices in already extracted samples where most inorganic salts are excluded through a first solid-phase extraction step. The specific objectives of this paper were to (i) connect, characterize, and calibrate a microfluidic spray-dryer with RP HPLC using an adjustable post-column flow splitter, (ii) define the lower and upper limits of quantification for QCM dry mass sensing, and (iii) validate the online approach against offline TOC fraction analysis of NOM. Lastly, we (iv) illustrate its applicability and analytical implications for the analysis of pesticides in brown rice through



Figure 4.1 Schematic overview of the coupled HPLC-QCM system. 1: HPLC grade solvents, 2: Binary HPLC pump, 3: Sample injector/autosampler, 4: Chromatographic column; 5: DAD detector, 6: Fraction collector, 7: Post-column adjustable flow splitter, 8: Microfluidic spray-dryer, a: connection to liquid channel, b: connection to gas channel, 9: QCM sensor.

qualitative assessment during separation of matrix compared with UV/Vis, and quantification of matrix effects in subsequent gas chromatography (GC)-MS analysis, respectively.

4.2 Experimental Section

4.2.1 Chemicals and Materials

A description of purchased chemicals, materials, as well as standard solutions used in this study are provided in the supporting information (section D.1).

4.2.2 Instrumental Setup of QCM Dry Mass Sensing

Coupling of QCM Dry Mass Sensing with RP HPLC using a Flow Splitter

An HPLC system, Figure 4.1 (**parts 1-6**), was coupled through an adjustable flow splitter, Figure 4.1 (**7**), to QCM dry mass sensing, Figure 4.1 (**8-9**). Chromatography was performed on a Nexera XR HPLC system (Shimadzu, Japan) equipped with a solvent delivery module (LC-20AD, Shimadzu, Japan) (**2**), an RP column (**4**) (XTerra RP18 Column, length: 150 mm, diameter: 3.0 mm, particle size: 3.5μ m, Waters, USA), a diode array detector (DAD) (**5**) (SPD-M20A, Shimadzu, Japan), and a fraction collector (**6**) (FRC-10A, Shimadzu, Japan). A flow rate of 0.5 mL/min, a sample injection volume of 200 μ L (**3**), and a column oven temperature of 40 °C were used for all HPLC measurements. Binary phase gradients with H₂O (A) and 90% CH₃OH 10% H₂O (B) were used as eluents (**1**).

The column effluent is split after the DAD using an analytical post-column adjustable flow splitter (7) (ASI 610-PO10-01, Analytical Scientific Instruments, USA, 50:1 to 1000:1 Split Ratio). Vernier scale settings were set to 65 unless otherwise stated. The high-flow port was connected with the fraction collector and the low flow port with a microfluidic spray-dryer (8) using polytetrafluorethylene (PTFE) tubing. The low-flow port was connected with the liquid channel of the spray-dryer via PTFE tubes (a) (tube 1: outer diameter 1/16 inch, inner diameter 0.010 inch; tube 2: outer diameter 1/32 inch, inner diameter 1/75 inch) that were connected through an

adapter (1/16 inch to 1/32 inch, PEEK, IDEX Health and Science) to meet the requirements of both the splitter and the spray-dryer.

We fabricated the microfluidic spray-dryer (8) in-house using an optimized protocol (details in section D.1) of a previously published standard polydimethylsiloxane (PDMS) soft-lithography approach.¹⁵² The microfluidic spray-dryer had two inlets, one connected to a nitrogen supply (b) set to 3 bar and another to the low-flow port of the flow splitter (a). The liquid channel had a length of 8.1 mm and a cross-section of 25 times 20 μ m², the gas channels had a length of 8.4 mm and a cross-section of 100 times 70 μ m². The mobile phase was sprayed onto the frequency counter QCM200 from Stanford Research Systems (USA) equipped with a 5 MHz QCM crystal (9) (Stanford Research Systems 100RX1, Cr/Au, USA); a gate time of 0.1 s was used. To this end, the spray-dryer was centered 3.5 cm above the QCM.

Determination of Split Ratios

Split ratios (R_{split}) were determined for different Vernier scale settings (56, 66, 73, 79, 94, 112) for three different CH₃OH/H₂O mobile phase compositions (85/15, 50/50, and 15/85 (v/v)) by spraying the mobile phase containing 500 mg/L NaCl for 30 min into a vial. The dried salt was reconstituted in 8 mL H₂O. The salt concentration in solution was determined by measuring the salinity using a salinometer (MultiLine F/SET-3, WTW, Germany).

$$\kappa_{corrected} = \kappa_{sample} - \kappa_{control} \tag{4.1}$$

$$c_{sample} = \frac{\kappa_{corrected}}{\Lambda_m^{NaCl}} \tag{4.2}$$

Dividing the corrected salinity ($\kappa_{corrected}$) by the molar conductivity of NaCl (Λ_m^{NaCl}) results in the concentration of the sample in the vial (c_{sample}) (see Eq 4.1 and 4.2).

$$Q_{spray} = \frac{m_{sample}}{c_{NaCl} \cdot t} \tag{4.3}$$

The flow to the spray-dryer (Q_{spray}) was calculated using Eq 4.3 by dividing the sprayed mass (m_{sample}), calculated using c_{sample} , by the sprayed time (t) and by the concentration of salt (C_{NaCl}) in the mobile phase.

$$R_{split} = \frac{Q_{input} - Q_{spray}}{Q_{spray}} \tag{4.4}$$

The split ratio (R_{split}) was calculated using Eq 4.4. Here, the high flow, which is the difference of the input flow (Q_{input}) and the low flow (Q_{spray}), is divided by the low flow.

Measurement, Calibration and Data Processing

Prior to each sample, a blank was run on the system described in Figure 4.1 under identical conditions where 200 μ L of 25/75 CH₃OH/H₂O (v/v) were injected instead of the sample. After the sample measurement, a one-point calibration was performed through constant mass spraying on the sensor achieved under the same chromatographic conditions but with the eluents containing NaCl (c_{cal} = 300 mg/L). The obtained frequencies given in Hz for each time point were translated into mass concentrations given in mg/L using Eq. 4.5, as well as detailed in a Matlab script (see section D.8).

$$c_{sample} = c_{cal} \cdot \frac{\partial \Delta f_{sample}}{\partial t} / \frac{\partial \Delta f_{cal}}{\partial t}$$
(4.5)

In this procedure, the blank (f_{blank}) is subtracted from both the sample (f_{sample}) and the calibration measurement (f_{cal}) to obtain corrected frequencies Δf_{sample} and Δf_{cal} , respectively. Then, the 1st derivative $(\partial \Delta f_{sample}/\partial t$ and $\partial \Delta f_{cal}/\partial t)$ is produced and smoothed using a Savitzky-Golay filter (polynomial order 3, 301 points). The derivatives ratio multiplied by the salt concentration for calibration (c_{cal}) yields mass concentrations in the sample (c_{sample}) .

Determination of Lower and Upper Limits of Detection and Quantification

The limits of detection (LOD) and limits of quantification (LOQ) of the system were determined for three different CH_3OH/H_2O mobile phase compositions (85/15, 50/50, and 15/85 (v/v)) according to the calibration method (DIN 32645).²³⁰ To this end, we sprayed the mobile phase containing NaCl in different concentrations (0, 30, 60, 90, 120, 150, and 180 mg/L) for 10 minutes onto the QCM. The average slope of quadruplicates of the frequency decrease was used for the signal intensity.

For the determination of the upper limit of the system for the three different mobile phase compositions, the mobile phase containing 500 mg/L NaCl was sprayed onto the QCM in triplicates. The upper limit was then estimated by calculating the amount of salt being sprayed till the resistance was by a factor of three higher than the starting resistance (12-17 ohm). This value was then converted into a maximal concentration for a 10 minute measurement.

Validation of QCM Dry Mass Sensing Approach

We compared dry-mass sensing with TOC analysis to validate our measurement approach. The elution of 1.65 mg NOM during a typical HPLC gradient (see Table A.4.2) was monitored and quantified online using QCM dry mass sensing and offline using TOC analysis. To this end, fractions of the HPLC eluate were taken every 30 s using a fraction collector (6). The fractionated eluate was evaporated to dryness under a gentle stream of N_2 at 30 °C and then reconstituted in 16 mL of H₂O. Organic carbon concentrations in each reconstituted sample were

determined using a TOC analyzer (TOC-L, Shimadzu, Japan) equipped with a combustion catalytic oxidation reactor (680 $^{\circ}$ C) and a non-dispersive infrared detector to analyze the generated CO₂.

4.2.3 Extraction Procedures to Isolate Environmental and Food Matrices

Extraction of Rice Matrix

Brown rice was treated using a modified version of the QuEChERS method.^{46,231} Frozen brown rice (500 g) was homogenized using cryogenic milling. Ten grams of the homogenized sample were weighed in a 50 mL centrifuge tube and soaked in 10 mL Milli-Q H₂O for 1 h. Afterwards, 10 mL of acetonitrile were added together with a buffer salt mixture of 4 g of magnesium sulfate anhydrous grit, 1 g of sodium chloride, 0.5 g of disodium hydrogen citrate sesquihydrate, and 1 g of trisodium citrate dihydrate. The mixture was shaken vigorously by hand for 1 minute and then centrifuged at $3500 \times g$ for 5 minutes. The acetonitrile phase was collected and stored at -18 °C for further experiments.

Extraction of Riverine NOM

Samples were taken from creek Wiesäckerbach (Garching, Germany, latitude 48.269009, longitude 11.667976) and filtered through glass microfiber filter membranes (1.2 μ m particle retention, 47 mm diameter, Whatman, UK). The filtered samples were passed over OASIS HLB cartridges under conventional solid-phase extraction conditions (Waters, 200 mg, 6 cc) using an automated SPE system (Smart Prep Extractor, Horizon Technology, USA) at 5 mL/min. The cartridges were subsequently dried under vacuum overnight and eluted in 5 mL of CH₃OH. The volume of combined eluates was reduced under a gentle stream of N₂ at 30 °C and then stored at -18 °C.

4.2.4 Experiments

Quantification of Brown Rice Matrix During Reversed-Phase Liquid Chromatography

Brown rice matrix collected from the acetonitrile phase was evaporated to dryness at 50 °C under a gentle stream of N_2 . The dry residues (2.6 mg) were then reconstituted in 250 µL H₂O/isopropanol 1/1 (v/v) and introduced using a manual injection valve into the HPLC-QCM dry mass sensing system with a Vernier scale setting of 65. The HPLC gradient parameters are listed in Table A.4.3. Matrix quantification data from the QCM dry mass sensing (Figure 4.1, **8**&**9**, low-flow port) were collected and processed after calibration with a blank measurement constituting a QuEChERS extract in absence of rice matrix for baseline correction. Data from the DAD detector (Figure 4.1, **5**) was collected using the software LabSolutions and chromatograms were extracted at wavelengths of 220, 254, and 310 nm. Comparison of data from QCM dry mass sensing and DAD

detector are plotted as intensity (mV) and mass concentration (mg/L), respectively, as a function of elution time after correction for the dead time (2.5 min) between the DAD detector and the QCM sensor.

Quantification of Matrix Effects in Residue Analysis of Pesticides Using GC-MS

Extracted brown rice matrix was fractionated into 5 portions after HPLC. Each fraction was evaporated to dryness under a gentle stream of N2 at 50 °C, reconstituted in CH3OH, and spiked with five different model analytes, namely 2,6-dichlorobenzamide (BAM), atrazine (ATZ), boscalid (BOSC), desethylatrazine (DEA), and propargite (Prop) to reach a volume of 1 mL and a pesticide concentration of 5 mg/L. The rice matrix fractions were measured using a GC-MS consisting of an Agilent 7890A GC system (Column: RestekTM RxiTM-5ms, 30 m, 250 µm i.d., 0.25 µm thickness, Restek Corporation, Bellefonte, USA) equipped with a 5975C Triple-Axis Detector MS from Agilent Technologies (Santa Clara, USA) and a High-Efficiency Source (HES). Liquid samples were injected (1 µL injection volume) using a CTC Pal combi-xt autosampler (CTC Analytics AG, Zwingen, Switzerland) with split injection mode (split-ratio 1:10) at an injection temperature of 250 °C with an injection liner pressure of 14.86 psi. The analyte separation was accomplished at a helium flow of 1.4 mL/min using the following temperature program of the GC oven: Starting temperature was 90 °C (0.5 min hold time), followed by a temperature ramp of 7.5 °C/min to 224 °C, a ramp of 25 °C/min to 290 °C and a ramp of 10 °C/min to 300 °C (4 min hold time). The electron ionization energy was 70 eV. For the MS detection single ion mode was used, retention times and masses are shown in Table A.4.4. Every sample was measured in triplicates and bracketed by triplicates of a standard containing the five pesticides in pure CH₃OH at the same concentration.

$$ME\% = \left(\frac{SignalArea_{\text{Sample}}}{SignalArea_{\text{Standard}}} - 1\right) \times 100 \tag{4.6}$$

The absolute matrix effect in percent (ME%) was calculated according to Eq. 4.6, in which the area of each pesticide in the sample (Signal Area_{Sample}) is divided by the mean of the area of the six bracketing standards (Signal Area_{Standard}).^{232,233}

4.3 Results and Discussion

4.3.1 Coupling, Flow Control, and Calibration

We coupled an HPLC system (1-6 in Figure 4.1, flow range = 0.1-1 mL/min) with a microfluidic spray-dryer and QCM sensor (8&9, respectively; flow range = 1-4 μ L/min) through an adjustable flow splitter (7). The narrow flow dynamic range of components 8&9 warrants accurate control of the split ratio under chromatographic conditions. Therefore, we evaluated split ratios for three different solvent compositions (CH₃OH/H₂O 15/85, 50/50, and 85/15 v/v) and six different Vernier scale settings in the range between 56 and 112 (see Figure 4.2a).



Figure 4.2 (a) Comparison of split ratios measured for the HPLC-QCM system at different Vernier scale settings for three different CH_3OH/H_2O compositions at 40 °C. The values were fitted with an exponential decay function. The values provided by the manufacturer at 25 °C for pure H_2O are shown in gray. (b) Viscosity values of CH_3OH/H_2O mixtures at 40 °C from Mikhail et al.²³⁴ in millipoise (mP). (c) Correlation of frequency slope and measured split ratios during a calibration (black). The eluent composition during the gradient run is shown in gray in vol. % of CH_3OH (containing constantly 300 mg/L NaCl).

The split ratios increase up to 2.4 times for the HPLC-QCM dry mass sensing system using CH₃OH/H₂O solvent compositions (Figure 4.2a blue, red, and green data) in comparison with the data provided by the manufacturer (Figure 4.2a, gray data), using only H_2O as a solvent with no restrictions after the flow splitter. Moreover, variations by a factor of 1.1 - 1.8 were observed for different solvent compositions in the order CH_3OH/H_2O 50/50 (blue) > 15/85 (red) > 85/15 (green). These variations are significant enough to induce shifts towards lower flow rates to the spray-dryer that may lead to operation outside its dynamic range (split ratios between 125 and 500), thus affirming the need to quantify split ratios for the system. The overall split ratio shift for the HPLC-QCM dry mass sensing system is caused by backpressure originating from the small inner diameter of the liquid channel of the spray-dryer ($25 \times 20 \ \mu m^2$), which is the only additional constriction in the system compared to manufacturer's data.^{235–237} In addition, the pressure in the system leads to a deformation of the liquid channel made of PDMS and thus to an increase of its hydraulic diameter (D_{hvd}) as reported by Kartanas et al.¹⁵³ This deformation strongly influences the hydraulic resistance $(R_{res} \propto 1/(D_{hyd})^4)$ and thus the generated backpressure. Since D_{hvd} is dependent on the liquid dynamic viscosity, the trend of the split ratios must follow the trend of the dynamic viscosities of the respective solvent compositions. Indeed, this is the case as shown in Figure 4.2b where the highest viscosity is for CH₃OH/H₂O 50/50 (10.5 mP, **blue**) > 10/90 (8.0 mP, red) > 90/10 (6.1 mP, green).

These results imply that while the split ratio, and thus the flow to the microfluidic spray-dryer, will stay constant during an isocratic HPLC run, flows will constantly change in a gradient HPLC mode. If the split ratio shifts are within the dynamic range (split ratios between 125 and 500), QCM dry mass sensing response is still expected to vary. Indeed, spraying a fixed concentration of solute (300 mg/L NaCl) returns a non-linear frequency response (Figure 4.2c) during CH₃OH/H₂O gradient run (Figure 4.2c, **gray**). The slope of the frequency change as a function of CH₃OH content follows in fact the observed shifts in split ratio earlier determined in the order CH₃OH 25-55% ($\partial \Delta f / \partial t$: -36, **blue**) < 10-25% & 55-90% ($\partial \Delta f / \partial t$: -44, **red&green**). Based on these results, we developed a calibration and data processing strategy, where we prepare calibration solvents (e.g., H₂O, CH₃OH) with an NaCl concentration of 300 mg/L for binary solvent systems and record the QCM response as a function of time during the same gradient run of the sample. This calibration is used to quantify the amount of solutes in the sample by dividing the frequency change of the sample with the one of the calibration. This strategy is not only valid for solute concentrations of 300 mg/L but also for large range of concentrations as the sprayed mass gives linear response of the frequency change in this range (30 to 500 mg/L, see supporting information Figure A.4.1).

4.3.2 Evaluation of Lower and Upper Quantification Limits

The concentration range in which accurate quantification of masses is achievable using the presented QCM dry mass sensing approach was investigated next by spraying different concentrations of NaCl (from 0 to 180 mg/L)

CH ₃ OH/H ₂ O	LOD	LOQ	upper limit
(v/v)	mg/L	mg/L	mg/L
15/85	15	52	336±7
50/50	4.3	16	408 ± 2
85/15	12	42	475±4

 Table 4.1 LODs, LOQs and upper limit determined for dry-mass sensing for three solvent compositions over 10 minute duration.

in a binary mobile phase system (i.e., CH_3OH/H_2O) for three different compositions (CH_3OH/H_2O 15/85, 50/50, and 85/15 (v/v)). The LOD and LOQ were determined according to the calibration method by using the slope of the frequency change per minute for each measurement as signal intensity term (y); the results are shown in Table 4.1.

The LOD for the different mobile phase compositions ranged from 4.3 mg/L to 15 mg/L, whereas the LOQ was found to be from 16 mg/L to 52 mg/L. The presented system's detection limits are at least 6 times lower than that estimated by Kartanas et al.¹⁵³ for aquatic conditions (LOQ: 100 mg/L). Although we observed lower noise levels in this study (5-15 Hz) compared with Kartanas et al.¹⁵³ (aquatic: 30 Hz), this cannot alone explain these results. In our study, the lowest detection limits were determined for CH₃OH/H₂O 50/50 composition (LOD = 4.3 mg/L, noise = 10 Hz), whereas the observed noise was found to be smallest for CH₃OH/H₂O 85/15 composition (LOD = 12 mg/L, noise = 5 Hz). Flow rates cannot fully explain the observed trends of the detection limits either, as they do not follow the same order we observed earlier. This indicates that the exact limits are not merely dependent on the noise and the flow rate, but also on other interconnected factors that are influenced by both the solvent composition and the flow rate including the spray cone dimensions, uniformity of the generated spray, droplet size, and evaporation rate of solvent(s).^{238–240}

There exists, however, not only a lower limit of the QCM quantification but also an upper limit, above which both trueness and precision of QCM dry mass sensing is compromised. Indeed, spraying a salt solution with high concentration (500 mg/L) on the QCM led over time to an increase in noise, to a shift of the slope of the frequency change, and to increased resistance values measured on the QCM (see Figure 4.3). Since higher resistance values indicate a change in oscillation behavior of the quartz crystal, and hence a change of the frequency-mass correlation,²⁴¹ we defined an operational upper limit when the measured resistance is by a factor of three higher than the starting resistance. This corresponds to a change of the noise over time ≤ 5 Hz/min and a difference of the frequency change ≤ 7 Hz/min among triplicates. For a 10 minute measurement, the upper limit was found to be above 330 mg/L for all solvent compositions (see Table 4.1), which corresponds to 2 measurements at $c_{sample} = 5000$ mg/L (injection volume = 200 µL) and $R_{split} = 200 - 290$. This suggests that cleaning the QCM sensor after each measurement may be necessary to guarantee reproducible and accurate results. Such a step was accomplished in this study by 2-3 gentle swipes of the QCM sensor surface using a wet microfiber cloth that proved to be effective with no significant deviation of frequency change over time even after



Figure 4.3 Frequency (blue) and resistance (orange) raw data of triplicate measurements of three different CH₃OH/H₂O compositions ((a): 15/85, (b): 50/50, (c): 85/15 (v/v)) containing 500 mg/L NaCl.

100 deposition and cleaning cycles (deviation from new sensor: $\partial \Delta f / \partial t = 0.4 \pm 2.4$ Hz/min). Alternatively, depositing a droplet of CH₃OH/H₂O on the surface and blowing it away using pressurized air was equally effective — a step that can be easily automated.

4.3.3 Validation of Online QCM Dry Mass Sensing Against Offline TOC Fraction Analysis for Organic Matrix

We validated the accuracy of QCM dry-mass sensing coupled to HPLC by real-time monitoring of an NOM extract during HPLC separation using our system and compared it with the results of offline TOC analysis of collected HPLC fractions during the same run as a reference strategy. This was possible since the extracted NOM could be reconstituted in H₂O without significant losses (NOM recovery \geq 98%) while inorganic salts



Figure 4.4 (a) Comparison of the NOM matrix monitoring results obtained by dry-mass sensing (blue line) with the results of offline TOC analysis of LC fractions (orange bar chart) during isocratic HPLC separation (CH₃OH/H₂O 30/70 v/v; 0.5 mL/min) of NOM (injected mass = 1 mg) on column (XTerra RP18, 150×3.0 mm, 3.5 µm). Orange dashed line: MQL of TOC analysis (13.2 mg/L). Blue dashed line: LOQ of QCM (40 mg/L). (b) Gray bar chart: Variance of QCM and TOC measurement per fraction shown as residual in %.

were already removed during the pre-extraction step. NOM quantification using QCM dry-mass sensing (see Figure 4.4a, **blue line**, see Figure A.4.3 for QCM raw data) is in good agreement with fraction analysis using TOC (Figure 4.4a, **orange bars**). Both detection techniques show that NOM elutes as an unresolved hump with maxima between 4 and 9 min, which is a typical behavior of NOM during RP HPLC using C18 separation columns of similar dimensions.^{242,243} Moreover, absolute recoveries obtained by real-time QCM dry mass sensing (= $103\pm10\%$) agree well with that of offline TOC fraction analysis (= $98\pm1\%$). These results confirm the suitability of QCM dry mass sensing for real-time monitoring of complex matrices during a typical HPLC separation. The lower precision achieved by QCM dry mass sensing (= $\pm10\%$) compared to TOC analysis (= $\pm1\%$) is conceivably the result of the variations associated with the continuous spraying/evaporation processes (typical precision of QCM measurements without spray-drying: 0.1 Hz).¹²⁰

Analysis of variance shows a tendency of QCM to overestimate NOM (see Figure 4.4b). This overestimation sums up to a total of $5\pm11\%$ until the retention time where limit of quantification for QCM is reached (t = 17.2 min, LOQ_{QCM} = 52 mg/L, Figure 4.4a **blue dashed line**), which is still within the measured QCM precision. Note that LOQ of dry mass sensing is 2.7 times higher than the method quantification limit of offline TOC analysis (MQL = 19.2 mg/L, Figure 4.4a **orange dashed line**, for calculation from LOD to MQL see Figure A.4.2). This narrow sensitivity gap could easily be closed by further fine-tuning the performance of the spray-dryer such as spraying a higher fraction of the mass in the mobile phase on the QCM.



Figure 4.5 (a) UV/Vis chromatogram of RP HPLC purification of rice matrix (injected mass = 2.6 mg) at three different wavelengths (brown; 220 nm, 254 nm, 310 nm). (b) Monitoring of rice matrix during the same RP HPLC purification using dry-mass sensing (blue).

4.3.4 Applicability and Analytical Implication of QCM Dry Mass Sensing for the Analysis of Pesticides in Food

After a successful coupling, characterization, and validation of QCM dry mass sensing, it is important to (i) assess its applicability, as a holistic detector of complex matrices, to a real-world analytical task, and (ii) examine the implications of the data collected by QCM dry mass sensing for sample preparation. To this end, we chose a typical example of pesticide analysis (DEA, BAM, ATZ, BOSC, and Prop) in brown rice as food matrix using GC-MS after QuEChERS extraction followed by a typical HPLC cleanup step.

Qualitative Assessment – Reversed-Phase Separation of Brown Rice Matrix and Monitoring Using UV/Vis Detection and QCM Dry Mass Sensing

We applied QCM dry-mass sensing during RP HPLC of brown rice matrix and compared the response of the DAD detector and the QCM. Figure 4.5a shows the HPLC chromatogram measured with the DAD detector at three different wavelengths (brown: 220 nm (dashed line), 254 nm (solid line), 310 nm (dotted)) while Figure 4.5b represents the results of the QCM dry-mass sensing (blue). Data were acquired over a range of 190 nm – 800 nm but no significant changes in intensity ratios were observed across the chromatogram within the visible range and hence not discussed.

There is a vast discrepancy between the validated data acquired by the QCM compared with the DAD detector where most matrix elutes in the time window 13.5-17.5 min whereas UV absorption shows only some scattered peaks. This demonstrates the unsuitability of using UV/Vis for food matrix monitoring and quantification purposes. This further confirms other studies that compared UV/Vis and TOC analysis during HPLC purification of NOM.^{243,244} It comes as no surprise that UV/Vis detection can not quantify matrix compounds since the response depends on the specific chemical compound/class and its molar absorptivity,²⁴⁵ as well as absorption wavelength (e.g., 220 nm: aromatic and carboxylic chromophores, 254 nm: aromatic groups with varying degrees of activation).^{114,246} Sugitate et al.²²⁸ identified monoacylglycerols as the most abundant chemical class found in GC-MS analysis of the QuEChERS extract of brown rice. The lack of UV/Vis absorption of most fatty acids can conceivably explain the discrepancy between QCM and UV/Vis data between minute 13.5 and 17.5.^{247,248} We identified, in fact, oleic acid as one of the main substances eluting in this range with GC-MS analysis using the NIST database (see Figure A.4.4). These results illustrate that mere reliance on UV detection during HPLC clean-up does not necessarily reveal information about the matrix's behavior and is thus inadequate to assess this analytical step's efficiency. Yet, combining the information gained from the DAD detector (i.e., insights into the compound structure and analyte retention times) with the complementary information obtained by QCM dry mass sensing (i.e., quantification of entire matrix) provides the analyst with a complete picture of the separation process.

Quantitative Implication – Matrix Effect Correlations in GC-MS Residue Analysis With QCM Dry Mass Sensing Data

We further examined the interpretability of acquired data using QCM dry mass sensing during a typical HPLC clean-up on a subsequent analysis using GC-MS as an example. To this end, five fractions that were quantified using QCM dry mass sensing (see retention windows in Table A.4.5) were collected during an HPLC clean-up of brown rice matrix, spiked with an analyte mixture (DEA, BAM, ATZ, BOSC, and Prop), and matrix effects associated with each analyte in each fraction were measured using GC-MS (see Figure 4.6 and Table A.4.5).

The relative amount of matrix in each fraction (matrix_{frac}/matrix_{total}) determined by QCM dry mass sensing correlates with the observed matrix effects (blue symbols in Figure 4.6). These correlations were found for all investigated compounds with signal enhancement for DEA ($R^2 = 0.99$), BAM (0.99), ATZ (0.99), and BOSC (0.99), and with signal suppression, observed for Prop (0.95). In contrast, such a correlation couldn't be observed when UV/Vis data were used to estimate the percentage of the total matrix in the respective fraction (brown symbols in Figure 4.6). Our findings, which primarily demonstrate signal enhancement, are consistent with the literature since this effect is the most common type (> 90%) observed in GC-MS residue analysis.^{155,228,249} While we can not explain the correlation for signal suppression since no mechanism has been proposed and accepted in literature for this phenomenon,^{155,228,249} the signal enhancement correlations



Figure 4.6 Observed matrix effects (ME) for DEA, BAM, ATZ, BOSC, and Prop during GC-MS analysis in 5 different fractions (A-E) of brown rice matrix after HPLC clean-up plotted against the percentage of total matrix contained in the respective fraction (matrix_{frac}/matrix_{total}) according to QCM dry mass sensing (blue symbols). GC-MS conditions were $V_{inj} = 1 \ \mu$ L, split ratio = 1/10, detection mode = SIM, column = RestekTMRxiTM-5ms, 30 m×0.25 mm, 0.25 μ m. Each HPLC fraction corresponds to a retention window of 1.5 min (see Table A.4.5). The respective DAD results at 220 nm are shown for comparison (brown symbols).

can be explained using the established mechanism of matrix-induced chromatographic response enhancement in GC. Signal enhancement is caused by matrix components competing with the analyte for the adsorption on active sites present in the injection liner and chromatographic column, which are mainly free silanol groups. In this way, analyte losses are reduced due to irreversible adsorption or catalytic decomposition.¹⁵⁵ Literature shows that the extent of such signal enhancement is dependent on (i) the mass of the matrix in the sample,^{228, 250} which the found correlations corroborate.

The extent of the signal enhancement further depends on (ii) the strength of interaction between the active sites and the components in the matrix, as well as (iii) the analyte properties.^{47,228,250} Although the limited number of investigated compounds in this study doesn't allow a comprehensive disentanglement of (ii) and (iii), the results still show that different compounds have different sensitivities to matrix effects as a function of the matrix mass (i.e. $\partial ME/\partial m_{matrix}$) following the order BAM (1.8±0.1) \approx ATZ (2.0±0.1) \approx DEA (2.2±0.1) < BOSC (5.8±0.4). This suggests that the late-eluting compound on GC BOSC (22.9 min) is the most susceptible to signal enhancement compared with the early-eluting DEA, BAM, and ATZ (12-13.9 min). This agrees with Anastassiades et al.,²⁵⁰ who illustrated that monoacylglycerols, the most abundant matrix component in brown rice,²²⁸ elutes in the late window of chromatography giving rise to the highest matrix effects for late-eluting pesticides. These results demonstrate that the data acquired by QCM dry mass sensing during a typical HPLC clean-up of a complex sample provide, in fact, meaningful information on the efficiency of this clean-up step. The analyst can use the acquired data to minimize matrix co-elution reducing thereby adverse matrix effects in the subsequent analysis.

4.4 Conclusion

The current work presents the successful coupling of a commercial HPLC system with a QCM using a microfluidic spray-dryer. We demonstrate that QCM dry mass sensing is suitable as a holistic detector for quantifying complex organic matrices during HPLC clean-up, in contrast to other detectors such as UV/Vis. Validation against offline TOC analysis confirmed the successful coupling, calibration and data processing strategy and its suitability within a precision of 10%. The demonstrated results of NOM and brown rice matrix, in conjunction with the system's current LOQ (16-52 mg/L), prove that the employed technique is relevant for a large range of real samples in environmental and food chemistry. This can possibly be further extended to other fields (e.g., archaeology, forensics) with similar loads of matrix, whereas further reduction of the systems LOQ may be necessary for more matrix-susceptible samples. The direct correlation found between the amount of brown rice matrix, quantified by QCM dry mass sensing, and matrix effects measured in GC-MS agrees with the established understanding of matrix-induced chromatographic response enhancement. This implies that the developed system can be a useful tool to minimize matrix co-elution reducing thereby adverse matrix effects in
a subsequent analysis, which is the ultimate goal of a clean-up. The exact potential gain of such an optimized clean-up is further evaluated in the companion paper.²²⁹

5 Quartz Crystal Microbalance as Holistic Detector for Quantifying Complex Organic Matrices During Liquid Chromatography: 2. Compound Specific Isotope Analysis

Abstract

In carbon-compound-specific isotope analysis (carbon-CSIA) of environmental micropollutants, purification of samples is often required to guarantee accurate measurements of a target compound. A companion paper has brought forward an innovative approach to couple quartz crystal microbalance (QCM) with high-performance liquid chromatography (HPLC) for online quantification of matrices during a gradient HPLC purification. This paper investigates the benefit for isotope analysis of polar micropollutants typically present in environmental samples. Here, we studied the impact of natural organic matter (NOM) on the isotopic integrity of model analytes and the suitability of the NOM-to-analyte ratio as a proxy for sample purity. We further investigated limitations and enhancement of HPLC purification using QCM on C_{18} and C_8 phases for single- and multiple-targets. Strong isotopic shifts of up to 3.3% towards the isotopic signature of NOM were observed for samples with a NOM-to-analyte ratio ≥ 10 . Thanks to QCM, optimization deteriorated when aiming for simultaneous purification of two or three compounds, leading to up to 2.5% less NOM removal. Our results suggest that one optimized HPLC purification can be achieved through systematic screening of 3 to 5 different gradients thereby leading to a shift of the boundaries of accurate carbon-CSIA by up to two orders of magnitude toward lower micropollutant concentrations.



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5.1 Introduction

Compound-specific isotope analysis (CSIA) has proven to be a powerful tool for identifying environmental contamination sources and delineating their natural and engineered degradation pathways by measuring isotopic ratios (i.e., ¹³C/¹²C, ¹⁵N/¹⁴N) of the contaminant/target analyte at natural abundance.^{2,3,17–19,30,31,33,251–253} To this end, gas chromatography combustion isotope ratio mass spectrometry (GC-c-IRMS) is typically used, where the contaminant is separated from other components in the sample using a GC, then converted in a combustion oven to a universal gas (i.e., CO₂, N₂), and measured using a sector field MS.^{6,21–23} The structural information of the compound gets, however, lost during this process, which makes accurate CSIA susceptible to interferences by concurrent carbon-/ nitrogen-containing constituents in the same sample.³⁻⁵ This represents a challenge for carbon CSIA of polar environmental contaminants that occur in low concentrations, such as pesticides and pharmaceuticals, for the following reasons. (i) The concentrations of such contaminants occur in the ng/L to µg/L range, whereas the potential interferences, namely natural organic matter (NOM), occur at 10^3 to 10^6 higher concentrations in the mg/L range.⁶² (ii) The heterogeneity of NOM, which consists of thousands of different organic compounds found in environmental samples like river water, renders an efficient separation of the target analyte and interferences challenging in one extraction step.^{50,80} While classical mass spectrometry can correct for adverse effects caused by such interferences using, for example, internal standards, ^{42–45} analyte protectants, ^{46,47} or matrix-matched calibration, ^{42,45,48} such corrections are not possible in GC-c-IRMS. Therefore, CSIA critically depends on highly purified samples.

Several purification strategies are at the analyst's disposal to separate target analytes from sample interferences, also referred to as matrix, in carbon-CSIA sample preparation. These strategies range from offline chromatographic techniques using conventional solid-phase extraction (SPE) materials,^{65,66} molecularly imprinted polymers (MIPs),⁵⁶ cyclodextrin polymers,⁵⁰ immunoaffinity chromatography,⁸¹ silica gel chromatography,^{73,74} or ion-exchange chromatography,⁷⁰ to different types of online chromatographic purification techniques including size-exclusion chromatography,⁷² or the most widely used reversed-phase (RP) high-performance liquid chromatography (HPLC).^{28,66,68,75–79} While the target analytes are monitored in most of these works, this is not necessarily the case for all interferences. For example, consider ¹³C/¹²C measurement of atrazine in a groundwater extract containing interfering NOM, where chromatographic clean-up is warranted prior to GC-c-IRMS. To screen for the optimal clean-up conditions, fractions have to be collected, organic solvents removed, the sample reconstituted in water, and each fraction measured using a total organic carbon (TOC) analyzer. On the other hand, quantification of matrix interferences during online purification procedures like HPLC is often hindered by a lack of suitable detectors.²⁵⁴ Detectors usually combined with HPLC are only able to monitor specific fractions of common matrices like NOM (i.e., chromophoric, fluorescent, or ionizable)^{114,115} or show inter-compound response differences, as discussed in detail in the companion paper.^{115–118,254} Alternatively, monitoring and quantifying potential interferences during the purification would, in fact, give insights into the success of the clean-up and its exact gain. We have brought forward in the companion study an innovative approach using quartz crystal microbalance (QCM) dry mass sensing that was coupled to RP HPLC and used to monitor and gravimetrically quantify different types of matrices (NOM, brown rice) during a gradient HPLC purification.²⁵⁴

In the current and the companion study,²⁵⁴ we spray a small part (<1%) of the column effluent on a QCM using a microfluidic spray-dryer, adopting elements of other works by Schulz et al.,¹⁵⁰ Müller et al.,¹⁵¹ and Kartanas et al.¹⁵³ In this process, the column effluent is nebulized into micron-sized droplets, which leads to the immediate evaporation of the solvent and deposits the non-volatile components on the QCM. Their absolute mass is measured due to the QCM's ability to measure mass changes on the oscillating piezoelectric quartz crystal with sub-nanogram resolution.^{119,121} Using this approach, it was possible to quantify matrix interferences in real-time during RP HPLC. Remarkably, these matrix interferences correlated with the extent of matrix effects on observable instrument response (signal enhancement/ suppression) observed during subsequent GC-MS analysis ($R^2 \ge 95$).²⁵⁴ This approach, hence, circumvented challenges for QCM dry mass sensing before application to RP HPLC clean-up through (i) enabling the use of organic solvents including gradients by using a microfluidic spray-dryer, (ii) characterizing variations of the QCM response caused by gradients, and (iii) alleviating the impact of the latter through a suitable calibration strategy.²⁵⁴ It seems ideal to apply this approach for environmental extracts intended for carbon-CSIA measurements after RP HPLC. Yet, a quantitative assessment of the gain of optimizing RP HPLC purification using real-time matrix monitoring has never been conducted — and its impact on accurate carbon-CSIA never been explored.

The work presented in this and the companion paper²⁵⁴ has the overall goal of exploring the feasibility of coupling a commercial HPLC with a microfluidic spray-dryer and a QCM for online monitoring of organic matrix components during RP HPLC gradient purification for different mass spectrometry-based applications in environmental and food sciences. Both studies focus on organic matrices in already extracted samples where most inorganic salts are excluded through a first SPE step. While the technical and fundamental groundwork for matrix online monitoring using QCM dry mass sensing during RP HPLC was laid out in the companion study,²⁵⁴ this paper systematically investigates the purification potential of RP HPLC before ¹³C/¹²C analysis of polar micropollutants present in environmental water samples using GC-c-IRMS. To this end, we (i) studied the impact of NOM on the isotopic integrity of model analytes and whether the NOM-to-analyte ratio ($C_{NOM}/C_{analyte}$, nmol C/nmol C) can be used as a proxy for the sample purity and (ii) investigated limitations and enhancement of HPLC purification using QCM dry mass sensing on C₁₈ and C₈ phases for single- and multiple-targets.

5.2 Experimental Section

5.2.1 Chemicals, Materials, and Samples

A list of purchased chemicals and materials, a description of standard solutions, and working solutions used in this study are provided in the supporting information (section E.1). NOM was extracted from surface water samples as detailed in the companion paper²⁵⁴ and summarized in section E.2. Samples for isotope analysis with different NOM/analyte ratios (10, 20, 50, 100), $C_{NOM}/C_{analyte}$ in mol C/mol C, were prepared in methanol by mixing the stock solution of extracted NOM with stock solution of corresponding analyte to reach an analyte concentration of 1667 nmol C/mL, corresponding to 5 nmol C per injection on GC-c-IRMS. Extracts for HPLC purification were prepared in methanol/water (25/75 v/v) and contained 3 mg/L of eight different model analytes, namely 2,6-dichlorobenzamide (BAM), atrazine (ATZ), azoxystrobin (AZOX), boscalid (BOSC), caffeine (CAF), desethylatrazine (DEA), desisopropylatrazine (DIA), and simazine (SIM), and 9000 mg/L of the extracted river water NOM. These extracts correspond to original water samples with 3.6 mg/L NOM and 120 ng/L analyte.

5.2.2 Chemical Analysis

Compound Specific Isotope Analysis

Carbon isotope measurements were performed on a GC-c-IRMS system consisting of a GC (TRACE GC Ultra multi-channel gas chromatograph, Thermo Fisher Scientific, Germany; Column: J&W DB-5MS UI column, $L = 30 \text{ m} \times \text{ID} = 0.25 \times \text{film thickness} = 1.0 \text{ µm}$, Agilent, Germany), a combustion interface (Finnigan GC Combustion III interface, Thermo Fisher Scientific, Germany), and an IRMS (Finnigan MAT 253 IRMS, Thermo Fisher Scientific, Germany). The combustion interface consisted of an oxidation reactor (1050 °C) with an alumina tube (L = 320 mm, ID = 0.5 mm, OD = 1.5 mm, Friatec, Germany) containing one platinum wire (D = 0.1 mm, 99.99% purity, Goodfellow, GB) and two nickel wires (D = 0.1 mm, 99.99% purity, Alfa Aesar, Germany). An identical alumina tube enclosing three copper wires (0.1 mm diameter, 99.99% purity, Alfa Aeser, Germany) was used for the reduction reactor (650 °C). Extracts in methanol were injected (3 µL injection volume) using an autosampler (GC PAL, CTC, Switzerland) with splitless injection mode (liner: ID = $5 \text{ mm} \times \text{L} = 105 \text{ mm}$, Thermo Fisher Scientific, Germany) at 250 at a surge pressure of 250 kPa. Analytes were separated at a helium flow of 1.4 mL/min using the following temperature program. The starting temperature was 120 °C (1 min hold time), followed by a temperature ramp of 22 °C/min to 250 °C, and a ramp of 40 °C/min to 325 °C (9 min hold time). The peaks were automatically detected and baseline-corrected (individual background algorithm) using the Isodat software of Thermo Fisher Scientific, Germany. Isotope ratios were calculated in relation to a CO₂ reference gas (Carbo, Germany) and are reported as arithmetic means of at least triplicate measurements as δ^{13} C values (in ∞) with the respective 95% Confidence Interval (CI) relative to the international reference material Vienna PeeDee Belemnite (VPDB).²⁵⁵ In addition, standard bracketing procedures were used to ensure identical treatment of standard and sample²⁵⁶ and method quantification limits were determined according to the moving mean procedure (see Figure A.4.1 and Table A.4.5).⁶⁴

High-Performance Liquid Chromatography

A Nexera XR HPLC system (Shimadzu, Japan) was used for chromatographic separation. It consists of a solvent delivery module (LC-20AD, Shimadzu, Japan), a diode array detector (DAD) (SPD-M20A, Shimadzu, Japan), and a fraction collector (FRC-10A, Shimadzu, Japan). As the stationary phase, two different columns were used: XTerra RP18 column (particle size = $3.5 \mu m$, L×D = $150 \times 3.0 mm$, pore size = 125 Å, Waters, USA) and Orbit 100 C8 column (particle size = $3.5 \mu m$, L×D = $150 \times 3.0 mm$, pore size = 100 Å, MZ Analysentechnik, Germany). As the mobile phase, binary gradients consisting of water (A) and methanol/water (90/10 v/v) (B) were used. A column oven temperature of 40, a flow rate of 0.5 mL/min, and a sample injection volume of 200 µL were used for all measurements. Using the DAD detector, the retention time and peak width of each analyte were determined at the corresponding maximum absorption wavelength and used to constrain the fraction in which the analyte was completely recovered. For HPLC optimization, the RP gradient conditions were systematically varied by changing the percentage of CH₃OH in the mobile phase at minute 7.5 (30, 40, 50, 60, 70, 80, or 90%) and minute 15 (60, 70, 80, or 90%) covering thereby linear, concave, and convex gradients. Twenty-two and 7 different gradients were studied for XTerra RP18 column and Orbit 100 C8 column, respectively (see Table A.4.7 and A.4.8).

QCM Dry Mass Sensing Coupled to HPLC

The QCM dry mass sensing system was coupled to the HPLC, characterized, and validated as described in detail in the companion paper.²⁵⁴ In short, the HPLC effluent was split after the DAD detector and prior to the fraction collector using a post-column adjustable flow splitter. The high-flow port was connected to the fraction collector, whereas the low-flow port to a microfluidic spray-dryer. The latter was fabricated in-house using a standard polydimethylsiloxane (PDMS) soft lithography approach.²⁵⁴ Using the spray-dryer, the HPLC effluent was sprayed onto a 5 MHz QCM crystal (100RX1, Cr/Au, Stanford Research Systems, USA) placed in a frequency counter (QCM200, gate time: 0.1 s, Stanford Research Systems, USA). Each measurement consisted of a blank run (methanol/water 25/75 v/v), the sample (NOM-containing extract), and a one-point calibration (c(NaCl) = 300 mg/L in mobile phase), which were used to derive the concentration of matrix in mg/L in the sample during chromatography.

5.2.3 Data Evaluation

QCM Dry Mass Sensing

The QCM dry mass sensing data was evaluated using a Matlab script as reported in the companion paper.²⁵⁴ In short, after correcting the frequency measurement of the sample and that of the calibration using the one of the blank, the 1st derivative was derived from the corrected frequencies. Then, 1st derivatives were smoothed using a Savitzky-Golay filter. To get the mass concentration of the sample in mg/L, the smoothed 1st derivative of the sample measurement was divided by the smoothed 1st derivative of the calibration measurement and multiplied by the concentration of the calibration solution (see Eq. 1 in companion paper²⁵⁴).

C_{NOM}/C_{analyte} Ratio and Gain Factor

The $C_{NOM}/C_{analyte}$ ratio in mol C/mol C before HPLC purification ($[C_{NOM}/C_{analyte}]_{no LC}$) was calculated by dividing the molar concentration of NOM by the molar concentration of the respective analyte in the extract. To calculate the $C_{NOM}/C_{analyte}$ ratio after the HPLC purification ($[C_{NOM}/C_{analyte}]_{LC}$), the integral of the NOM data measured using QCM dry mass sensing during the HPLC purification was taken over the corresponding time window of the analyte peak (area_{fraction}). The latter was divided by the integral of the NOM data over the whole chromatogram (area_{total}), where complete recovery of NOM was validated, to get the percentage of NOM co-eluting during the analyte fraction (see Eq. 5.1).

$$NOM_{co-elution} = \frac{area_{fraction}}{area_{total}} \cdot 100$$
(5.1)

 $[C_{NOM}/C_{analyte}]_{no LC}$ was multiplied by the percentage of NOM co-eluting in the respective fraction to get $[C_{NOM}/C_{analyte}]_{LC}$ (see Eq. 5.2).

$$[C_{\text{NOM}}/C_{\text{analyte}}]_{\text{LC}} = \frac{\text{NOM}_{\text{co-elution}} \cdot [C_{\text{NOM}}/C_{\text{analyte}}]_{\text{no LC}}}{100}$$
(5.2)

The gain factor, which is the factor by which the $C_{NOM}/C_{analyte}$ was improved, was calculated by dividing $[C_{NOM}/C_{analyte}]_{no LC}$ by $[C_{NOM}/C_{analyte}]_{LC}$ (see Eq 5.3).

$$gain \ factor = \frac{[C_{\text{NOM}}/C_{\text{analyte}}]_{\text{no LC}}}{[C_{\text{NOM}}/C_{\text{analyte}}]_{\text{LC}}}$$
(5.3)

Matrix Removal for Individual and Multiple Compounds

The matrix removal in % for individual compounds was calculated by subtracting the percentage of co-eluting NOM from 100 (see Eq. 5.4).

matrix removal_{individual} =
$$100 - \text{NOM}_{\text{co-elution}}$$
 (5.4)



Figure 5.1 Gradient screening for the individual compounds CAF and BOSC and their NOM co-elution average for HPLC purification on XTerra RP18 of both compounds at the same time (CAF+BOSC). The optimal gradient with the lowest NOM co-elution is encircled both for the individual compound purification (CAF, BOSC, gradient_i) and multiple compound purification (CAF+BOSC, gradient_m). The arrows show the difference between the optimal gradient_i and the optimal gradient_m, the number next to the arrows the difference of NOM co-elution in % between gradient_i and gradient_m.

To determine the maximal matrix removal during multiple compound purification, we added for each investigated HPLC gradient the respective matrix removal of the individual compounds and divided the value by the number of compounds n to get the average matrix removal for n-compounds (matrix removal_{n-compounds}) (see Eq. 5.5; see examples in Figure 5.1 and A.4.15).

matrix removal_{n-compounds} =
$$\frac{\sum_{k=1}^{n} \text{matrix removal } (k)}{n}$$
 (5.5)

This calculation was made for each HPLC gradient separately. The gradient with the highest matrix removal_{n-compounds} (gradient_m) was selected as the optimal gradient for the respective combination of compounds. The exact matrix removal of each of the compounds for gradient_m was used as the maximal matrix removal for this exact purification problem. The difference between the optimal gradient determined for the individual compound (gradient_i) and gradient_m is reported as loss in matrix removal. Repeating this procedure for several combinations of two or three early, middle, and late eluting compounds (see Table A.4.17 and A.4.18) made it possible to determine an average matrix removal and to plot the different determined numbers in a box plot (see Figure 5.5).

5.3 Results and Discussion

5.3.1 Natural Organic Matter-to-Analyte Ratio as Proxy for Sample Purity and its Impact on Isotopic Integrity

We assessed the NOM/analyte ratio, $C_{NOM}/C_{analyte}$ in mol C/mol C, as representative indicator of sample purity and its impact on accurate isotope analysis. Figure 5.2a shows measured δ^{13} C values on GC-c-IRMS of four different model analytes, namely DIA (δ^{13} C = -36.8±0.5‰), ATZ (-29.6±0.5‰), DEA (-29.4±0.5‰), and CAF (δ^{13} C = -1.2±0.5‰), in extracts containing different C_{NOM}/C_{analyte} ratios (10, 20, 50, 100 mol C/mol C) and compared to standard measurements in the absence of NOM. Analyte concentrations were kept constant for all



Figure 5.2 (a) The isotope value of standard measurements of four different analytes (DEA: green, ATZ: black, DIA: red, CAF: blue) is plotted against the isotope value measured in extracts containing NOM in different $C_{NOM}/C_{analyte}$ ratios (10: triangle up, 20: triangle down, 50: circle, 100: diamond). The range of typical NOM isotope values ($\delta^{13}C = 27\pm1\%$) is highlighted (brown circle). (a1-a3) show the enlarged areas of the four analytes. (a1) gray: Extract with concentration of NOM equal to ratio 100 was subjected to HPLC clean-up using XTerra RP18 (see HPLC gradient in Table A.4.4). The respective fraction of DIA was collected, the solvents evaporated, NOM reconstituted and spiked with DIA to reach an analyte concentration of 1667 nmol C/mL and a total volume equal to the original NOM extract (200 µL). (b1-b4) Correlation of the background intensity (m/z 44/ mV) at the respective analyte retention time in the GC-c-IRMS chromatogram and the amount of NOM injected.

samples at 5 nmol C injected in each measurement, corresponding to concentrations of 57.9 mg/L (DIA), 44.9 mg/L (ATZ), 52.1 mg/L (DEA), and 40.5 mg/L (CAF) in the extract. The corresponding background intensities at m/z 44 are depicted in Figure 5.2b at the respective analyte retention time in the GC-c-IRMS chromatogram as a function of $C_{NOM}/C_{analyte}$.

We observed significant δ^{13} C shifts in the presence of NOM for DIA (Figure 5.2a1, red data, positive shift) and CAF (Figure 5.2a3, blue data, negative shift), while no significant shifts are visible for ATZ and DEA (Figure 5.2a2, black and green data). The absence of isotopic shifts for ATZ and DEA confirms the observation of Glöckler et al.⁵⁰ that compounds with an isotopic signature close to the one of NOM do not suffer from isotopic shifts induced by the sample matrix. Indeed, $\delta^{13}C$ of ATZ (-29.6±0.5‰) and DEA (-29.4±0.5‰) are both in the proximity of that of NOM $(-27\pm1\%)^{257}$ on the carbon isotopic scale. This implies that the obtained δ^{13} C values of the analytes are not only attributable to the compound but, strictly speaking, a bulk measurement of analyte and matrix. In contrast, the effect of NOM on δ^{13} C integrity of DIA (-36.8±0.5‰) and CAF $(-1.2\pm0.5\%)$ is evident and becomes most pronounced the greater the distance of their isotopic signatures to that of NOM is. This is corroborated by the direction of the isotopic shift, which consistently goes in the direction of the isotopic signature of NOM (postive for DIA, negative for CAF), and the magnitude of the shift, which is greater for CAF ($\delta^{13}C_{sample} - \delta^{13}C_{standard}$ for $C_{NOM}/C_{analyte}$ ratio 100: -3.3±0.8‰) compared to DIA $(+1.3\pm0.6\%)$ reflecting the greater difference to the one of NOM on the isotopic scale (CAF-NOM = +25.8±1.1, DIA-NOM = -9.8 ± 1.1). Even the magnitude of isotopic shifts is progressively following the C_{NOM}/C_{analyte} ratios (see arrow in Figure 5.2a1&a3 and Figure A.4.2 in the supporting information). The observed deviation is, however, not precisely the composite of the background and the peak due to the applied individual background algorithm implemented in the Isodat software: The measured shift for CAF for $C_{NOM}/C_{analyte}$ ratio 100 ($\Delta \delta$ ¹³C = -3.3‰) is, for example, four times smaller than the theoretically determined isotope shift using the ratio of background area to analyte area (-14.5%) (see Table A.4.6). This shows that the applied background correction can reduce the influence of NOM but not entirely compensate for it, as already illustrated by Glöckler et al.⁵⁰

The influence of the matrix NOM on the measurement can also be seen in the IRMS chromatograms. A distinct hump-shaped baseline rise is visible in the samples containing NOM (see Figure 5.3). We found a direct correlation ($R^2 \ge 0.999$) between the amount of NOM injected and the background intensity (m/z 44) recorded on the IRMS at the respective analyte retention times for all compounds (see Figure 5.2b). Consequently, the ratio of injected matrix and analyte, $C_{NOM}/C_{analyte}$, seems to be a good proxy of sample purity as proposed by Bakkour et al.⁵⁶ and Glöckler et al.⁵⁰ Accurate isotope values of DIA were only measured for $C_{NOM}/C_{analyte} \le 10$ (Figure 5.2a1 and Figure A.4.2). To further probe for this, we moved the $C_{NOM}/C_{analyte}$ ratio from 100 to 8 using HPLC purification and were thus able to recover the isotope integrity of the analyte (Figure 5.2a1 grey data point). For CAF, a $C_{NOM}/C_{analyte}$ of 10 was not sufficient to resolve the target analyte peak and guarantee accurate isotope analysis (Figure 5.2a3 and Figure A.4.2). Upon comparing these findings with data



Figure 5.3 GC-IRMS chromatograms of DEA and CAF for different C_{NOM}/C_{analyte} ratios.

published in the existing literature for other analytes, a noticeable range of approximately a $C_{NOM}/C_{analyte}$ ratio of 10 or slightly less emerges.^{49,50} The exact $C_{NOM}/C_{analyte}$ ratio guaranteeing accurate isotope analysis varies depending on the analyte, the distance between the signature of the analyte and NOM on the isotopic scale, and the used GC method. This highlights the importance of (i) including standards spanning over a range of isotope signatures in carbon-CSIA method development and (ii) the purity of the sample as a strategy to avoid systematic bias in isotope values. Samples containing NOM in higher amounts therefore warrant sufficient sample purification procedures to guarantee accurate isotope analysis.

5.3.2 Limitations and Enhancement of Preparative Chromatography Revealed by QCM Dry Mass Sensing

To quantitatively assess the limits and possible enhancement of typical preparative chromatography clean-up steps in removing organic matrix from a sample extract, we selected 8 model compounds (CAF, BAM, DIA, DEA, SIM, ATZ, AZOX, BOSC; $\log K_{OW}$ range: -0.07-2.96) present in an extract containing NOM as organic matrix and subjected them to HPLC clean-up using a C₁₈ stationary phase (XTerra RP18), a classical phase used in many CSIA applications (see Table A.4.19). Binary solvent mixtures of water and CH₃OH were systematically varied by changing the percentage of CH₃OH in the mobile phase at minute 7.5 and minute 15 thus covering linear, concave, and convex gradients (see illustrative gradients in Figure 5.4a; all gradients in Table A.4.7 and A.4.8). NOM concentrations in the HPLC effluent were acquired using QCM dry mass sensing, whereas analyte retention times were monitored using UV-Visible spectroscopy (UV/Vis) detection at the corresponding maximum absorption wavelength. Figure 5.4b depicts fractions of analytes at the corresponding retention time window where the analyte is completely recovered (coloured vertical bars), whereas the area underneath



Figure 5.4 (a) Seven out of the 22 measured gradients with varying % of CH₃OH in the mobile phase till minute 7.5 (blue; 30, 40, 50, 60, 70, 80, or 90%) and minute 15 (grey; 60, 70, 80, or 90%). (b) Chromatogram (gradient 10-60-70) shows both the analyte peaks detected using UV/Vis for CAF, DEA, SIM, and BOSC (dotted grey line) and NOM in %/min quantified using QCM dry mass sensing (black line). The amount of co-eluting NOM during the analyte retention time is integrated (colorful areas) and divided by the total amount of NOM measured to receive a number of the percentage of NOM co-eluting with the analyte (corresponding colour). (c-f) The NOM co-elution in % is plotted for the 22 different gradients for 4 analytes ((c): CAF, (d): DEA, (e): SIM, (f): BOSC). The second axis shows the $C_{NOM}/C_{analyte}$ ratio after the purification step corresponding to BOSCs ratio in the original extract of 2383. The minima are encircled using a black dotted line, the maxima using a black solid line.

Table 5.1 Reduction of the $C_{NOM}/C_{analyte}$ ratio during HPLC purification of the Oasis HLB extract of a water sample containing 120 ng/L of each respective analyte and 1.8 mgC/L NOM. The Table displays the $C_{NOM}/C_{analyte}$ (nmol C/nmol C) ratio in the extract (no LC), the reduced ratio for the gradient on XTerra RP18 that showed the highest (LC_{XTerra RP18}) and the lowest (optim-LC_{XTerra RP18}) NOM co-extraction, and the lowest (optim-LC_{Orbit 100 C8}) co-extraction on Orbit 100 C8. It also shows the gain factor, which is calculated by dividing the $C_{NOM}/C_{analyte}$ ratio before the clean-up ("no LC") by the $C_{NOM}/C_{analyte}$ ratio after the respective clean-up. The matrix removal in % is shown in brackets. The analytes are classified in early-, middle-, and late-eluting substances depending on their retention behaviour during the 22 investigated gradients and listed in the order of their retention time.

	ea	arly-elutii	ng	middle	-eluting	1	ate-elutin	g
	CAF	BAM	DIA	DEA	SIM	ATZ	AZOX	BOSC
logKow	-0.07	0.77	1.50	1.51	2.18	2.61	2.50	2.96
no LC	3034	3393	4343	3909	3601	3370	2292	2383
LC _{XTerra RP18}	448	347	548	453	417	403	264	207
gain factor	7	10	8	9	9	8	9	12
matrix removal (%)	(85.3)	(89.8)	(87.4)	(88.4)	(88.4)	(88.0)	(88.5)	(91.3)
optim-LC _{XTerra RP18}	242	215	296	281	192	107	53	47
gain factor	13	16	15	14	19	31	44	51
matrix removal (%)	(92.0)	(93.7)	(93.2)	(92.8)	(94.7)	(96.8)	(97.7)	(98.0)
optim-LC _{Orbit 100 C8}	96	156	206	271	129	78	14	4
gain factor	32	22	21	14	28	44	167	556
matrix removal (%)	(96.8)	(95.4)	(95.3)	(93.1)	(96.4)	(97.7)	(99.4)	(99.8)

represents the percentage of co-eluting NOM in the respective fraction and thus the $C_{NOM}/C_{analyte}$ ratio. Changes of NOM co-eluting in each fraction are shown as heat maps for different gradients in Figure 5.4c-f, where the x-axis represents the percentage of CH₃OH in the mobile phase at minute 7.5 and the left y-axis at minute 15, whereas the colour code represents the percentage of co-eluting NOM as well as $C_{NOM}/C_{analyte}$ ratio at the right y-axis. To reduce the complexity of the figure, data for CAF, DEA, SIM, and BOSC are shown here, whereas the data for BAM, DIA, ATZ, and AZOX are shown in Figure A.4.3 (all NOM co-elution data are summarized in Table A.4.10 and A.4.11).

Gains from an Individual Compound Perspective

A single HPLC purification of an extract of a 5L water sample containing 1.8 mgC/L NOM (post-spiked after the extraction with each respective analyte to correspond to 120 ng/L in the original water sample) could remove between 85-91% of the co-extracted NOM (see Table 5.1, "LC_{XTerra RP18} matrix removal"). This corresponds to a remaining percentage of co-eluting NOM in each fraction of between 9-15% of the original NOM concentration (see Figure 5.4c-f solid marked areas). The C_{NOM}/C_{analyte} ratio in the extract could thus be reduced by a factor of 7 to 12 from ratios ranging between 2292 and 4343 to down to between 207 and 548. While these results show the substantial purification potential of HPLC using a typical C₁₈ column without any method development, the C_{NOM}/C_{analyte} ratio is still too high for accurate carbon-CSIA (\leq 10). This highlights the need for optimizing HPLC purification. In fact, screening for 22 gradients using QCM dry mass sensing made it possible to remove an additional 6.7% NOM in the retention window of CAF, 3.7% in the window of DEA, 6.3% of SIM, and



Figure 5.5 Removal of NOM (in %) in the fraction of early-, middle-, or late-eluting compounds during the purification of one individual compound or multiple compounds for both columns. The dashed upward arrow annotates the trend of elution regions early<middle<late, the dotted downward arrow the compound number trend 1>2>3.

6.7% of BOSC (see Figure 5.4c-f, dashed marked areas). These gains are significant considering the associated uncertainties between 0.1% and 1.1% according to triplicate to sextuplicate measurements (see Table A.4.10 and A.4.11). Using the QCM optimized HPLC purification, the $C_{NOM}/C_{analyte}$ ratios could be reduced to between 47 and 296 ("optim-LC_{XTerra RP18}"), corresponding to gain factors between 13 and 51 compared to no clean-up ("no LC") and to gain factors between 2 to 5 compared to not optimized LC ("LC_{XTerra RP18}").

An optimized single clean-up on XTerra RP18 leads to larger gain factors for late-eluting compounds (31-51), compared with early- (13-16) and middle-eluting compounds (14-19). These results are meaningful given the shape of the NOM hump that can be influenced more for the late eluting compounds than for the early and middle ones eluting directly with the main part of the NOM hump (see Figure 5.4b). Yet, $C_{NOM}/C_{analyte} =$ 47-296 are significantly above the required value for accurate carbon-CSIA (≤ 10). This is not surprising given the concentration of the target analytes and NOM in the investigated water sample (1.8 mgC/L NOM, 120 ng/L analyte). This highlights that residuals of NOM of as low as 2% in the collected fraction of such a sample require further optimization, even when recovering 100% of the target analyte. Therefore, we assessed the potential for NOM removal on a different stationary HPLC phase, namely a column Orbit 100 C8, which offers a higher theoretical plate number (see Table A.4.9) for the investigated compounds and, thereby, possesses a higher retention and smaller peak width presumably leading to an even lower NOM co-elution and thus lower C_{NOM}/C_{analyte} ratios. Indeed, it was possible to reach an NOM removal of between 93.1 and 99.8% (see results for all gradients in A.4.12 and A.4.13) leading to gain factors for early- (21-32), middle- (14-28), and late-eluting compounds (167-556) as shown in Table 5.1 "optim-LC_{Orbit 100 C8}". Thanks to the QCM, it was therefore possible to remove up to 99.8% of the matrix for BOSC with a single optimized clean-up leading to a $C_{NOM}/C_{analyte}$ ratio = 4, which is smaller than the suggested value of 10.

Trade-Offs between Single- and Multiple-Targets

Purifying more than one compound in a single HPLC purification run is expected to lead to trade-offs in the potential of maximal NOM removal. Therefore, we quantified the maximal NOM removal (lowest percentage of co-eluting NOM depicted in the dashed area of Figure 5.4 and A.4.3) when optimizing HPLC purification for only one compound at a time and compared it with the NOM removal determined for the optimised purification for multiple targets over the whole chromatographic run, covering thereby combinations of early, middle, and late eluting compounds (see Figure 5.5).

Efficiency of HPLC purification deteriorates when aiming for simultaneous purification of two (orange) or three compounds (blue) compared to an individual compound (black) as seen by the maximal NOM removal denoted as dotted downward arrows in Figure 5.5. For (a) early eluting compounds on XTerra RP18, 92.0% NOM can be removed on average when purifying two compounds and 91.0% during the purification of three compared with one (93.0%). The same holds true for (b) middle (1: 93.7%, 2: 92.4%, 3: 92.0%) and (c) late eluting compounds (1: 97.5%, 2: 96.0%, 3: 95.2%). The trend of the NOM removal for individual and multiple compounds is consistent within each elution region following the order early<middle<late (denoted as dashed upward arrow). This picture may vary dependent on the chromatographic behaviour of different matrices, as well as on the exact combination of compounds used (see Table A.4.17 and A.4.18 and Figure 5.1 and A.4.13-A.4.15). For example, the maximal NOM removal determined for late eluting compounds in combination with middle eluting ones (96.7%) is higher in comparison to the simultaneous purification with early eluting compounds (95.3%).

Similar trends were observed on a different column, namely Orbit 100 C8, which further corroborates the acquired results (see Figure 5.5d,e). The data on the middle eluting compounds on Orbit 100 C8 is not shown since we did not determine any variations between the different combinations. Nonetheless, the determined maximal NOM removal on Orbit 100 C8 is higher in comparison with the XTerra RP18 column. In fact, the average NOM removal for three compounds on Orbit 100 C8 ("early": 93.1%, "late": 97.5%, see Figure 5.5d,e) is equal to the individual compound NOM removal on XTerra RP18 ("early": 93.0%, "late": 97.5%, see Figure 5.5a,c), highlighting the importance of column choice. Although the differences in the maximal NOM removal for one, two, or three compounds might seem small, they are significant considering the precision of these measurements ($\pm 0.1-1.1\%$) and their impact on the C_{NOM}/C_{analyte} ratios. This can be illustrated using the example of BOSC, where the C_{NOM}/C_{analyte} ratio changes from 4 for the individual compound to 26 on average for two and to 44 on average for three compounds, thus preventing accurate carbon-CSIA measurements in the latter cases.



Figure 5.6 Dependence of accurate isotope analysis on the analyte and NOM concentration in the real-world water sample for (a) BAM (early-eluting) and (b) BOSC (late-eluting) for different sample preparation strategies: SPE using Oasis HLB (black), plus an HPLC purification (red), or plus an optimized HPLC purification (blue).

5.4 Conclusion and Analytical Implications

The present work systematically demonstrates that QCM dry mass sensing is a valuable auxiliary tool for optimizing matrix removal during a classical clean-up of extracts prior to carbon-CSIA. In fact, this is the first study to report quantitative efficiencies of RP HPLC clean-up that amounted to matrix removal up to 99.8% upon optimization. On average, the maximal matrix removal within a precision of 1% could be determined by screening 3 to 5 different gradients, including convex, concave, and linear gradients (see Table A.4.14 and A.4.15 and Figures A.4.5-A.4.12), thus demonstrating that a systematic method development with the help of QCM dry mass sensing yields substantial benefits with reasonable efforts.

The discrepancies in gain factors of an HPLC clean-up between early- and late-eluting compounds have analytical implications for carbon-CSIA. This is depicted in Figure 5.6 for one early-eluting compound (BAM, Figure 5.6a) and one late-eluting compound (BOSC, Figure 5.6b), where limits of accurate carbon-CSIA are shown as a function of environmental analyte concentration (x-axis), NOM concentration (y-axis), and efficiency of the HPLC purification (red and blue arrows). While for both model compounds these limits can be shifted by approximately a factor of 10 to lower analyte concentrations using one HPLC purification (red arrow), a factor of up to 500 can be gained instead for a late-eluting compound by optimizing the HPLC purification (blue arrow). In contrast, only a factor of approximately 20 can be gained for an early-eluting compound. These findings are meaningful since the challenge of separating small polar compounds using RP columns is well known.^{258–260} Potentially, a column phase engineered for these compounds (e.g., HILIC)^{261,262} could result in a better separation of early eluting compounds and NOM and thus a higher NOM removal during purification. To put these findings in a larger context of complete sample preparation for carbon-CSIA, an overall higher removal can become possible when combining the targeted HPLC cleanup presented here with the use of more selective SPE materials (e.g., cyclodextrins)⁵⁰ to replace OASIS HLB in the first extraction step, making it possible to measure concentrations ≥ 100 ng/L for BAM and ≥ 3 ng/L for BOSC in a groundwater sample containing 0.5 mgC/L NOM.

The use of NOM elution data for a given matrix is, furthermore, not limited to the 8 model compounds investigated in this study. Combined with software tools that can predict the analyte retention time and peak width,²⁶³⁻²⁶⁵ it is possible to determine the C_{NOM}/C_{analyte} ratio for any given analyte and thus the feasibility of carbon-CSIA. Creating in the future an openly available database for different samples and matrices can be very useful for researchers and can open the door to training artificial intelligence and prediction tools to assist in the optimization of sample preparation for targeted analysis.

6 Conclusion and Outlook

The overarching goal of this dissertation was to expand the applicability of CSIA to polar, non-volatile compounds present in real-world samples in the low ng/L concentration range. In particular, the research focused on addressing the significant analytical challenges associated with the lack of selectivity in compound-specific isotope analysis (CSIA) sample preparation and the tediousness of these sample preparation workflows. To this end, the present work investigated the effectiveness of strategies to optimize the matrix removal during the purification of sample extract prior to gas chromatography isotope ratio mass spectrometry (GC-IRMS) isotope analysis. This work supplements earlier research efforts addressing the identical analytical issue, wherein substantial efforts were dedicated to introducing new selective extraction/purification techniques to the CSIA sample preparation workflow. The results of this dissertation stress the importance of optimizing the matrix removal during sample purification in a targeted way to enable accurate CSIA of complex real-world samples. In particular, the presented approach of optimizing reversed-phase high-performance liquid chromatography (RP HPLC) purification by online quantifying matrix compounds using quartz crystal microbalance (QCM) dry mass sensing paves the way for (i) faster development of purification methods, (ii) a significantly improved selectivity of chromatographic purification, and (iii) new applications of CSIA for compounds present in complex samples at low to mid ng/L concentrations.

6.1 Implications of Charge of the Sample Matrix on its Sorption on Molecularly Imprinted Polymers

Chapter 2 investigated the influence of the charge of natural organic matter (NOM) on non-specific sorption of NOM during molecularly imprinted solid phase extraction (MISPE) by reducing the charge density of NOM using methylation of acidic functional groups. Breakthrough curves revealed a stronger interaction between the methylated NOM and the MIP, leading to nearly 30% more NOM binding to the MIP. This is most likely the result of smaller electrostatic repulsion between NOM molecules resulting from the significantly reduced charge density. These results demonstrate the importance of studying the underlying intermolecular mechanisms to understand non-specific sorption of matrix compounds on selective sorbent materials like MIPs. Further research should focus on developing techniques to use this electrostatic repulsion to increase the selectivity of MISPE and, thus, matrix removal before CSIA.

6.2 Effectiveness and Limitations of Quartz Crystal Microbalance for Online Quantification of Matrix Compounds during Liquid Chromatography

The central part of the thesis addressed the challenge of developing a detection technique that can quantify matrix components online during liquid chromatography. It was hypothesized that such a detector could help to optimize the separation of the target analyte and the matrix, thus significantly improving the removal of co-extracted sample matrix during the respective chromatographic purification of the sample extract to reduce adverse effects of the sample matrix during the subsequent measurement of the target analyte using GC-MS and GC-IRMS. The present work systematically investigated the possibilities and limitations of using QCM liquid sensing (see chapter 3) and QCM dry mass sensing (see chapters 4 and 5) for this purpose.

6.2.1 Effectiveness and Limitations of QCM Liquid Sensing

To quantify matrix components in the liquid phase using QCM liquid sensing, first, the challenge of finding a suitable coating for the QCM sensor that (i) can extract the entirety of NOM previously extracted from the water sample with a (ii) sufficient capacity had to be tackled. Chapter 3 demonstrates for the first time the successful grafting of a hyper crosslinked divinylbenzene ethylene glycol dimethacrylate (DVB-EGDMA) co-polymer layer onto a QCM sensor using radical polymerization. It was possible to graft the polymer layer with a 200-300 nm thickness inside the dynamic range of QCM measurements.^{120,216} Humic acids did sorb onto the grafted co-polymer during sorption experiments leading to a frequency decrease of 18-20 Hz. This is at the higher end of the frequency decrease observed in other studies for a variety of polymer coatings.^{131,134,136,143} However, this number is still too low for the purpose of matrix online monitoring. Additionally, it was not possible to regenerate the sorption abilities of the grafted DVB-EGDMA co-polymer layer by (i) increasing the layer thickness while staying inside the QCM's dynamic range and (ii) further improving the homogeneity of the grafted polymer layer. Furthermore, future research can build upon the established grafting and characterization procedure to coat the QCM sensor with other co-polymers to gain valuable insights into sorption processes.

6.2.2 Effectiveness and Limitations of QCM Dry Mass Sensing

While there is still a long way to go to monitor matrix compounds online using QCM liquid sensing, QCM dry mass sensing proved to be suitable as a holistic detector for the quantification of complex organic matrices during gradient RP HPLC purification. Chapters 4 and 5 systematically investigated how a QCM can be coupled to a commercial HPLC using a post-column adjustable flow splitter and a microfluidic spray-dryer, developed a measurement and data processing strategy, assessed how it can be used for the quantification of matrix

components during a typical gradient RP HPLC purification, and applied it to different mass spectrometrybased applications. It was possible to overcome challenges of organic solvent gradients (i.e., constantly changing spraying/evaporation behavior) for QCM dry mass sensing by calibrating the system using a constant NaCl concentration in the HPLC eluate. Validating the measurement approach and characterizing the system's upper and lower limit of quantification, precision, and accuracy confirmed the relevance of the approach for a large set of real-world samples in environmental and food chemistry and demonstrated the successful integration of QCM dry mass sensing as auxiliary detector into HPLC purification workflows. Comparing the results acquired with the QCM for a chromatographic application of a complex food sample with the ones obtained with UV-Visible spectroscopy (UV/Vis) detection demonstrated the unsuitability of UV/Vis for such a complex sample. It emphasized again the need for a universal detector like a QCM for the chromatographic separation of target analytes from complex matrices.

Optimizing HPLC purification of an environmental extract using the combined data of UV/Vis detection for the retention of the target analyte and QCM for the retention of matrix compounds led to 93-99.8% NOM being removed from target analytes eluting at retention times spanning over the whole chromatogram. Furthermore, using the data measured with the QCM, it was possible to find optimal HPLC gradients for the simultaneous purification of multiple targets; this, however, led to up to 2.5% less NOM removal. On average, the maximal matrix removal could be determined by screening 3 to 5 different gradients, thus demonstrating that a systematic method development with the help of QCM dry mass sensing yields substantial benefits with reasonable effort.

Applying the QCM as a holistic detector for quantifying complex organic matrices during RP HPLC for subsequent (i) pesticide residue analysis in food using GC-MS and (ii) carbon-CSIA of environmental aquatic micropollutants demonstrated the validity and the applicability of the approach and the benefit this technique can bring to many matrix susceptible analytical applications. (i) In GC-MS residue analysis, significantly different matrix effects (up to 345%) were determined for different chromatographic fractions for several model compounds (DEA, BAM, ATZ, Prop, BOSC). Together with the newly established correlation between the amount of matrix quantified by QCM dry mass sensing and matrix effects measured during the subsequent GC-MS analysis, this shows that QCM dry mass sensing can be a valuable tool to the analyst where HPLC clean-up is routinely performed to reduce adverse effects caused by the sample matrix. (ii) Carbon-CSIA, especially, proved to be highly susceptible to the sample matrix. A direct correlation was found between the mass of NOM injected and the background intensity measured. This matrix background highly affected the accuracy of the isotope measurement, leading to strong isotopic shifts of up to 3.3% and becoming greater the higher the amount of matrix in the sample was and the greater the distance of the isotopic signature of the target analyte to that of NOM was. Systematic investigations of the impact of the ratio of injected matrix and analyte, C_{NOM}/C_{analyte}, on the accuracy of carbon-CSIA further corroborated the hypothesis and findings of Bakkour et al.⁵⁶ and Glöckler et al.⁵⁰ that the C_{NOM}/C_{analyte} ratio is a good proxy of sample purity and that accurate carbon-CSIA necessitates a $C_{NOM}/C_{analyte}$ ratio in the purified sample extract of below 10. This highlights the importance of (i) including standards spanning over a range of isotope signatures in carbon-CSIA method development and (ii) the purity of the sample as a strategy to avoid systematic bias in isotope values. Carbon-CSIA can thus benefit significantly from a sample purification optimized with a semi-universal detector like the QCM, whose purification power can shift the boundaries of accurate carbon-CSIA by up to two orders of magnitude toward lower micropollutant concentrations.

6.3 Perspectives for Micropollutant CSIA in Field Studies

Altogether, the findings of chapters 4 and 5 emphasize the importance (i) of suitable detection techniques for the specific requirements of analytical tasks and (ii) of optimized, highly selective, and automated purification techniques for sample clean-up to use the full potential of CSIA. To put these findings in a larger context of complete sample preparation for carbon-CSIA and to provide the analyst with a more general tool at hand, Table 6.1 summarizes the sample preparation strategies for different NOM and analyte concentration levels expressed as $C_{NOM}/C_{analyte}$ ratios.

For highly contaminated fields (level 1), an extraction using a classical sorbent like Oasis HLB is enough (Ext; NOM removal: 90-95%). For pollutants in the low μ g/L range (level 2), using a more selective SPE during the extraction of the water sample can already be the solution to rising amounts of NOM in the extract (Ext⁺; NOM removal: 95-99%; i.e., cyclodextrin polymers).⁵⁰ While this shows that CSIA for pollutants in the low μ g/L range can be achieved using only a selective sample extraction, CSIA of non-volatile organic micropollutants in the ng/L range was limited in the past by the low concentrations of micropollutants in the environment and a lack of suitable sample preparation procedures. As a result, field applications were scarce (see Figure 1.1). This work, together with very recent advancements in CSIA sample preparation, have the potential to change this since field samples with analyte concentrations in the low to mid ng/L region (compare Table 6.1 C_{BAM}, C_{DEA}, and C_{BOSC}) can now be processed. Purifying the SPE extract by adding one HPLC clean-up makes it possible to accurately measure isotope ratios of pollutants present in the sample in mid to high ng/L concentrations (level 3, NOM removal: 99-99.95%) or even in the low to mid ng/L micropollutant concentrations (level 4) if the pollutants were extracted during the first step using a selective SPE material (NOM removal: 99.99.99%).

For very low concentrated pollutants (level 5), it might, however, still be necessary to add a second clean-up step (NOM removal: 99.99-99.999%). To this end, procedures that were already successfully used in the field of CSIA, like two-dimensional chromatography or MIPs can be used,⁵⁶ or other purification techniques using selective materials like covalent organic frameworks (COFs),²⁶⁶ or metal organic frameworks (MOFs),²⁶⁷ which still have to be investigated in the future for their use in CSIA sample preparation. Furthermore, additional advancements on the instrumental end to increase the chromatographic resolution of the hyphenated

Level	C _{NOM} /C _{analyte}	C_{BAM}^{1}	C_{DEA}^{1}	C_{BOSC}^{1}	NOM removal	Sa	mple Pi	ep. Strat	egy
	ratio range				in %	Ext	Ext ⁺	HPLC	pur.
1	1-200	>11000	>13000	>8000	90-95	Х			
2	200-1000	>2300	>2600	>1600	95-99		х		
3	1000-20000	>500	>900	>15	99-99.95	х		Х	
4	3000-100000	>100	>180	>3	99.9-99.99		х	Х	
5	30000-1000000	>10	>18	>0.3	99.99-99.999		Х	х	х
1: in ng/L for a NOM concentration of 1 mgC/L									

Table 6.1 Sample preparation strategies for different NOM and analyte concentration regimes in environmental real-world samples expressed as $C_{NOM}/C_{analyte}$ ratios.

Extraction (Ext): analyte recovery: 90-100%, NOM removal: 90-95%.⁵⁰ selective Extraction (Ext⁺): analyte recovery: 90-100%, NOM removal: 95-99%.⁵⁰ HPLC: analyte recovery: 90-100%, NOM removal: 93-99% additional purification (pur.): analyte recovery: 90-100%, NOM removal: 90%

GC and IRMS sensitivity might help close the gap to the level 5 concentrations. There are already strategies available to increase the chromatographic resolution using, for example, longer columns,⁵¹ multidimensional chromatography,^{34,52–55} or new reactor design that reduces peak broadening.²⁶⁸ Alongside with optimized sample preparation procedures, they are expected to boost new applications of CSIA in the future.

All in all, this shows that there are several strategies available to reach level 5. Selectivity optimization alongside automation of procedures is vital for all of them. QCM dry mass sensing paves the way to efficiently develop optimized purification strategies for various purification problems using a large range of liquid chromatographic solid phase materials and modes. Combining the efficient development of selective purification methods using the QCM with the strategy of comparing $C_{matrix}/C_{analyte}$ ratios before and after each chromatographic purification helped to compare two different RP columns objectively for clean-up of an environmental extract for CSIA. In the future, such a selectivity assessment strategy has to be developed/validated for different matrices and applications of CSIA to enable targeted optimization. To extend the applicability of QCM dry mass sensing even further, future research should focus on optimizing the spray-dryer to make it resistant to solvents other than methanol, acetonitrile, or water²⁶⁹ and to be able to increase the dynamic range of the flow-range to increase the sensitivity of the measuring process. Furthermore, while QCM dry mass sensing was successfully applied to optimize the sample preparation for subsequent isotope analysis using GC-IRMS and residue analysis using GC-MS, it might be potentially useful in the future to other matrix susceptible techniques (i.e., LC-MS)¹⁵⁵ or could even be used to quantify particles (i.e., nanoparticles, micro/nanoplastic).

Last but not least, QCM dry mass sensing enabled online method development and optimization for CSIA sample preparation for environmental extracts, thus taking a big step towards a fully automated method development. The future generation of more data on the behavior of matrix during chromatographic purification using a holistic detector like the QCM could open the door to training artificial intelligence as a method development assistant, getting even closer to the goal of a fully automated, highly selective sample preparation.

A Supporting Information to Introduction Figure 1.1

Table A.1 Publications in CSIA in environmental chemistry are classified as work on new methods to measure a given compound with isotope analysis (method), as a study on the lab scale (lab), or as a field study using real-world samples (field) for several compound classes, namely PAHs (polycyclic aromatic hydrocarbon), pesticides (atrazine, acetochlor, meto-lachlor, chloridazon, desethylatrazine, desphenylchloridazon, 2,6-dichlorobenzamide, isoproturon, parathion, glyphosate, metalaxyl, bromoxynil, dimetomorph), HCHs (hexachlorocyclohexane), 1H-benzotriazole, BTEX (aromatic hydrocarbons benzene, toluene, ethylbenzene, and xylene), PCB+PCDD (polychlorinated biphenyl, polychlorinated dibenzodiox-ins), pharmaceuticals (diclofenac, ibuprofen, sulfamethoxazole, sulfonamide), explosives (2,4,6-trinitrotoluene, hexogen, 2,4-dinitrotoluene), fuel oxygenates (tert-butyl methyl ether, ethyl tert-butyl ether, tert-butyl alcohol), and volatile chlorinated aliphatics (trans-1,2-dichloroethene, cis-1,2-dichloroethene, trichloroethene, terachloroethene, dichloromethane, chloroform, carbon tetrachloride, 1,2-dichloroethane, 1,1-dichloroethylene, tetrachloromethane). Only publications on micropollutants in water or soil measured with IRMS were considered but no reviews and no exhaust analytics. Source: Kuntze et al.⁵⁷ and Web of Science. Publications were considered till 04.10.2023.

Publication	Year	Method/ Lab/ Field
РАН		
Hammer et al. ²⁷⁰	1998	field
McRae et al. ²⁷¹	2000	field
Fabbri et al. ²⁷²	2003	field
Walker et al. ²⁷³	2005	field
Saber et al. ²⁷⁴	2006	field
Bosch et al. ²⁷⁵	2015	field
Richnow et al. ²⁷⁶	2003	field
O'malley et al. ²⁷⁷	1996	field
Richnow et al. ²⁷⁸	2003	field
Micić et al. ²⁷⁹	2007	field
Morasch et al. ²⁸⁰	2011	field
Mahro et al. ²⁸¹	2014	field
Steinbach et al. ²⁸²	2004	field
Blum et al. ²⁸³	2009	field
Griebler et al. ²⁸⁴	2004	field
Marquès et al. ²⁸⁵	2016	lab

Blessing et al. ²⁸⁶	2015	method
Kümmel et al. ²⁸⁷	2016	lab
Morasch et al. ²⁸⁸	2007	lab
Li et al. ²⁸⁹	2009	method
Tolosa et al. ²⁹⁰	2019	method
Yanik et al. ²⁹¹	2003	lab
Zhang et al. ²⁹²	2019	field
Mikolajczuk et al. ²⁹³	2009	method
Lichtfouse et al. ²⁹⁴	1995	method
Yan et al. ²⁹⁵	2006	field
Cennerazzo et al. ²⁹⁶	2017	lab
McRae et al. ²⁹⁷	1996	lab
McRae et al. ²⁹⁸	1998	lab
Ou et al. ²⁹⁹	2010	field
O'malley et al. ³⁰⁰	1994	field
Kim et al. ³⁰¹	2005	method
Bergmann et al. ³⁰²	2011	lab
Buczynska et al. ³⁰³	2014	method
Ternon et al. ³⁰⁴	2015	method
Kim et al. ³⁰⁵	2008	field
Smirnov et al. ³⁰⁶	1998	field
Kim et al. ³⁰⁷	2006	field
Yang et al. ³⁰⁸	2020	lab
McRae et al. ³⁰⁹	2000	field
Vinzelberg et al. ³¹⁰	2005	field
Mazéas et al. ³¹¹	1999	field
Zhang et al. ³¹²	2014	field
Okuda et al. ³¹³	2002	field
Petrisic et al. ³¹⁴	2013	field
O'malley et al. ³¹⁵	1997	lab
Zhang et al. ³¹⁶	2014	method
Gauchotte-Lindsay et al. ³¹⁷	2014	method
Wang et al. ³¹⁸	2004	method
McRae et al. ³¹⁹	1999	lab

Boyd et al. ³²⁰	2006	method
Marozava et al. ³²¹	2019	lab
Mazéas et al. ³²²	2001	method
Liu et al. ³²³	2021	lab
Meckenstock et al. ³²⁴	2004	lab
Mazéas et al. ³²⁵	2002	lab
Jautzy et al. ³²⁶	2013	field
Meckenstock et al. ³²⁷	1999	lab
Morasch et al. ³²⁸	2002	lab
Tolosa et al. ³²⁹	2004	method
Dickhut et al. ³³⁰	2004	lab
Tian et al. ³³¹	2023	method
van Leeuwen et al. ³³²	2022	field

pesticides

Chen et al. ³³³	2017	lab
Chen et al. ³³⁴	2019	lab
Penning et al. ³³⁵	2010	lab
Reinnicke et al. ³³⁶	2012	method
Schreglmann et al. ⁶⁸	2013	field
Ehrl et al. ³³⁷	2018	lab
Masbou et al. ³³⁸	2018	lab
Ehrl et al. ³³⁹	2018	lab
Torrento et al. ⁶⁵	2019	field
Ponsin et al. ³⁴⁰	2019	method
Meyer et al. ³⁴¹	2008	method
Elsayed et al. ³⁴²	2014	lab
Lutz et al. ³⁴³	2017	field
Lihl et al. ³⁴⁴	2019	method
Alvarez-Zaldívar et al. ²⁵³	field	
Imfeld et al. ³⁴⁵	2018	lab
Melsbach et al. ³⁴⁶	2019	method
Schürner et al. ³⁴⁷	2016	lab
Jin et al. ³⁴⁸	2016	lab

Wu et al. ³⁴⁹	2018	lab
Wu et al. ³⁵⁰	2018	field
Kujawinski et al. ³⁵¹	2013	method
Mogusu et al. ³⁵²	2015	method
Hartenbach et al. ³⁵³	2008	lab
Yamamoto et al. ³⁵⁴	2004	lab
Lutz et al. ³⁵⁵	2013	lab
Meyer et al. ³⁵⁶	2009	lab
Penning et al. ³⁵⁷	2007	method
Reinnicke et al. ³⁵⁸	2012	lab
Maier et al. ³⁵⁹	2013	method
Wu et al. ³⁶⁰	2014	method
Jin et al. ³⁶¹	2016	method
Wu et al. ³⁶²	2017	method
Tang et al. ³⁶³	2017	lab
Chen et al. ³⁶⁴	2019	lab
Melsbach et al. ⁶⁶	2020	field
Limon et al. ³⁶⁵	2020	method
Torabi et al. ³⁶⁶	2020	lab
Knossow et al. ³⁶⁷	2020	lab
Shi et al. ³⁶⁸	2022	lab
Masbou et al. ³⁶⁹	2018	method
Melsbach et al. ³⁷⁰	2020	lab
Droz et al. ³⁷¹	2021	lab
Drouin et al. ³⁷²	2021	lab
Torrentó et al. ³⁷³	2021	method
Gilevska et al. ³⁷⁴	2023	field
Gilevska et al. ³⁷⁵	2022	field
Glöckler et al. ⁵⁰	2023	method
Liang et al. ³⁷⁶	2023	lab
Chen et al. ³⁷⁷	2022	lab
Li et al. ³⁷⁸	2022	lab
Arar et al. ³⁷⁹	2023	lab
Prieto-Espinoza et al. ³⁸⁰	2022	lab

Kundu et al. ³⁸¹	2022	lab
Sun et al. ³⁸²	2022	lab
Marks et al. ²³⁶	2022	method
Meite et al. ³⁸³	2022	lab

HCH

Badea et al. ³⁸⁴	2011	field
Bashir et al. ³⁸⁵	2015	field
Chartrand et al. ³⁸⁶	2015	field
Liu et al. ³⁸⁷	2017	field
Wu et al. ³⁸⁸	2019	field
Zhang et al. ³⁸⁹	2014	lab
Badea et al. ³⁹⁰	2015	method
Jin et al. ³⁶¹	2016	method
Qian et al. ³⁹¹	2019	lab
Badea et al. ³⁹²	2009	lab
Bashir et al. ³⁹³	2013	lab
Schilling et al. ³⁹⁴	2019	lab
Schilling et al. ³⁹⁵	2019	lab
Ivdra et al. ³⁹⁶	2014	method
Gui et al. ³⁹⁷	2015	method
Bashir et al. ³⁹⁸	2018	lab
Liu et al. ³⁹⁹	2020	lab
Gao et al. ⁴⁰⁰	2022	field
Liu et al. ⁴⁰¹	2022	lab
Liu et al. ⁴⁰²	2019	lab
Badea et al. ⁴⁰³	2021	lab
Kannath et al.404	2019	method
Ivdra et al. ¹²	2017	lab
Liu et al. ⁴⁰⁵	2022	field
Zhu et al. ⁴⁰⁶	2023	lab
Liu et al. ⁴⁰⁷	2022	lab
Gao et al. ⁴⁰⁰	2022	field
Liu et al. ⁴⁰⁸	2023	field

Aamir et al. ⁴⁰⁹	2023	field
1H-benzotriazole		
Bakkour et al. ⁵⁶	2018	field
Huntscha et al.410	2014	lab
Spahr et al. ⁴¹¹	2013	method
Wu et al. ⁴¹²	2021	lab
BTEX		
Kelley et al. ⁴¹³	1997	field
Mancini et al.414	2008	field
Lutz et al. ⁴¹⁵	2014	field
Beckley et al. ⁴¹⁶	2016	field
Richnow et al. ⁴¹⁷	1999	field
Stehmeier et al.418	1999	field
Bugna et al. ⁴¹⁹	2004	field
Bugna et al. ⁴²⁰	2005	field
Micić et al. ²⁷⁹	2007	field
Beller et al. ⁴²¹	2008	field
Gelman et al. ⁴²²	2008	field
Mahro et al. ²⁸¹	2014	field
Kolhatkar et al. ⁴²³	2017	field
Moshkovich et al. ⁴²⁴	2018	field
BenIsrael et al.425	2019	field
Vieth et al. ⁴²⁶	2001	field
Mancini et al.427	2002	field
Meckenstock et al.428	2002	field
Richnow et al. ⁴²⁹	2002	field
Richnow et al. ²⁷⁶	2003	field
Richnow et al. ²⁷⁸	2003	field
Fischer et al. ⁴³⁰	2004	field
Griebler et al. ²⁸⁴	2004	field
Peter et al. ⁴³¹	2004	field
Steinbach et al. ²⁸²	2004	field

Vieth et al. ⁴³²	2005	field
Fischer et al. ⁴³³	2006	field
Mak et al. ⁴³⁴	2006	field
Stelzer et al. ⁴³⁵	2006	field
Fischer et al. ⁵⁸	2007	field
Bouchard et al. ⁴³⁶	2008	field
Batlle-Aguilar et al. ⁴³⁷	2009	field
Blum et al. ²⁸³	2009	field
Mäurer et al. ⁴³⁸	2009	field
Prommer et al.439	2009	field
De Biase et al. ⁴⁴⁰	2011	field
Morasch et al. ²⁸⁰	2011	field
Rakoczy et al.441	2011	field
Van Keer et al. ⁴⁴²	2012	field
Batlle-Aguilar et al. ⁴⁴³	2014	field
Ponsin et al.444	2015	field
Gilevska et al. ⁴⁴⁵	2019	field
McKelvie et al. ⁴⁴⁶	2005	field
Feisthauer et al. ⁴⁴⁷	2012	field
Xiong et al. ⁴⁴⁸	2012	field
Wei et al. ⁴⁴⁹	2015	field
Shayan et al. ⁴⁵⁰	2018	field
Wei et al. ⁴⁵¹	2018	field
Wanner et al. ⁴⁵²	2019	field
Imfeld et al. ⁴⁵³	2014	lab
Ponsin et al. ⁴⁵⁴	2017	method
Breukelen et al. ⁴⁵⁵	2007	method
Vogt et al. ⁴⁵⁶	2008	lab
Fischer et al. ⁴⁵⁷	2009	lab
Herrero-Martín et al. ⁴⁵⁸	2015	method
Ebongué et al. ⁴⁵⁹	2009	method
Dempster et al. ⁴⁶⁰	1997	method
Sherwood Lollar et al. ⁴⁶¹	1999	lab
Ahad et al. ⁴⁶²	2000	lab

Slater et al. ⁴⁶³	2000	lab
Wang et al. ⁴⁶⁴	2003	lab
Harrington et al. ⁴⁶⁵	1999	lab
Aeppli et al. ⁴⁶⁶	2008	method
Kampara et al. ⁴⁶⁷	2008	lab
Tobler et al. ⁴⁶⁸	2008	lab
Langenhoff et al. ⁴⁶⁹	2009	lab
Seeger et al. ⁴⁷⁰	2011	lab
Dorer et al. ⁴⁷¹	2014	method
Jin et al. ⁴⁷²	2014	lab
Busch-Harris et al. ⁴⁷³	2008	lab
Jin et al. ⁴⁷⁴	2014	lab
Ward et al. ⁴⁷⁵	2000	lab
Mancini et al. ⁴⁷⁶	2003	lab
Dias et al. ⁴⁷⁷	1997	method
Slater et al. ⁴⁷⁸	1999	lab
Elsner et al. ⁴⁷⁹	2006	method
Morasch et al. ²⁸⁸	2007	lab
Mancini et al.414	2008	lab
Herrmann et al. ⁴⁸⁰	2009	lab
Amaral et al. ⁴⁸¹	2010	method
Jechalke et al. ⁴⁸²	2013	lab
Centler et al. ⁴⁸³	2013	method
Bouchard et al. ⁴⁸⁴	2014	method
Passeport et al.485	2014	method
Dorer et al. ⁴⁸⁶	2016	lab
Bouchard et al. ⁴⁸⁷	2017	method
Morasch et al. ⁴⁸⁸	2001	lab
Morasch et al. ⁴⁸⁹	2004	lab
Mancini et al.490	2006	lab
Qiu et al. ⁴⁹¹	2013	lab
Khan et al. ⁴⁹²	2018	lab
Klisch et al. ⁴⁹³	2012	method
Nagel et al.494	2011	field

Knöller et al. ⁴⁹⁵	2006	lab
Schüth et al. ⁴⁹⁶	2003	lab
Sun et al. ⁴⁹⁷	2021	lab
Ahad et al. ⁴⁹⁸	2008	lab
Teramoto et al.499	2020	field
van Leeuwen et al. ³³²	2022	field
Müller et al. ⁵⁰⁰	2020	field
Passeport et al. ²⁰	2016	field
Keller et al. ⁵⁰¹	2017	lab
Feng et al. ⁵⁰²	2021	method
Solano et al. ⁵⁰³	2018	lab
Gilevska et al. ⁵⁰⁴	2021	field
Willach et al. ⁵⁰⁵	2020	method
Rostkowski et al. ⁵⁰⁶	2021	lab
van Breukelen et al. ⁵⁰⁷	2008	method
Hunkeler et al. ⁵⁰⁸	2001	lab
Shin et al. ⁵⁰⁹	2010	lab
Poulson et al. ⁵¹⁰	2010	lab
Fischer et al. ⁵¹¹	2008	lab
Kopinke et al. ⁵¹²	2005	lab
Rolle et al. ⁵¹³	2017	lab
Oba et al. ⁵¹⁴	2008	lab
Rakoczy et al. ⁵¹⁵	2013	lab
Höhener et al. ⁵¹⁶	2012	lab
Bouchard et al. ⁵¹⁷	2008	lab
Jochmann et al. ⁶⁴	2006	method
Aüllo et al. ⁵¹⁸	2016	lab
Vieth et al. ⁵¹⁹	2006	lab
Chen et al. ⁵²⁰	2022	lab
Khan et al. ⁵²¹	2022	lab

PCB+PCDD

Horii et al. ⁵²²	2005	method
Vetter et al. ⁵²³	2007	method

Drenzek et al. ⁵²⁴	2004	lab
Drenzek et al. ⁵²⁵	2001	lab
Huang et al. ⁵²⁶	2020	field
Böttcher et al. ⁵²⁷	2010	field
Liu et al. ⁵²⁸	2010	lab
Ewald et al. ⁵²⁹	2007	lab

pharmaceuticals

Schürner et al. ³⁴⁷	2016	field
Maier et al. ⁵³⁰	2014	method
Jin et al. ³⁴⁸	2016	method
Maier et al. ¹⁷	2016	lab
Birkigt et al. ⁵³¹	2015	lab
Gilevska et al. ¹³	2015	lab
Willach et al. ⁵³²	2017	lab
Willach et al. ⁵³³	2018	lab
Kujawinski et al. ⁵³⁴	2012	method
Bennett et al. ⁵³⁵	2017	field
Ouyang et al. ⁵³⁶	2022	lab

explosives

Coffin et al. ⁵³⁷	2001	field
Amaral et al. ⁵³⁸	2009	field
Bernstein et al. ⁵³⁹	2010	field
Moshe et al. ⁵⁴⁰	2010	field
Wijker et al. ¹⁶	2013	field
Miyares et al.541	1999	field
Pennington et al.542	2001	field
Hatzinger et al.543	2018	field
Gelman et al. ⁵⁴⁴	2011	method
Berg et al. ⁵⁴⁵	2007	method
Bernstein et al.546	2008	lab
Lott et al. ⁵⁴⁷	2015	method
Hofstetter et al.548	2008	lab
Tobler et al. ⁵⁴⁹	2007	lab
--------------------------------	------	-------
Hartenbach et al.550	2006	lab
Ulrich et al. ⁵⁵¹	2018	lab
Tong et al. ⁵⁵²	2020	lab
Berens et al. ⁵⁵³	2019	lab
Fuller et al. ⁵⁵⁴	2020	field
Smith et al. ⁵⁵⁵	2015	lab
Bernstein et al.556	2013	lab
Fuller et al. ⁵⁵⁷	2016	lab
Ippoliti et al. ⁵⁵⁸	2023	lab
Hlohowskyj et al.559	2023	lab

fuel oxygenates

Oudijk et al. ⁵⁶⁰	2008	field
Day et al. ⁵⁶¹	2003	field
Day et al. ⁵⁶²	2003	field
Kolhatkar et al. ⁵⁶³	2002	field
Spence et al. ⁵⁶⁴	2005	field
McKelvie et al. ⁵⁶⁵	2007	field
Gelman et al. ⁴²²	2008	field
De Biase et al. ⁴⁴⁰	2011	field
Thornton et al. ⁵⁶⁶	2011	field
Lu et al. ⁵⁶⁷	2016	field
Moshkovich et al.424	2018	field
van der Waals et al. ⁵⁶⁸	2018	field
Kuder et al. ⁵⁶⁹	2005	field
Wilson et al. ⁵⁷⁰	2005	field
Zwank et al. ⁵⁷¹	2005	field
McKelvie et al. ⁵⁷²	2007	field
Gafni et al. ⁵⁷³	2016	field
Berg et al. ⁵⁷⁴	2005	field
Lesser et al. ⁵⁷⁵	2008	field
Kujawinski et al. ⁵⁷⁶	2010	field
Jechalke et al. ⁵⁷⁷	2010	field

Fayolle-Guichard et al.578	2012	field
Bombach et al. ⁵⁷⁹	2015	field
Bastida et al. ⁵⁸⁰	2010	lab
Youngster et al. ⁵⁸¹	2010	lab
Hunkeler et al.582	2001	lab
Smallwood et al. ⁵⁸³	2001	method
Wang et al. ⁴⁶⁴	2003	lab
Zwank et al. ⁶³	2003	method
Jochmann et al. ⁶⁴	2006	method
Somsamak et al.584	2006	lab
Elsner et al. ⁴⁷⁹	2006	method
van Breukelen et al. ⁵⁸⁵	2007	method
van Breukelen et al. ⁴⁵⁵	2007	method
Eweis et al. ⁵⁸⁶	2007	lab
Aeppli et al. ⁴⁶⁶	2008	method
Busch-Harris et al.473	2008	lab
Kuder et al. ⁵⁸⁷	2009	lab
Gauchotte et al. ⁵⁸⁸	2009	method
Amaral et al. ⁴⁸¹	2010	method
Youngster et al. ⁵⁸⁹	2010	lab
Seeger et al. ⁴⁷⁰	2011	lab
North et al. ⁵⁹⁰	2012	lab
Jin et al. ⁴⁷²	2014	lab
Herrero-Martín et al. ⁴⁵⁸	2015	method
Liu et al. ⁵⁹¹	2016	lab
Rosell et al. ⁵⁹²	2007	lab
Rosell et al. ⁵⁹³	2012	lab
Zhang et al. ⁵⁹⁴	2015	lab
McKelvie et al. ⁵⁹⁵	2009	lab
Schmidt et al. ⁵⁹⁶	2004	lab
Heo et al. ⁵⁹⁷	2012	lab
McKelvie et al. ⁵⁹⁸	2010	lab
Somsamak et al. ⁵⁹⁹	2005	lab
Shin et al. ⁶⁰⁰	2013	lab

Rosell et al. ⁶⁰¹	2010	lab
Youngster et al. ⁵⁸¹	2010	lab
Elsner et al. ⁶⁰²	2007	lab
O'Sullivan et al. ⁶⁰³	2008	lab
Tremblay et al. ⁶⁰⁴	2009	method
Bouchard et al. ⁶⁰⁵	2022	lab
Ji et al. ⁶⁰⁶	2023	lab

volatile chlorinated aliphatics

Hunkeler et al. ⁶⁰⁷	2004	field
Blessing et al. ⁶⁰⁸	2009	field
Hunkeler et al. ⁶⁰⁹	2011	field
McHugh et al. ⁶¹⁰	2011	field
Kaown et al. ¹⁵	2014	field
Filippini et al. ⁶¹¹	2018	field
Eberts et al. ⁶¹²	2008	field
Nijenhuis et al. ⁶¹³	2013	field
Badin et al. ⁶¹⁴	2015	field
Beneteau et al. ⁶¹⁵	1999	field
Wang et al. ⁶¹⁶	2010	field
Wang et al. ⁶¹⁷	2013	field
Beckley et al.416	2016	field
McKelvie et al. ⁵⁶⁵	2007	field
Mundle et al. ⁶¹⁸	2012	field
Damgaard et al. ⁶¹⁹	2013	field
Puigserver et al. ⁶²⁰	2016	field
Kirchholtes et al. ⁶²¹	2004	field
Vanstone et al. ⁶²²	2005	field
Chapman et al. ⁶²³	2007	field
Nijenhuis et al. ⁶²⁴	2007	field
Imfeld et al. ⁶²⁵	2008	field
Morrill et al. ⁶²⁶	2009	field
Courbet et al. ⁶²⁷	2011	field
Révész et al. ⁶²⁸	2014	field

Lee et al. ⁶²⁹	2015	field
Filippini et al. ⁶³⁰	2016	field
Hallsworth et al. ⁶³¹	2017	field
Pierce et al. ⁶³²	2018	field
Schaefer et al. ⁶³³	2018	field
Vogel et al. ⁶³⁴	2018	field
Blázquez-Pallí et al. ⁶³⁵	2019	field
Buchner et al. ⁶³⁶	2019	field
Richards et al. ⁶³⁷	2019	field
Sturchio et al. ⁶³⁸	1998	field
Hunkeler et al. ⁶³⁹	1999	field
Song et al. ⁶⁴⁰	2002	field
Kirtland et al. ⁶⁴¹	2003	field
Carreón-Diazconti et al. ⁶⁴²	2009	field
Kuhn et al. ⁶⁴³	2009	field
McLoughlin et al. ⁶⁴⁴	2014	field
Velimirovic et al. ⁶⁴⁵	2014	field
Sonne et al. ⁶⁴⁶	2017	field
Wilkin et al. ⁶⁴⁷	2018	field
Pooley et al. ⁶⁴⁸	2009	field
Elsner et al. ⁶¹	2010	field
Amaral et al. ⁶⁴⁹	2011	field
Broholm et al. ⁶⁵⁰	2014	field
Hermon et al. ⁶⁵¹	2018	field
Wanner et al. ⁶⁵²	2018	field
Vieth et al. ⁶⁵³	2003	field
Morrill et al. ⁶⁵⁴	2005	field
Martin et al. ⁶⁵⁵	2006	field
Hirschorn et al. ⁶⁵⁶	2007	field
Mäurer et al. ⁴³⁸	2009	field
Patterson et al. ⁶⁵⁷	2013	field
Sherwood Lollar et al. ²⁵²	2001	field
Hunkeler et al. ⁶⁵⁸	2003	field
Chartrand et al.659	2005	field

Hunkeler et al. ⁶⁶⁰	2005	field
Abe et al. ⁶⁶¹	2009	field
Hamonts et al. ⁶⁶²	2012	field
Appelo et al. ⁶⁶³	2010	field
Torrentó et al. ⁶⁶⁴	2014	field
Aeppli et al. ⁶⁰	2010	field
Hunkeler et al. ⁶⁶⁵	2011	field
Lojkasek-Lima et al. ⁶⁶⁶	2012	field
Lojkasek-Lima et al. ⁶⁶⁷	2012	field
Wiegert et al. ⁶⁶⁸	2012	field
Petitta et al. ⁶⁶⁹	2013	field
Palau et al. ⁵⁹	2014	field
Audí-Miró et al. ⁶⁷⁰	2015	field
Kaown et al. ⁶⁷¹	2016	field
Palau et al. ⁶⁷²	2016	field
Clark et al. ⁶⁷³	2017	field
Dogan-Subasi et al. ⁶⁷⁴	2017	field
Schiefler et al. ⁶⁷⁵	2018	field
Segal et al. ⁶⁷⁶	2018	field
Jochmann et al. ⁶⁴	2006	method
Imfeld et al. ⁶⁷⁷	2008	lab
Cichocka et al. ⁶⁷⁸	2008	lab
Haluska et al. ⁶⁷⁹	2019	field
van Breukelen et al. ⁶⁸⁰	2017	lab
Alvarez-Zaldívar et al. ⁶⁸¹	2016	lab
Schmidt et al. ⁶⁸²	2014	lab
Kuder et al. ⁶⁸³	2013	method
Chan et al. ⁶⁸⁴	2012	lab
Fletcher et al. ⁶⁸⁵	2011	lab
Morrill et al. ⁶⁸⁶	2004	method
Harding et al. ⁶⁸⁷	2013	lab
Liu et al. ⁶⁸⁸	2018	lab
Rosell et al. ⁶⁸⁹	2019	lab
Gafni et al. ⁶⁹⁰	2019	field

van Breukelen et al. ⁶⁹¹	2005	lab
Vanstone et al. ⁶⁹²	2008	lab
Hunkeler et al. ⁶⁹³	2009	method
Fletcher et al. ⁶⁹⁴	2009	lab
Amaral et al. ⁴⁸¹	2010	method
Chiang et al. ⁶⁹⁵	2012	lab
Wiegert et al. ⁶⁹⁶	2013	lab
Shouakar-Stash et al. ⁶⁹⁷	2013	method
Wanner et al. ⁶⁹⁸	2015	lab
Kret et al. ⁶⁹⁹	2015	lab
Wanner et al. ⁷⁰⁰	2016	field
Ebert et al. ⁷⁰¹	2017	method
Goli et al. ⁷⁰²	2017	method
Blázquez-Pallí et al. ⁷⁰³	2019	lab
Shouakar-Stash et al. ⁷⁰⁴	2006	method
Leitner et al. ⁷⁰⁵	2017	lab
Zwank et al. ⁶³	2003	method
Kuder et al. ⁷⁰⁶	2013	lab
Rodríguez-Fernández et al. ⁷⁰⁷	2017	lab
Wanner et al. ⁷⁰⁸	2019	lab
Rodríguez-Fernández et al. ⁷⁰⁹	2018	lab
Zwank et al. ⁷¹⁰	2005	lab
Rodríguez-Fernández et al. ⁷¹¹	2018	field
Mundle et al. ⁷¹²	2017	lab
van Breukelen et al. ⁵⁸⁵	2007	lab
Chartrand et al. ⁷¹³	2007	method
Heckel et al. ⁷¹⁴	2017	method
Slater et al. ⁴⁷⁸	1999	lab
Elsner et al. ⁴⁷⁹	2006	method
Bouchard et al. ⁴⁸⁴	2014	method
Bouchard et al.487	2017	method
Ertl et al. ⁷¹⁵	1996	lab
Dayan et al. ⁷¹⁶	1999	lab
Numata et al. ⁷¹⁷	2002	method

Poulson et al. ⁷¹⁸	2002	lab
Slater et al. ⁷¹⁹	2002	lab
Shouakar-Stash et al. ⁷²⁰	2003	lab
Slater et al. ⁷²¹	2003	lab
Chu et al. ⁷²²	2004	lab
Sakaguchi-Söder et al. ⁷²³	2007	lab
Elsner et al. ⁷²⁴	2008	lab
Liang et al. ⁷²⁵	2009	lab
Aeppli et al. ⁷²⁶	2009	lab
Bernstein et al. ⁷²⁷	2011	lab
Marchesi et al. ⁷²⁸	2012	lab
Klisch et al. ⁴⁹³	2012	method
Gan et al. ⁷²⁹	2013	method
Audí-Miró et al. ⁷³⁰	2013	lab
Cretnik et al. ⁷³¹	2013	lab
Marchesi et al. ⁷³²	2013	lab
Cretnik et al. ⁷³³	2014	lab
Jin et al. ⁴⁷²	2014	lab
Renpenning et al. ⁷³⁴	2014	lab
Lee et al. ⁷³⁵	2015	lab
Buchner et al. ⁷³⁶	2015	lab
Liu et al. ⁷³⁷	2016	lab
Liu et al. ⁷³⁸	2016	lab
Badin et al. ¹⁹	2016	lab
Gafni et al. ⁷³⁹	2018	lab
Heckel et al. ⁷⁴⁰	2018	lab
Yu et al. ⁷⁴¹	2018	lab
Liu et al. ⁷⁴²	2018	lab
Jian-Ye et al. ⁷⁴³	2019	method
Thouement et al. ⁷⁴⁴	2019	lab
Lihl et al. ³⁴⁴	2019	method
Gafni et al. ⁷⁴⁵	2020	lab
Gui et al. ³⁹⁷	2015	method
Walaszek et al. ⁷⁴⁶	2020	lab

Franke et al. ⁷⁴⁷	2020	lab
Franke et al. ⁷⁴⁸	2017	lab
Hirschorn et al. ⁷⁴⁹	2007	lab
Carpani et al. ⁷⁵⁰	2021	field
Heckel et al. ⁷⁵¹	2022	lab
Yankelzon et al. ⁷⁵²	2020	lab
Palau et al. ⁷⁵³	2014	method
Head et al. ⁷⁵⁴	2020	lab
Hunkeler et al. ⁷⁵⁵	2000	lab
Palau et al. ⁷⁵⁶	2017	lab
Hirschorn et al. ⁷⁵⁷	2004	lab
Hunkeler et al. ⁷⁵⁸	2002	lab
Wanner et al. ⁷⁵⁹	2017	field
Abe et al. ⁷⁶⁰	2009	lab
Soder-Walz et al. ⁷⁶¹	2021	lab
Palau et al. ⁷⁶²	2017	lab
Hart et al. ⁷⁶³	2022	field
Liu et al. ⁷⁶⁴	2021	lab
Rodríguez-Fernández et al. ⁷⁰⁷	2017	lab
Heckel et al. ⁷⁶⁵	2017	lab
Liang et al. ⁷⁶⁶	2007	lab
Rodríguez-Fernández et al. ⁷⁰⁹	2018	lab
Neumann et al. ⁷⁶⁷	2009	lab
Elsner et al. ⁷⁶⁸	2007	lab
Stewart et al. ⁷⁶⁹	2018	lab
Elsner et al. ⁷⁷⁰	2004	lab
Breider et al. ⁷⁷¹	2013	lab
Rostkowski et al. ⁵⁰⁶	2021	lab
Arnold et al. ⁷⁷²	2008	lab
Torrentó et al. ⁷⁷³	2017	lab
Breider et al. ⁷⁷⁴	2014	lab
Asfaw et al. ⁷⁷⁵	2020	method
Chen et al. ⁷⁷⁶	2018	lab
Heckel et al. ⁷⁷⁷	2019	lab

Aeppli et al. ⁷⁷⁸	2013	lab
Hunkeler et al. ¹⁴	2012	field
Benbow et al. ⁷⁷⁹	2008	method
Nikolausz et al. ⁷⁸⁰	2006	lab
Torgonskaya et al. ⁷⁸¹	2019	lab
Nadalig et al. ⁷⁸²	2013	lab
Prieto-Espinoza et al. ⁷⁸³	2021	lab
Cichocka et al. ⁷⁸⁴	2007	lab
Nijenhuis et al. ⁷⁸⁵	2005	lab
Büsing et al. ⁷⁸⁶	2019	lab
Béranger et al. ⁷⁸⁷	2006	lab
Renpenning et al. ⁷⁸⁸	2015	lab
Jeannottat et al. ⁷⁸⁹	2012	lab
Numata et al. ⁷¹⁷	2002	lab
Palau et al. ⁷⁹⁰	2010	field
Thullner et al. ⁷⁹¹	2008	method
Badin et al. ⁷⁹²	2014	lab
Barth et al. ⁷⁹³	2002	lab
Jeannottat et al. ⁷⁹⁴	2013	lab
Gan et al. ⁷⁹⁵	2014	lab
Morrill et al. ⁷⁹⁶	2006	lab
Höhener et al. ⁷⁹⁷	2015	method
Lihl et al. ⁷⁹⁸	2019	lab
Marco-Urrea et al. ⁷⁹⁹	2011	lab
Smits et al. ⁸⁰⁰	2011	lab
Imfeld et al. ⁸⁰¹	2011	field
Ottosen et al. ⁸⁰²	2021	field
Damgaard et al. ⁸⁰³	2013	field
Murray et al. ⁸⁰⁴	2019	field
Åkesson et al. ⁸⁰⁵	2020	field
Hellal et al. ⁸⁰⁶	2020	field
Schwarzbauer et al. ⁸⁰⁷	2005	method
Ghezzi et al. ⁸⁰⁸	2021	field
Halloran et al. ⁸⁰⁹	2021	method

Ottosen et al. ⁸¹⁰	2020	field
Liu et al. ⁸¹¹	2014	lab
Schmidt et al. ⁸¹²	2014	lab
Yu et al. ⁸¹³	2014	lab
Bloom et al. ⁸¹⁴	2000	lab
Horst et al. ⁸¹⁵	2020	lab
Schüth et al. ⁸¹⁶	2003	lab
Kopinke et al. ⁵¹²	2005	method
Bill et al. ⁸¹⁷	2001	lab
Schüth et al. ⁴⁹⁶	2003	lab
Tiehm et al. ⁸¹⁸	2008	lab
Dong et al. ⁸¹⁹	2011	lab
Clingenpeel et al. ⁸²⁰	2012	lab
Han et al. ⁸²¹	2018	lab
Horst et al. ⁸²²	2016	lab
Höhener et al.516	2012	lab
Li et al. ⁸²³	2022	lab
Julien et al. ⁸²⁴	2018	method
Imfeld et al. ⁸²⁵	2010	lab
Schmidt et al. ⁸²⁶	2010	lab
Abe et al. ⁸²⁷	2009	lab
Gilevska et al. ⁸²⁸	2015	method
Holt et al. ⁸²⁹	2001	method
Brungard et al. ⁸³⁰	2003	lab
Heraty et al. ⁸³¹	1999	lab
Bouchard et al. ⁶⁰⁵	2022	lab
Lincker et al. ⁸³²	2022	lab
Buchner et al. ⁸³³	2022	method
Wienkenjohann et al. ⁸³⁴	2023	lab
Willmann et al. ⁸³⁵	2023	lab
Phillips et al. ⁸³⁶	2022	lab
Asfaw et al. ⁸³⁷	2023	lab
Cai et al. ⁸³⁸	2022	lab
Emsbo-Mattingly et al. ⁸³⁹	2022	field

Yuan et al. ⁸⁴⁰	2022	field
Ji et al. ⁶⁰⁶	2023	lab

B Supporting Information to Chapter 2

B.1 Chemicals, Materials, and Standard Solutions

All chemicals and materials purchased commercially and used in this work are summarized in Table B.1.

Chemical	Purity/Grade/Type	Supplier
dichloromethane	≥99%	Sigma-Aldrich
formic acid	≥88%	Sigma-Aldrich
hydrochloric acid	ACS reagent, 37%	Sigma-Aldrich
methanol	≥99%	Sigma-Aldrich
sodium chloride	≥99.5%	Fisher Scientific
sodium hydroxide solution	0.1 N	Carl Roth
(trimethylsilyl)diazomethane solution	2.0 M in hexane	Sigma-Aldrich

Ultrapure H₂O (18.2 M Ω cm at 25 °C) was obtained from a Milli-Q[®] direct reference H₂O purification system from Merck MilliPore (Burlington, USA).

B.2 Methylation: Mechanistic Details



Figure B.1 Reaction mechanism of methylation of NOM carboxylic acid groups (1) using TMSD (2) according to Kühnel et al.⁸⁴¹ **2** deprotonates the carboxylic acid group of **1** and is subsequently desilylated by the excess of methanol (**3**). The nucleophilic attack of the deprotonated carboxylic acid group at diazomethane (**4**) leads to the release of nitrogen and the final methylated product (**5**).

B.3 Supplementary Data on the Titration



Figure B.2 Triplicate acid-base titration measurements of NOM (3 mgC).

B.4 Supplementary Data on the Breakthrough Curves



Figure B.3 Validation of time methylated NOM samples have to be ultrasonicated using an ultrasonic lab homogenizer to fully reconstitute all organic compounds in water.



Figure B.4 Breakthrough curves of a control measurement on MISPE. For the control measurement, the same reaction conditions used for methylated NOM were used except of no NOM was included. The gray bars show the amount of DOC in the breakthrough and indicate the amount of contamination in the different fractions originating from the methylation procedure.

C Supporting Information to Chapter 3

C.1 Chemicals, Materials, and Standard Solutions

All chemicals and materials purchased commercially and used in this work are summarized in Table C.1.

Chemical	Purity/Grade/Type	Supplier
1-vinyl-2-pyrrolidone	stabilizer: sodium hydroxide	Sigma-Aldrich
2,2'-azobis(2-methylpropionitrile)	≥98%	Sigma-Aldrich
γ -methacryloxypropyltrimethoxysilane	≥97%	Sigma-Aldrich
acetone	technical grade	in-house supply
acetonitrile	≥99%	Sigma-Aldrich
divinylbenzene	stabilizer: 4-tert-butylpyrocatechol	Sigma-Aldrich
ethylene glycol dimethacryate	stabilizer: hydroquinone monomethyl ether	Sigma-Aldrich
humic acids	technical grade	Sigma-Aldrich
hydrochloric acid	ACS reagent, 37%	Sigma-Aldrich
isopropyl alcohol	≥99%	Sigma-Aldrich
magnesium sulfate	anhydrous, ≥98.0%	Sigma-Aldrich
methanol	≥99%	Sigma-Aldrich
sodium hydroxide solution	1 N	Carl Roth
toluene	≥99%	Sigma-Aldrich
trimethylol-propane trimethacrylate	stabilizer: monomethyl ether hydroquinone	Sigma-Aldrich

Table C.1 List of reagents, solvents, and analytical standards.

Ultrapure H₂O (18.2 M Ω cm at 25 °C) was obtained from a Milli-Q[®] direct reference H₂O purification system from Merck MilliPore (Burlington, USA).

Before using DVB for the synthesis, the respective monomer was sequentially washed twice with NaOH (1 M) and once with water to remove the stabilizer and. then dried over MgSO₄. The stabilizer was removed from EGDMA using a vacuum destillation at 140 °C and 40 mbar. The purified monomers were stored at -80 °C. To purify AIBN, it was recrystallized in methanol and stored at 4 °C.

The carbon content of the above-mentioned humic acids was determined to be $37\% \pm 3\%$ by measuring a suspension of 0.5 mg humic acids in 1 mL water with a Total Organic Carbon Analyzer (TOC-L, Shimadzu, Germany) and used for mass calculations.

C.2 Sensor Holder



Figure C.1 Sensor holder used during the coating reaction to guarantee only the upper sensor surface being coated. (a) Scheme of the sensor holder: 1: Custom-made teflon sensor holder, 2: Screws, 3: O-rings made of FFKM (11.1 mm x 1.6 mm, Techniparts, Wezep, Netherlands), 4: QCM sensor. (b) Setup during the reaction: The sensor holder is placed in the middle of the flask using wire.

C.3 Data Evaluation

Listing A.4.1 Peak picking for the interval experiments with the shutter in which outliers were eliminated manually.

```
# In[1]:
### RUN ME
import pandas as pd
import scipy.signal as signal
import numpy as np
import scipy
from matplotlib import pyplot as plt
import seaborn as sns
import os
# In[2]:
### RUN ME
def count_experiments(data):
    n = 1
    experiments = {n: {'relative_time': [], 'frequency': []}}
```

```
for i, row in data.iterrows():
        if (i>0 and data.Relative_time.loc[i] <
        data. Relative_time.loc[i-1]):
            n += 1
            experiments[n] = { 'relative_time ': [], 'frequency ': []}
        experiments [n]['relative_time']. append (row. Relative_time)
        experiments [n]['frequency']. append (row. Resonance_Frequency)
    return n, experiments
def get_peaks(experiment, distance=200, prominence=1):
    peaks, _ = signal.find_peaks(experiment['frequency'],
    prominence=prominence, distance=distance)
    return np. array (experiment ['relative_time']) [peaks],
    np.array(experiment['frequency'])[peaks]
def clean_peaks(timepoints_peaks, values_peaks, thrh=20):
    to_delete = []
    for i, val in enumerate(values_peaks):
        if i > 0 and i < len(values_peaks) - 1 and
        abs(values_peaks[i]-values_peaks[i-1])<=thrh and
        abs(values_peaks[i]-values_peaks[i+1]) <= thrh:
            to_delete.append(i)
    values_peaks = np.delete(values_peaks, to_delete)
    timepoints_peaks = np.delete(timepoints_peaks, to_delete)
    return timepoints_peaks, values_peaks
def get_value(param, defult_param):
    if param == '':
        return defult_param
    else:
        return int(param)
```

In[3]:

path = os.path.join('~', 'Desktop', 'Interval',

```
'202100830_Interval-100mgC-3.x1sx')
data = pd.read_excel(path, sheet_name='Tabelle2')
data = data.rename(columns={
    'Time<sub>u</sub>(s)': 'Relative_time',
    'Delta_{\Box}F_{\Box}(Hz)': 'Resonance_Frequency'
})
n, experiments = count_experiments(data)
print (f'Based \Box on \Box the \Box timeline \Box there \Box were \Box {n} \Box experiments \Box detected ')
# In [4]:
### Compute the picks for the experiment
n = int(input('Choose_experiment_to_plot:'))
distance = input(Approximate_min_distance_between_peaks_(default=200):')
prominence = input('Prominence_value_for_peaks_(default_1):')
threshold = input('Threshold \Box for \Box peaks \Box removal (default \Box 20): ')
timepoints_peaks, values_peaks = get_peaks(
    experiment=experiments[n],
    distance=get_value(distance, 200),
    prominence=get_value(prominence, 1)
)
timepoints_peaks, values_peaks = clean_peaks(
    timepoints_peaks=timepoints_peaks,
    values_peaks=values_peaks,
    thrh=get_value(threshold, 20)
)
### Approximate min distance between peaks (default=200): 200
### Prominence value for peaks (default 1):1
### Threshold for peaks removal(default 20):0
# In [5]:
```

```
### Plot the results
plt.figure(figsize=(20,10))
```

```
sns.lineplot(x=experiments[n]['relative_time'],
y=experiments[n]["frequency"], ci=None)
sns.scatterplot(x=timepoints_peaks, y=values_peaks, color='r')
plt.ylabel('Resonance_Frequency', fontsize=20);
plt.xlabel('Relative_Time', fontsize=20);
plt.title(f'Peak_Detection_in_Experiment_{n}', fontsize=20);
```

```
# In[6]:
### To Save
data = pd.DataFrame(experiments[n])
data['peak_frequency'] = data[['relative_time', 'frequency']].apply(
    lambda x: x[1] if (x[0], x[1]) in
    [(t, v) for (t,v) in zip(timepoints_peaks, values_peaks)] else None,
    axis=1
)
```

```
# In[7]:
path_to_save = input(f'Path_to_save_experiment_{n}:_')
data[['frequency', 'relative_time', 'peak_frequency']].to_excel(
        path_to_save, index=False
)
```

Listing A.4.2 Linear regression for changes in resonance frequency.

```
import pandas as pd
from scipy.stats import linregress
```

```
FILE = "./Date_Name.csv"
COLUMNS = ["t", "F"]
```

#input t in min and F in Hz

```
dataset = pd.read_csv(FILE, sep=";")
```

```
print(len(dataset))
```

```
for col in COLUMNS:
    dataset[col] = dataset[col].apply(lambda x:
    float(x.replace(",", ".")))
for col in COLUMNS[1:]:
    X = dataset['t']
    y = dataset[col]
    s, i, r, p, std = linregress(X, y)
    print(col)
    print(s *60, std *60)
    print(s *60 *4.42, std *60 *4.42)
```

```
#output Hz/h and ng/hcm^2
```

```
Listing A.4.3 Smoothing of resonance frequency baselines for calculation of the baseline drift.
```

import pandas as pd
import seaborn as sns

FILE = "./Date_Name.csv" COL = "F" C = [701]

```
df = pd.read_csv(FILE, sep=";")
```

```
df[COL] = df[COL].apply(lambda x: float(x.replace(",", ".")))
```

```
for c in C:
    print(c)
    name = f"{COL}_smoothed_{c}"
    df[name] = df[COL].rolling(c).median()
```

df[name] = df[name].apply(lambda x: str(x).replace(".", ","))

df[COL] = df[COL].**apply**(**lambda** x: **str**(x).replace(".", ","))

df.to_csv("./Date_Name_smooth.csv", sep=";")

C.4 Raman Measurement



Figure A.4.1 Raman spectrum of a silica QCM sensor coated with a DVB-EGDMA polymer.



C.5 Supplementary Data on Flow Experiments

Figure A.4.2 Frequency change (black) during (a) humic acid sorption experiment on an uncoated sensor and (b) water passed over a coated sensor. (a) Humic acid sorption experiment 1 on an uncoated QCM sensor. Water was passed constantly over the sensor with a flow rate of 30μ L/min. Using an injection valve, humic acid solutions were injected during the flow experiments. The brown bars visualize the time when the humic acid solution is passed over the sensor. (b) Water is passed over a coated sensor with a flow rate of 30μ L/min. Using an injection valve, water was injected. The blue bar visualizes the time when the injected water is passed over the sensor.

D Supporting Information to Chapter 4

D.1 Chemicals, Materials, Standard Solutions, and Spray Fabrication

Chemical	Purity/Grade	Supplier		
QuEChERS extraction				
brown rice (Oryza)	n.a.	Euryza GmbH		
disodium hydrogen citrate sesquihydrate	≥99 %	Sigma-Aldrich		
magnesium sulfate anhydrous grit	≥98 %	Sigma-Aldrich		
sodium chloride	≥99.5 %	Fisher Scientific		
trisodium citrate dihydrate	≥99 %	Sigma-Aldrich		
Solvents				
acetonitrile	≥99 %	Sigma-Aldrich		
isopropanol	≥99 %	Sigma-Aldrich		
methanol	≥99 %	Sigma-Aldrich		
Analytical Standards				
2,6-dichlorobenzamide (BAM)	PESTANAL [®] , anal. st.	Sigma-Aldrich		
atrazine (Atz)	PESTANAL [®] , anal. st.	Sigma-Aldrich		
boscalid (Bosc)	PESTANAL [®] , anal. st.	Sigma-Aldrich		
desethylatrazine (DEA)	PESTANAL [®] , anal. st.	Sigma-Aldrich		
propargite (Prop)	PESTANAL [®] , anal. st.	Sigma-Aldrich		
n.a. = not available, anal. st. = analytical standard				

Table A.4.1 List of reagents, solvents, and analytical standards.

Ultrapure H₂O (18.2 M Ω cm at 25 °C) was obtained from a Milli-Q[®] direct reference H₂O purification system from Merck MilliPore (Burlington, USA). Stock solutions of analytical standards (1 g/L) were prepared in CH₃OH and stored at -18 °C.

The microfluidic spray-dryers were fabricated in-house at the Heinz Nixdorf-Chair of Biomedical Electronics at the Center for Translational Cancer Research of the Technical University of Munich (TranslaTUM). Fast and reliable production of microfluidic spray-dryers was achieved using a two-layer soft lithography approach according to a previously published protocol.¹⁵² Microfluidic channels were designed in AutoCAD 2021 (Autodesk GmbH). Negative resists SU8-3025 and SU8-3050 (MicroChem Corp.) were spin-coated and patterned using a maskless laser lithography system (Dilase 250, Kloe, France) on a 3" Si substrate to obtain the negative master mold. The first layer has a thickness of 20 µm and contains the channel for the liquid sample, while the second layer has a thickness of 70 µm and contains the channel for the gas. PDMS (Sylgard 184, Dow

Corning) was mixed at a ratio of 9:1 (w/w), degassed, and cured in the negative SU8 master mold for 60 min at 65 °C. Microfluidic devices were cut along alignment marks using a razor blade, and holes for tubings were punched using a 0.5 mm biopsy punch (World Precision Instruments). Individual PDMS devices were cleaned using isopropanol and acetone and blown dry with nitrogen. PDMS devices were activated using oxygen plasma for 60 s at 30 W (Zepto, Diener electronic GmbH, Germany). A drop of deionized water was applied to the surface to facilitate the alignment of two PDMS devices under a stereo microscope for the final microfluidic device. A permanent bond between PDMS parts is formed by curing the assembled devices for 60 min at 85 °C. The cross-section of the channels for liquid and gas delivery were measured to be $27 \times 20 \,\mu\text{m}^2$ (w × h) and $110 \times 70 \,\mu\text{m}^2$ (w × h), respectively.



D.2 Determination of Limits of Detection and Quantification

Figure A.4.1 a-c: Frequency raw data of three different CH_3OH/H_2O compositions ((a): 15/85, (b): 50/50, (c): 85/15 (v/v)) containing NaCl in different concentrations (0, 30, 60, 90, 120, 150, 180 and 500 mg/L). d-f: The average slope of quadruplicates of dry mass sensing experiments using different CH_3OH/H_2O compositions ((d): 15/85, (e): 50/50, (f): 85/15 (v/v)) containing NaCl in different concentrations (0, 30, 60, 90, 120, 150, 180 and 500 mg/L). The slopes were used for the calculation of the LOD and the LOQ.

D.3 TOC Validation

% CH ₃ OH
10
40
80
90
90

 Table A.4.2 HPLC gradient conditions for the TOC validation measurement.



Figure A.4.2 Flow chart of offline TOC measurement of HPLC fractions. The mobile phase is split using a post-column adjustable flow splitter. The high flow goes to a fraction collector; each fraction is collected for 30 seconds (volume: 0.25 mL). The fraction is evaporated and reconstituted in 16 mL H₂O and measured using TOC analysis.



Figure A.4.3 Frequency raw data (blank = black, sample = blue, calibration = red) of the QCM measurement during the TOC validation experiment. The grey bar shows the measurement window (2.5 min dead time).

D.4 HPLC Parameters for Rice Matrix Measurement

Time/ min	% CH ₃ OH
0	10
0.5	10
6	80
13	100
17	100
20	10
22	10

 Table A.4.3 HPLC gradient conditions for the brown rice measurement.

D.5 GC-MS: Measurement Details and Analyte Retention Time

Table A.4.4 SIM parameters for	or GC-MS	analysis and	pesticide	retention	times
--------------------------------	----------	--------------	-----------	-----------	-------

Analyte	Retention Time/ min	Measured Ion m/z
Desethylatrazine	12.0	172.0
2,6-Dichlorobenzamide	12.4	172.9
Atrazine	13.9	200.0
Propargite	16.3	135.1
Boscalid	22.9	140.0

D.6 Correlation of Relative Detector Intensity and Matrix Effect

Table A.4.5 Absolute matrix effect (in %) of five pesticides (in order of their retention time; see Table A.4.4) during GC-MS measurement of LC fractionated brown rice matrix of triplicate sample measurements (standard deviation: \pm in %)

fraction	А	В	С	D	Е	
retention window/ min	6 - 7.5	8.5 - 10	11 - 12.5	12.7 - 14.2	15 - 16.5	
		absolute matrix effect/ %				
Desethylatrazine	6.0±7.3	3.8±8.2	9.0±6.3	17±11	130±33	
2,6-Dichlorobenzamide	4.1 ± 9.9	-1.1±7.3	5.3 ± 4.4	14±9	101±62	
Atrazine	-2.0 ± 5.7	0.8 ± 8.6	3.9 ± 5.9	10±7	110±33	
Propargite	-36±7	-31±6	-34±8	-55±11	-83±4	
Boscalid	25±8	29±10	23±8	31±11	345±132	

D.7 GC-MS Chromatograms for Collected Fractions and Mass Spectrum of Oleic Acid



Figure A.4.4 (a) Overlapped GC chromatograms of the five brown rice matrix fractions. GC chromatograms were recorded in full scan mode (0-4000 m/z). There is no data available before minute 12 because of solvent delay. (b) Mass spectrum of the brown rice matrix fraction 5 peak at minute 19. The main component is oleic acid according to the NIST database.

D.8 Matlab Script for QCM Data Processing

```
1
   clc
2
3
   clear
4
   para.Projecttitle=('10-80-90');
5
   para.Endtime=22;
6
7
   MEOHpercentOmin=10;
   MEOHpercent75min=80;
8
9
   MEOHpercent15min=90;
   GradientX=[0 7.5 15 16.5 18 19 para.Endtime];
10
   GradientY=[MEOHpercentOmin MEOHpercent75min MEOHpercent15min 90 90
11
       10 10];
12
   figure
13
   plot(GradientX, GradientY, '-k')
14
   title('Solvent Gradient')
15
   xlabel('time /min')
16
17
   ylabel('MeOH %')
```

```
xlim([0 para.Endtime])
18
  ylim([0 100])
19
20
  otherweise
  %%%%%%%%%%%%%%%%%% type in any nr.
21
  QuechersBlank=0;
22
23
  UV without Blank subtraction
  namelist=dir('*.txt');
24
25
  len=length(namelist);
26
27
  UVfilename='./UV/10_80_90.txt'%namelist(1).name;
  % UVfilename="220324_isochratic30percent_NOMextractsample.txt";
28
29
   [RetentionTime, Intensity]=textread(UVfilename, '%s%s', 'headerlines'
30
     ,25);
31
32
  RetentionTime=strrep(RetentionTime,',','.');
33
   [inx_Time,~,~]=find(contains(RetentionTime, 'Time'));
34
   [inx_R,~,~]=find(contains(RetentionTime, 'R'));
35
36
   [inx_Wave,~,~]=find(contains(RetentionTime,'Wave'));
37
  Wavelength=Intensity(inx_Wave);
38
  Starttxt='Bandwidth(nm)';
39
  Endtxt='[PDA';
40
  [inx_Start,~,~]=find(contains(RetentionTime,Starttxt));
41
  inx_Start=inx_Start+3;
42
43
  [inx_End,~,~]=find(contains(RetentionTime,Endtxt));
44
  inx_End=inx_End-1;
45
  inx_End=inx_End(2:end);
46
  inx_End=[inx_End;length(RetentionTime)];
47
48
49
  for i=1:length(Wavelength)
```

```
50
       UVtime{i}=RetentionTime(inx_Start(i): inx_End(i),1);
51
       UVtime{i}= str2double(convertCharsToStrings(UVtime{i}));
52
53
       UVintensity{i}=Intensity(inx_Start(i): inx_End(i),1);
54
       UVintensity{i}= str2double(convertCharsToStrings(UVintensity{i
55
          }));
  end
56
57
   Raw data extraction
58
  %%figurename must match the sequence of filelist
59
   % figurename={'Blank1', 'Blank2', 'Blank3', 'Calibration01_1','
60
      Calibration01_2', 'Calibration01_3', ...
   % 'Calibration02_1', 'Calibration02_2', 'Calibration02_3', '
61
      Sample01_1', 'Sample01_2', 'Sample01_3','Sample02_1', '
      Sample02_2', 'Sample02_3'};
   para.figurename={'blank1', 'blank2', 'cali1', 'cali2', 'sample1'};
62
63
  %%%read the file from QCM
64
65
  QCMnamelist=dir('*.txt');
66
  len=length(QCMnamelist);
67
  n=1;
68
   TableTimeDeltaF=[];
69
70
   for i=1:len
71
       filename{i}=QCMnamelist(i).name;
72
73
       [RawF{i},
                                    DeltaF{i}, DeltaR{i}, DeltaMass{
74
                   RawR{i} ,
                Thickness{i},
                                Time{i},
                                                 Tag{i}]=textread(
         i}.
          filename{i},'%s%s%s%s%s%s%s%s','headerlines',16);
75
       DeltaF_num{i}=strrep(DeltaF{i},',','.');
       DeltaF_num{i}=cell2mat(DeltaF_num{i});
76
```

```
77
        %
              DeltaF_num{i}=str2double(convertCharsToStrings(
           DeltaF_num{i});
        DeltaF_num{i}=str2num(DeltaF_num{i});
78
79
        DeltaR_num{i}=strrep(DeltaR{i},',','.');
80
        DeltaR_num{i}=cell2mat(DeltaR_num{i});
81
        %
              DeltaF_num{i}=str2double(convertCharsToStrings(
82
           DeltaF_num{i});
83
        DeltaR_num{i}=str2num(DeltaR_num{i});
84
85
        RawR_num{i}=strrep(RawR{i},',','.');
        RawR_num{i}=cell2mat(RawR_num{i});
86
87
        %
              DeltaF_num{i}=str2double(convertCharsToStrings(
           DeltaF_num{i});
        RawR_num{i}=str2num(RawR_num{i});
88
89
90
        Time_num{i}=strrep(Time{i},',','.');
91
        Time_num{i}=cell2mat(Time_num{i});
        % Time_num{i}=str2double(convertCharsToStrings(Time_num{i}));
92
93
        Time_num{i}=str2num(Time_num{i});
94
        Time_min{i}=Time_num{i}./60;
95
96
        % write time and delte freq to excel file.
97
98
99
        T{i}=table(Time_min{i},DeltaF_num{i});
100
        T{i}.Properties.VariableNames = {'Time_min', 'DeltaF'};
101
102
        TableTimeDeltaF=T{i};
103
104
        excelcolumn={'A2','C2','E2','G2','I2', 'K2', 'M2','O2','Q2', '
          S2', 'U2'};
105
        excelfilename = [para.Projecttitle 'TableTimeDeltaF.xlsx'];
106
```

```
107
        writetable(TableTimeDeltaF, excelfilename, 'Sheet', 1, 'Range',
           excelcolumn{i})
108
        [TF{i},S1{i},S2{i}] = ischange(DeltaF_num{i},'linear','
109
           Threshold',30000);
   end
110
111
   filename
112
    add title for excel columns
113
114
115
    for n=1: length(para.figurename)
116
        excelcolumn={'A1','C1','E1','G1','I1', 'K1', 'M1','01','Q1', '
117
           S1', 'U1'};
118
119
        excelfilename = [para.Projecttitle 'TableTimeDeltaF.xlsx'];
        writecell(para.figurename(n),excelfilename,'Sheet',1,'Range',
120
           excelcolumn{n})
121
122
   end
123
   Enter the index of blank/calibration/sample!!
   blank_index=[1:2];
124
   calibration_index=[3:4];
125
   sample_index= [5];
126
127
    Compare blanks and calibrations via figures
128
129
    figure
130
   hold on
    for i=blank_index
131
132
133
        plot(Time_min{i},DeltaF_num{i})
134
135
   end
136
```

```
137
    for j=sample_index
138
139
        plot(Time_min{j},DeltaF_num{j})
140
141
   end
142
   hold off
143
144
   xlim([0,25])
145
   legend([para.figurename(blank_index),para.figurename(sample_index)
146
       ],"Location", 'best')
147
   title('CompareBlank')
   figure
148
149
   hold on
   for i=blank_index
150
151
152
        plot(Time_min{i}, RawR_num{i})
153
154
   end
155
156
    for j=sample_index
157
158
        plot(Time_min{j},RawR_num{j})
159
160
    end
161
   hold off
162
163
   xlim([0,para.Endtime])
   legend([para.figurename(blank_index),para.figurename(sample_index)
164
       ],"Location", 'best')
165
   title('Compare Blanks and Smaple R')
166
    figure
167
168
   hold on
```

```
for i=calibration_index
169
170
171
        plot(Time_min{i},DeltaF_num{i})
172
173
   end
174
175
   for j=sample_index
176
        plot(Time_min{j},DeltaF_num{j})
177
178
   end
179
180
   hold off
181
182
183
   xlim([0,25])
   legend([para.figurename(calibration_index),para.figurename(
184
       sample_index)],"Location","best" )
185
   title('\DeltaF comparation')
186
   ylabel('\DeltaF /Hz')
   xlabel('time /min')
187
188
189
   xlim([0.0 26])
   figure
190
191
   hold on
    for i=calibration_index
192
193
194
        plot(Time_min{i}, RawR_num{i})
195
   end
196
197
198
    for j=sample_index
199
200
        plot(Time_min{j},RawR_num{j})
201
```

```
202
   end
203
204
   hold off
205
   xlim([0,para.Endtime])
206
   legend([para.figurename(calibration_index),para.figurename(
      sample_index)],"Location",'best')
207
   title('R-value comparation')
   ylabel('R-value /Ohms')
208
   xlabel('time /min')
209
   Select Blank and Calibration
210
   %%%%%%Blank=3 means Blank3
211
   %%%%%%Cali=5 means Calibration1; C=5 or 6 or 7 for four blanks and
212
        three Cali
213
   %-----select Blank and Calibration
214
   Cali=4;
215
   Blank=2;
   Export template file for selected calibration and sample with
216
      selected blank
217
   %-----Export template file for selected calibration
218
219
   Caliexcelfilename = [para.Projecttitle 'Template_Calibration.xlsx'
      ];
220
   writematrix(BLANKfinal_frequency,Caliexcelfilename,'Sheet',1,'
221
      Range', 'A1')
222
   writematrix(Califinal_frequency, Caliexcelfilename, 'Sheet', 1, 'Range
      ', 'C1')
223
   %-----Export template file for Sample
224
225
226
   Samexcelfilename = [para.Projecttitle 'Template_Sample.xlsx'];
227
228
   writematrix(BLANKfinal_frequency,Samexcelfilename,'Sheet',1,'Range
       ', 'A1')
```
```
229
   writematrix(SAMPLEfinal_frequency,Samexcelfilename,'Sheet',1,'
      Range', 'C1')
230
   Control subtraction, filtration, derivate calculation
   For Calibraition:
231
232
233
   %-----Load data
234
   %Specify path:
235
236
   path_to_excel_file = Caliexcelfilename;
   sheet_name_in_excel = "Sheet1";
237
238
   data = xlsread(path_to_excel_file, sheet_name_in_excel);
239
   %-----Compute the difference:
240
   %-----since timepoints are not aligned the difference is
241
      computed between two closest in time points
242
   %define the row
243
   time_control = 1;
244
   frequency_control = 2;
245
   time_calib = 3;
246
247
   frequency_calib = 4;
248
   control_timepoints = data(:,time_control);
   calib_timepoints = data(:,time_calib);
249
   control_freq = data(:, frequency_control);
250
251
   calib_freq = data(:,frequency_calib);
252
253
   %Specify path:
   path_to_excel_file = Caliexcelfilename;
254
   sheet_name_in_excel = "Sheet1";
255
256
   data = xlsread(path_to_excel_file, sheet_name_in_excel);
257
   %-----Compute the difference:
258
259
   %-----since timepoints are not aligned the difference is
      computed between two closest in time points
```

```
260
   %define the row
261
262
   time_control = 1;
263
   frequency_control = 2;
264
   time_calib = 3;
265
   frequency_calib = 4;
266
   control_timepoints = data(:,time_control);
    calib_timepoints = data(:,time_calib);
267
268
    control_freq = data(:, frequency_control);
269
    calib_freq = data(:,frequency_calib);
270
271
   %%%%%%%%%%%%%%% consider the data length of Calibration
   validEND=sum(~isnan(calib_freq));
272
273
   if validEND > 2000
274
       validEND=2000;
   end
275
276
   calib_freq=calib_freq(1:validEND);
277
   calib_timepoints=calib_timepoints(1:validEND);
278
   %searching for the nearest time_control and subtract control
279
      frequency from
   %calibration
280
281
   %searching for the nearest time_control
282
283
284
    calib = zeros(length(calib_timepoints), 2);
    for i = 1 : length(calib_timepoints)
285
286
        calib(i, 1) = calib_timepoints(i);
        [~,Index] = min(abs(control_timepoints-calib_timepoints(i)));
287
        calib(i, 2) = calib_freq(i) - control_freq(Index);
288
289
   end
290
291
   %-----calculating derivate
292
   %type in approx_step to adjust the timestep in regression
```

```
293
294
   approx_step = 100;
295
   derivate_data = zeros(length(calib_timepoints) - approx_step,2);
296
    for i = 1 : (length(calib_timepoints)-approx_step)
297
        approx_timepoint = zeros(approx_step, 1);
298
        approx_frequency = zeros(approx_step, 1);
299
        for j = 1 : approx_step
300
            approx_timepoint(j) = calib(i+j-1, 1);
301
            approx_frequency(j) = calib(i+j-1, 2);
        end
302
303
        X = [ones(size(approx_timepoint)), approx_timepoint];
304
        Y = approx_frequency;
305
        derivate = X \setminus Y;
306
        derivate_data(i, 1) = calib(i + floor(approx_step/2), 1);
        derivate_data(i, 2) = derivate(2);
307
   end
308
   position = "C";
309
310
   position_app = position + floor((length(calib_freq)-length(
      derivate_data(:,2)))/2);
   derivate_data(end,1)
311
312
   %-----Applying filter
313
   % odd num only
   window_length =801;
314
315
   polyorder = 3;
316
   filt_calib = sgolayfilt(derivate_data, polyorder, window_length);
317
   filt_calib(end,1)
318
   figure
319
   plot(calib(:, 1), calib(:, 2), '-r', derivate_data(1:end,1),
      derivate_data(1:end,2), '-b')
   hold on
320
   plot(filt_calib(1:end,1), filt_calib(1:end,2),'-k','LineWidth',2)
321
322
   hold off
   xlim([0 27])
323
```

```
legend('\DeltaF', '1st Derivate', 'Filtered Derivate', 'Location',"
324
      best")
325
   title('Calibration', 'Data processing')
   xlabel('time /min')
326
327
   ylabel({'Frequency /Hz'; '1^st Derivate of \DeltaF'})
328
   plot( derivate_data(:,1), derivate_data(:,2), '-b')
   hold on
329
   plot(filt_calib(:,1), filt_calib(:,2),'-k','LineWidth',2)
330
331
   hold off
   ylim([-200 150])
332
   xlim([0 27])
333
334
   x0 = 10;
   y_0 = 10;
335
336
   width=1200;
337
   height=400;
   set(gcf, 'position', [x0, y0, width, height])
338
339
   For Sample:
   path_to_excel_file = Samexcelfilename;
340
   sheet_name_in_excel = "Sheet1";
341
   data = xlsread(path_to_excel_file, sheet_name_in_excel);
342
343
   %-----Compute the difference:
344
345
   %-----since timepoints are not aligned the difference is
      computed between two closest in time points
346
347
   %define the row
348
   time_control = 1;
349
    frequency_control = 2;
   time_calib = 3;
350
   frequency_calib = 4;
351
352
   control_timepoints = data(:,time_control);
   calib_timepoints = data(:,time_calib);
353
354
   control_freq = data(:, frequency_control);
355
    calib_freq = data(:,frequency_calib);
```

```
356
357
   %searching for the nearest time_control
358
359
   calib = zeros(length(calib_timepoints), 2);
360
   for i = 1 : length(calib_timepoints)
361
       calib(i, 1) = calib_timepoints(i);
362
        [~,Index] = min(abs(control_timepoints-calib_timepoints(i)));
363
       calib(i, 2) = calib_freq(i) - control_freq(Index);
364
   end
365
366
   %-----calculating derivate
   %type in approx_step to adjust the timestep in regression
367
368
369
   approx_step = 30;
370
   derivate_data = zeros(length(calib_timepoints) - approx_step,2);
371
   for i = 1 : (length(calib_timepoints)-approx_step)
372
        approx_timepoint = zeros(approx_step, 1);
373
        approx_frequency = zeros(approx_step, 1);
374
       for j = 1 : approx_step
375
            approx_timepoint(j) = calib(i+j-1, 1);
376
            approx_frequency(j) = calib(i+j-1, 2);
       end
377
378
       X = [ones(size(approx_timepoint)), approx_timepoint];
379
       Y = approx_frequency;
380
       derivate = X \setminus Y;
       derivate_data(i, 1) = calib(i + floor(approx_step/2), 1);
381
382
       derivate_data(i, 2) = derivate(2);
383
   end
   position = "C";
384
   position_app = position + floor((length(calib_freq)-length(
385
      derivate_data(:,2)))/2);
386
   %-----Applying filter
387
   window_length = 301;
388
```

```
389
   polyorder = 3;
   filt_SAMPLE = sgolayfilt(derivate_data, polyorder, window_length);
390
391
392
   %-----plot data
393
   figure
   plot(calib(:, 1), calib(:, 2), '-r', derivate_data(:,1),
394
      derivate_data(:,2), '-b')
   hold on
395
396
   plot(filt_SAMPLE(:,1), filt_SAMPLE(:,2),'-k','LineWidth',2)
   hold off
397
398
   xlim([0 27])
   legend('\DeltaF', '1st Derivate', 'Filtered Derivate', 'Location',"
399
      best")
400
   title('Sample', 'Data processing')
   xlabel('time /min')
401
   ylabel({'Frequency /Hz'; '1^st Derivate of \DeltaF'})
402
   %----zoom
403
404
   plot( derivate_data(:,1), derivate_data(:,2), '-b')
405
   hold on
406
407
   plot(filt_SAMPLE(:,1), filt_SAMPLE(:,2),'-k','LineWidth',2)
408
   hold off
   ylim([-200 150])
409
410 xlim([0 20])
411
   x0 = 10;
412 |y0=10;
   width=1200;
413
414
   height=400;
   set(gcf, 'position', [x0, y0, width, height])
415
   %-----saving data to the file
416
417
   %first row is time
418
   %second row is calb.frequency
419
420
   head = {'time_calib', 'frequency_calib'};
```

```
421
   file_name = "Sample_Frequency-filtered.xlsx";
   if exist(file_name, 'file') == 1
422
423
        delete(file_name);
   end
424
   writematrix(calib, file_name, 'range', 'A2');
425
   writematrix("time_calib", file_name, 'range', 'A1');
426
427
   writematrix("frequency_calib", file_name, 'range', 'B1');
   writematrix("filtered gravity", file_name, 'range', 'C1');
428
   writematrix(derivate_data(:, 2), file_name, 'range', position_app)
429
430
   Correction of time (shift, cut off)
   df_dm = 0.1415;
431
432
433
   %-----input timeshift
434
   timeshift = -2.50;
435
436
    shifted_filt_calibtime=filt_calib(:,1)+timeshift;
437
438
    shifted_filt_SAMPLEtime=filt_SAMPLE(:,1)+timeshift;
439
440
441
   %//////cut off the negative timeframe
442
   cutted_shifted_filt_calibtime=shifted_filt_calibtime(
443
      shifted_filt_calibtime >0 & shifted_filt_calibtime <20);</pre>
444
445
   cutted_shifted_filt_SAMPLEtime=shifted_filt_SAMPLEtime(
      shifted_filt_SAMPLEtime >0 & shifted_filt_SAMPLEtime <20);</pre>
446
   cutted_shifted_filt_calibfreq=filt_calib(:,2);
447
   cutted_shifted_filt_calibfreq=cutted_shifted_filt_calibfreq(
448
      shifted_filt_calibtime >0 & shifted_filt_calibtime <20);</pre>
449
   cutted_shifted_filt_SAMPLEfreq=filt_SAMPLE(:,2);
450
```

```
451
   cutted_shifted_filt_SAMPLEfreq=cutted_shifted_filt_SAMPLEfreq(
      shifted_filt_SAMPLEtime >0 & shifted_filt_SAMPLEtime <20);</pre>
452
453
   figure
454
   plot(cutted_shifted_filt_SAMPLEtime,cutted_shifted_filt_SAMPLEfreq
      )
   Gradient construction: run if HPLC with Gradient
455
   GRADIENT.startMEOH=0.111;
456
457
458
   459
   GRADIENT.m1 = 5.2952;
460
   GRADIENT.m2=3.7;
461
   GRADIENT.m3 = 11.1;
462
   GRADIENT.t1=8.4524;
463
464
   GRADIENT.t2=26;
   GRADIENT.t3 = -77.6;
465
466
   %-----input sample concentrations in H20 and MeOH
467
468
469
   GRADIENT.sample_meoh=300;
470
   GRADIENT.sample_h2o=300;
471
472
   gradientcomposition=zeros(length(cutted_shifted_filt_calibtime),1)
      ;
   gradientcomposition(cutted_shifted_filt_calibtime <= 0.5) = GRADIENT.
473
      startMEOH;
474
    gradientcomposition(cutted_shifted_filt_calibtime>0.5 &
      cutted_shifted_filt_calibtime <=11) =(</pre>
      cutted_shifted_filt_calibtime(cutted_shifted_filt_calibtime>0.5
       & cutted_shifted_filt_calibtime <=11).* GRADIENT.m1 + GRADIENT.
      t1)/100;
475
   gradientcomposition(cutted_shifted_filt_calibtime>11 &
      cutted_shifted_filt_calibtime <=14) =(</pre>
```

```
cutted_shifted_filt_calibtime(cutted_shifted_filt_calibtime>11
      & cutted_shifted_filt_calibtime <=14).* GRADIENT.m2 + GRADIENT.
      t2)/100;
476
    gradientcomposition(cutted_shifted_filt_calibtime>14 &
      cutted_shifted_filt_calibtime <=16) = (</pre>
      cutted_shifted_filt_calibtime(cutted_shifted_filt_calibtime>14
      & cutted_shifted_filt_calibtime <=16).* GRADIENT.m3 + GRADIENT.
      t3)./100;
477
    gradientcomposition(cutted_shifted_filt_calibtime >16) = 1;
478
479
   plot(cutted_shifted_filt_calibtime,gradientcomposition)
480
   figure
481
   yyaxis left
482
   plot(cutted_shifted_filt_calibtime,gradientcomposition.*90)
   ylim([0 100])
483
484
485
   yyaxis right
486
   plot(CaliDF(:,1), CaliDF(:,2));
487
    legend('Solvent Gradient','Calibration \DeltaF','Location',"south
488
      ")
    xlim([0 20])
489
490
    concentration_sprayed=ones(length(cutted_shifted_filt_calibtime)
       ,1);
491
492
    concentration_sprayed=gradientcomposition.*GRADIENT.sample_meoh +
      (1-gradientcomposition).* GRADIENT.sample_h2o;
493
    figure
494
495
    plot(cutted_shifted_filt_calibtime, concentration_sprayed)
496
    Calculation of sprayed concentration
497
    Isocratic: Run if isocratic, input the solvent composition of MeOH
498
499
```

```
%
500
      Isocratic!!++++++calculation of sprayed conc.
501
   %%% deactive if with Gradient
   % GRADIENT.sample_meoh=290.6055516;
502
   % GRADIENT.sample_h2o=290.2358244;
503
504
   %
505
   % gradient_HPLC=0.3333;
506
   %
507
   % concentration_sprayed=GRADIENT.sample_meoh.*gradient_HPLC+
      GRADIENT.sample_h2o.*(1-gradient_HPLC);
   sample concentration calculated
508
   if length(cutted_shifted_filt_calibfreq)< length(</pre>
509
      cutted_shifted_filt_SAMPLEfreq)
510
        cutted_shifted_filt_SAMPLEfreq=cutted_shifted_filt_SAMPLEfreq
          (1:length(cutted_shifted_filt_calibfreq));
        cutted_shifted_filt_SAMPLEtime=cutted_shifted_filt_SAMPLEtime
511
           (1:length(cutted_shifted_filt_calibfreg));
512
        concentration_sprayed=concentration_sprayed(1:length(
          cutted_shifted_filt_calibfreq));
   else
513
        cutted_shifted_filt_calibfreq=cutted_shifted_filt_calibfreq(1:
514
          length(cutted_shifted_filt_SAMPLEfreq));
        cutted_shifted_filt_calibfreq=cutted_shifted_filt_calibfreq(1:
515
          length(cutted_shifted_filt_SAMPLEtime));
516
        concentration_sprayed=concentration_sprayed(1:length(
          cutted_shifted_filt_SAMPLEfreq));
517
   end
518
519
                 -----sample concentration calculated
520
   concentration_sample_passedColumn=cutted_shifted_filt_SAMPLEfreq./
521
      cutted_shifted_filt_calibfreq.*concentration_sprayed;
522
523
   %//////plot
524
```

```
525
   %%%%%Mass Calculation
526
527
   para.MassInteEndtime=20;
528
   validtimeframe=cutted_shifted_filt_SAMPLEtime>=0 &
529
       cutted_shifted_filt_SAMPLEtime <= para.MassInteEndtime &</pre>
       concentration_sample_passedColumn >=0;
530
531
    SprayTotalMass=trapz(cutted_shifted_filt_SAMPLEtime(validtimeframe
      ), concentration_sample_passedColumn(validtimeframe))/2000
    SprayTotalMass = 1.9785
532
533
   TheoInjectedNOM=1.80;
   MassBalance=SprayTotalMass/TheoInjectedNOM
534
535
   FinalResult=table(cutted_shifted_filt_SAMPLEtime,
       concentration_sample_passedColumn);
536
537
   % % % % % % % % % % % % % % % % % % export excel
538
   FinalResult=table(cutted_shifted_filt_SAMPLEtime,
539
       concentration_sample_passedColumn);
540
541
   FinalResult.Properties.VariableNames = { 'Time_min', 'Mass Conc. /
      mg/L'};
542
543
   TableFinalResult=FinalResult;
544
    excelcolumn={'A2','C2','E2','G2','I2', 'K2', 'M2','O2','Q2', 'S2',
        'U2','W2', 'Y2'};
545
    excelfilename = [para.Projecttitle 'TableFinalResult.xlsx'];
546
547
    writetable(TableFinalResult, excelfilename, 'Sheet', 1, 'Range',
      excelcolumn{1})
548
549 \mid f = figure;
550 | u = f.Units;
```

```
551
    f.Units = 'normalized';
552
553
   % % legend([p1 p3],{'First','Third'})
554
555
   xlim([0,20])
556
557
    g_1=gca;
558
559
    plot_1=plot(cutted_shifted_filt_SAMPLEtime,
       concentration_sample_passedColumn, 'LineWidth',2,"Color",'k');
   ylim ([-10,700])
560
561
   xlim([0,20])
   g_1.YColor = 'k';
562
563
   xlabel('Time /min');
564
   % legend('QCM')
565
566
   Y1=ylabel('Mass /mg');
                              label
    xlim_1=get(g_1, 'xlim');
567
   ylim_1=get(g_1, 'ylim');
568
569
570
   pos_2=get(g_1, 'position');
571
   g_2=axes('Position',pos_2,'Color','none','XTick',[],'YAxisLocation
       ', 'right');
   Y2=ylabel('UV-Vis'); label
572
573
   g_2.YColor='k';
574
   hold on;
   plot_2=plot(UVtime{1}, UVintensity{1},'-','LineWidth',1,"Color",'
575
       #0072BD');
576
577
   xlim([0,20])
578
   % ylim ([0,100])
579
   pos_1=g_1.Position;
580
   pos_1(1) = pos_1(1) - 0.03;
581
   pos_1(3)=pos_1(3)*0.9;
```

```
582
   g_3=axes('Position', pos_1, 'Color', 'none', 'XTick', [], 'YTick', []);
583
584
   set([g_1;g_2;g_3], 'position', pos_1);
585
   hold on;
586
   plot_3=plot(GradientX,GradientY,'-','LineWidth',1,"Color", '#
587
      D95319');
   % legend('Gradient: MeOH %')
588
589
   xlim([0,20])
590
   ylim ([0,100])
591
592
   pos_4=pos_1;
   pos_4(3) = pos_4(3) + 0.1;
593
594
   g_4=axes('Position',pos_4,'Color','none','XTick',[],'YLim',[0
      100], 'YTick', [0:10:100], 'YAxisLocation', 'right');
595
596
   Y3=ylabel('MeOH %'); label
   legend([plot_1,plot_2, plot_3], {'QCM','220nm PestMix','Gradient:
597
      MeOH %'}, 'Location', "northwest", "Box", "off")
598
599
   g_4.YColor='k';
600
   grid off;
   title(para.Projecttitle)
601
   602
603
   Peaktime=[];
   Peaktime(1,:)=[6.258 6.883];
604
   Peaktime(2,:)=[6.700 7.317];
605
   Peaktime(3,:)=[6.983 7.575];
606
   Peaktime(4,:)=[8.125 8.675];
607
   Peaktime(5,:)=[9.183 9.750];
608
609
   Peaktime(6,:)=[9.908 10.433];
610
   Peaktime(7,:)=[10.125 10.783];
   Peaktime(8,:)=[10.367 10.908];
611
612
```

D Supporting Information to Chapter 4

613	<pre>for i=1:length(Peaktime)</pre>
614	<pre>Peak_Starttime=Peaktime(i,1);</pre>
615	<pre>Peak_Endtime=Peaktime(i,2);</pre>
616	<pre>Peaktimedata=cutted_shifted_filt_SAMPLEtime>=Peak_Starttime&</pre>
	<pre>cutted_shifted_filt_SAMPLEtime <= Peak_Endtime;</pre>
617	<pre>Spray_Peak_NOMMass(i)=trapz(cutted_shifted_filt_SAMPLEtime(</pre>
	<pre>Peaktimedata),concentration_sample_passedColumn(</pre>
	Peaktimedata))/2000;
618	
619	end
620	Spray_Peak_NOMMass
621	RelNOM_Peak=Spray_Peak_NOMMass/SprayTotalMass*100

E Supporting Information to Chapter 5

E.1 Chemicals, Materials, and Standard Solutions

All chemicals and materials purchased commercially and used in this work are summarized in Table A.4.1. Additional information on the selected model analytes can be found in Table A.4.2.

Chemical	Purity/Grade	Supplier				
2,6-dichlorobenzamide (BAM)	PESTANAL [®] , anal. st.	Sigma-Aldrich				
atrazine (ATZ)	PESTANAL [®] , anal. st.	Sigma-Aldrich				
azoxystrobin (AZOX)	PESTANAL [®] , anal. st.	Sigma-Aldrich				
boscalid (BOSC)	PESTANAL [®] , anal. st.	Sigma-Aldrich				
caffeine (CAF), USGS63		USGS				
desethylatrazine (DEA)	PESTANAL [®] , anal. st.	Sigma-Aldrich				
desisopropylatrazine (DIA)	PESTANAL [®] , anal. st.	Sigma-Aldrich				
methanol	≥99%	Sigma-Aldrich				
simazine (SIM)	PESTANAL [®] , anal. st.	Sigma-Aldrich				
sodium chloride	≥99.5%	Fisher Scientific				
anal, st. = analytical standard						

 Table A.4.1 List of reagents, solvents, and analytical standards.

Ultrapure H₂O (18.2 M Ω cm at 25 °C) was obtained from a Milli-Q[®] direct reference H₂O purification system from Merck MilliPore (Burlington, USA). Stock solutions of analytical standards (1 g/L) were prepared in CH₃OH and stored at -18 °C.

Table A.4.2 Additional information on the selected model analytes including the chemical formula, the isotope signature of the specific batch used, the molecular weight, the $\log K_{OW}$ and the charge at pH7.

Name	Formula	Isotope Signature	Molecular Weight	logK _{OW}	Charge pH 7
			[g/mol]	[-]	[-]
BAM	C7H5Cl2NO	n.a.	190.02	0.77	n
ATZ	C ₈ H ₁₄ ClN ₅	-29,56	215.68	2.61	n
AZOX	$C_{22}H_{17}N_3O_5$	n.a.	403.4	2.50	n
BOSC	$C_{18}H_{12}Cl_2N_2O$	n.a.	343.2	2.96	n
CAF	$C_8H_{10}N_4O_2$	-1,17	194.19	-0.07	n
DEA	$C_6H_{10}ClN_5$	-29,39	187.63	1.51	n
DIA	C ₅ H ₈ ClN ₅	-36,78	173.60	1.50	n
SIM	$C_7H_{12}ClN_5$	n.a.	201.66	2.18	n

n.a. = not available, n = neutral.

E.2 Extraction of Riverine NOM

Surface water samples (Wiesäckerbach, latitude 48.269009, longitude 11.667976, Garching, Germany) were filtered using glass microfiber filter membranes (1.2 μ m particle retention, 47 mm diameter, Whatman, UK). NOM was extracted using Oasis HLB SPE material (Waters, 200 mg, 6 cc) and an automated SPE system (Smart Prep Extractor, Horizon Technology, USA). The extraction was performed using conventional SPE conditions at 5 mL/min. The Oasis HLB cartridges were dried overnight under vacuum and eluted using 5 mL of CH₃OH. The eluates were combined, reduced under a gentle stream of nitrogen at 30 °C, and stored at -18 °C. TOC analysis (TOC-L, Shimadzu, Japan) was used to determine the carbon content of the eluate. Elemental analysis (EURO-EA, HEKATech, Germany) was used to determine the percentage of carbon in the extracted NOM (see Table A.4.3).

Content in %
51.20
6.56
2.02
0.51
39.71

Table A.4.3 Elemental analysis of NOM extracted from Wiesäckerbach using Oasis HLB.

E.3 Compound Specific Isotope Analysis: Method Detection Limits, $\Delta \partial^{13}$ C Data, and Chromatogram Background Data

Table A.4.4 HPLC gradient used for purifying NOM sample prior to GC-c-IRMS measurement.

t/ min									
0	0 7.5 15 16.5 18								
% of CH ₃ OH									
10 90 90 90 90									

Table A.4.5 Method detection limits (nmol C) for GC-IRMS measurements determined according to the moving mean procedure with an uncertainty limit of $\pm 0.5\%$ and the corresponding analyte amplitude at m/z 44 in mV.

Analyte	MQL nmol C on column	Amplitude/ mV
ATZ	1	818 ± 24
DIA	2	1172 ± 156
DEA	3	2489 ± 78
CAF	4	3643 ± 71

Data



Figure A.4.1 Determination of Method detection limits (nmol C) for GC-IRMS measurements with an uncertainty limit of $\pm 0.5\%$ (dotted lines) for four analytes: (a) DEA, (b) DIA, (c) ATZ, and (d) CAF. The measured ∂^{13} C values are shown in black, and the respective peak amplitude in red (m/z 44 in mV). Isotope values and amplitudes are arithmetic means of at least triplicate measurements with their respective standard deviation.

Table A.4.6 Determined ratio of background area to analyte area in the GC-IRMS chromatogram is shown as matrix fraction (f_{matrix}) in %. Using this ratio, theoretically determined isotope shifts were calculated ($\Delta \partial^{13}C_{calc}$ in ‰) using the isotope value of the analyte and NOM ($\partial^{13}C \approx 27\pm1$). The experimentally determined isotope shifts are shown for comparison as $\Delta \partial^{13}C_{exp}$ in ‰.

compound	NOM/analyte ratio	f _{matrix}	$\Delta \partial^{13} C_{calc}$	$\Delta \partial^{13} C_{exp}$
		[%]	[‰]	[‰]
	10	17.8 ± 0.5	1.74 ± 0.05	0.43 ± 0.23
DIA	20	26 ± 4	2.54 ± 0.39	0.58 ± 0.07
DIA	50	42 ± 6	4.11 ± 0.59	0.99 ± 0.42
	100	54 ± 8	5.18 ± 0.78	1.33 ± 0.60
	10	11.1 ± 0.1	0.26 ± 0.00	0.18 ± 0.20
	20	20 ± 1	0.47 ± 0.01	-0.04 ± 0.19
DEA	50	36 ± 2	0.87 ± 0.05	-0.08 ± 0.45
	100	48 ± 7	1.15 ± 0.17	-0.44 ± 0.20
	10	9.5 ± 0.2	0.24 ± 0.00	0.46 ± 0.40
۸ Т7	20	15.6 ± 0.4	0.40 ± 0.01	0.34 ± 0.16
AIL	50	33 ± 3	0.84 ± 0.07	0.40 ± 0.30
	100	49 ± 2	1.25 ± 0.05	0.42 ± 0.38
	10	20 ± 1	-5.17 ± 0.23	-1.02 ± 0.44
CAE	20	22 ± 1	-5.79 ± 0.16	-0.79 ± 0.09
CAF	50	40 ± 4	-10.34 ± 1.03	-1.89 ± 0.23
	100	56 ± 11	-14.48 ± 2.84	-3.30 ± 0.78



Figure A.4.2 Deviations of carbon isotope values ($\Delta \partial^{13}$ C in black) of (a) DIA, (b) DEA, (c) ATZ, and (d) CAF during the measurement of samples containing NOM in different amounts (NOM/analyte ratios: 10, 20, 50, 100) from the values of standard measurements. The dotted black lines show the uncertainty limit of carbon isotope analysis using GC-IRMS ($\pm 0.5\%$). The error bars resemble the 95% confidence interval of triplicate measurements. The red data point shows a measurement after an HPLC clean-up using 10-60-90 gradient and column 1 of a sample containing NOM/analyte ratio 100 with an expected final NOM/analyte ratio of 8 after the clean-up.

E.4 Details on HPLC Gradients and QCM Dry Mass Sensing Results

Table A.4.7 22 HPLC gradients used to optimize separation of analytes and NOM on XTerra RP18. Mobile phase consistsof methanol and water.

		t/ mi	n					
0	7.5	15	16.5	18				
% of methanol								
10	30	60	90	90				
10	30	70	90	90				
10	30	80	90	90				
10	30	90	90	90				
10	40	60	90	90				
10	40	70	90	90				
10	40	80	90	90				
10	40	90	90	90				
10	50	60	90	90				
10	50	70	90	90				
10	50	80	90	90				
10	50	90	90	90				
10	60	60	90	90				
10	60	70	90	90				
10	60	80	90	90				
10	60	90	90	90				
10	70	70	90	90				
10	70	80	90	90				
10	70	90	90	90				
10	80	80	90	90				
10	80	90	90	90				
10	90	90	90	90				

Table A.4.8 7 HPLC gradients used to optimize separation of analytes and NOM on Orbit 100 C8. Mobile phase consists of methanol and water.

t/ min							
0	7.5	15	16.5	18			
	% o	f met	hanol				
10	30	60	90	90			
10	40	80	90	90			
10	50	60	90	90			
10	60	70	90	90			
10	70	90	90	90			
10	80	90	90	90			
10	90	90	90	90			

Table A.4.9 Theoretical plate number for gradient 10-70-90.

	CAF	BAM	DIA	DEA	SIM	ATZ	AZOX	BOSC
XTerra RP18	822	800	2061	5639	11294	13795	28775	27699
Orbit 100 C8	10384	10605	15990	28947	41653	49415	50835	54224



Figure A.4.3 The NOM co-elution in % on XTerra RP18 column is plotted for the 22 different gradients for 4 analytes ((a): BAM, (b): DIA, (c): ATZ, (d): AZOX). The x-axis represents the % of methanol at minute 7.5 during the HPLC clean-up and the y-axis % of methanol at minute 15.

Gradient	CAF	BAM	DIA	DEA
10-30-60	14.8 ± 0.8	10.2 ± 0.8	11.7	10.6
10-30-70	14.8 ± 0.8	10.2 ± 0.8	12.6	9.8
10-30-80	14.8 ± 0.8	10.2 ± 0.8	11.0	8.9
10-30-90	14.8 ± 0.8	10.2 ± 0.8	11.7	8.6
10-40-60	12.3 ± 1.0	8.7 ± 0.7	10.5	10.2
10-40-70	12.3 ± 1.0	8.7 ± 0.7	9.2	9.6
10-40-80	12.3 ± 1.0	8.7 ± 0.7	9.7 ± 0.3	10.5 ± 0.9
10-40-90	12.3 ± 1.0	8.7 ± 0.7	8.8	9.3
10-50-60	11.3 ± 0.7	8.8 ± 0.7	9.1 ± 0.8	10.9 ± 0.5
10-50-70	11.3 ± 0.7	8.8 ± 0.7	9.1 ± 0.8	10.3
10-50-80	11.3 ± 0.7	8.8 ± 0.7	9.1 ± 0.8	10.2
10-50-90	11.3 ± 0.7	8.8 ± 0.7	9.1 ± 0.8	8.7
10-60-60	8.2 ± 0.1	7.5 ± 0.2	8.5 ± 1.1	11.0
10-60-70	8.2 ± 0.1	7.5 ± 0.2	8.5 ± 1.1	11.6
10-60-80	8.2 ± 0.1	7.5 ± 0.2	8.5 ± 1.1	10.4
10-60-90	8.2 ± 0.1	7.5 ± 0.2	8.5 ± 1.1	10.3
10-70-70	8.0 ± 0.8	6.5 ± 0.6	6.8 ± 0.8	9.7
10-70-80	8.0 ± 0.8	6.5 ± 0.6	6.8 ± 0.8	9.2
10-70-90	8.0 ± 0.8	6.5 ± 0.6	6.8 ± 0.8	8.6
10-80-80	8.0 ± 0.5	6.4 ± 0.5	6.9 ± 0.6	8.7 ± 0.9
10-80-90	8.0 ± 0.5	6.4 ± 0.5	6.9 ± 0.6	8.7 ± 0.9
10-90-90	8.6	6.8	7.8	7.2

Table A.4.10 NOM co-elution in % shown for 22 HPLC gradients on XTerra RP18. Gradient: first number represents % of methanol at min 0, second number at min 7.5, and third number at min 15.

Gradient	SIM	AT7	170Y	BOSC
10-30-60	0.0	5.2	2.5	5.2
10-30-70	6.5	4.6	3.6	3.4
10-30-80	7.4	5.2	4.0	2.8
10-30-90	5.3	5.0	5.8	4.6
10-40-60	8.0	5.3	3.7	2.0
10-40-70	7.6	5.8	3.7	2.6
10-40-80	6.5 ± 0.6	5.6 ± 0.6	4.7 ± 0.3	3.8 ± 0.3
10-40-90	6.2	5.0	6.1	5.7
10-50-60	7.2 ± 0.7	5.4 ± 0.4	4.4 ± 0.8	2.4 ± 0.4
10-50-70	8.1	5.8	4.5	2.0
10-50-80	8.1	5.8	5.0	2.7
10-50-90	7.8	5.3	5.2	3.3
10-60-60	11.6	10.3	9.6	6.1
10-60-70	9.3	7.4	8.8	4.3
10-60-80	7.9	6.8	8.8	5.9
10-60-90	7.3	5.6	7.9	5.8
10-70-70	10.0	8.3	9.3	6.9
10-70-80	8.5	7.4	9.9	7.4
10-70-90	8.4	8.0	11.5	8.7
10-80-80	10.9	12.0	8.3	7.7
10-80-90	9.6 ± 0.4	8.2 ± 0.5	7.2 ± 0.6	6.6 ± 0.7
10-90-90	8.3	10.2	8.2	7.6

Table A.4.11 NOM co-elution in % shown for 22 HPLC gradients on XTerra RP18. Gradient: first number represents % of methanol at min 0, second number at min 7.5, and third number at min 15.

Table A.4.12 NOM co-elution in % shown for 7 HPLC gradients on Orbit 100 C8. Gradient: first number represents % of methanol at min 0, second number at min 7.5, and third number at min 15.

Gradient	CAF	BAM	DIA	DEA
10-30-60	7.4	7.5	8.8	6.9
10-40-80	5.0	6.0	5.7	7.2
10-50-60	4.5	6.3	7.2	13.2
10-60-70	4.6	6.0	6.5	7.7
10-70-90	4.7	5.5	5.3	7.6
10-80-90	3.2	4.6	5.1	7.0
10-90-90	4.9	4.9	4.7	7.9

Table A.4.13 NOM co-elution in % shown for 7 HPLC gradients on Orbit 100 C8. Gradient: first number represents % of methanol at min 0, second number at min 7.5, and third number at min 15.

Gradient	SIM	ATZ	AZOX	BOSC
10-30-60	3.6	2.9	2.7	1.9
10-40-80	6.3	5.1	3.5	2.7
10-50-60	8.9	2.3	0.6	0.2
10-60-70	10.0	6.8	2.5	1.7
10-70-90	8.0	6.0	10.4	6.8
10-80-90	8.1	6.9	8.3	6.6
10-90-90	9.0	8.2	7.6	5.9



Figure A.4.4 Comparison of NOM retention on XTerra RP18 (blue) and Orbit 100 C8 (grey). The bands resemble all measured NOM values (in %/min) between the maximal and the minimal value determined for 22 gradients in case of column 1 (XTerra RP18 Column, 150×3.0 mm, 3.5 µm, pore size 125 Å) and 7 gradients in case of column 2 (Orbit 100 C8 Column, 150×3.0 mm, 3.5 µm, pore size 100 Å).



Figure A.4.5 Gradient screening of CAF using 3, 5, 7, 10, 12, 15, 18, or 22 different gradients on XTerra RP18.



Figure A.4.6 Gradient screening of BAM using 3, 5, 7, 10, 12, 15, 18, or 22 different gradients on XTerra RP18.



Figure A.4.7 Gradient screening of DIA using 3, 5, 7, 10, 12, 15, 18, or 22 different gradients on XTerra RP18.



Figure A.4.8 Gradient screening of DEA using 3, 5, 7, 10, 12, 15, 18, or 22 different gradients on XTerra RP18.



Figure A.4.9 Gradient screening of SIM using 3, 5, 7, 10, 12, 15, 18, or 22 different gradients on XTerra RP18.



Figure A.4.10 Gradient screening of ATZ using 3, 5, 7, 10, 12, 15, 18, or 22 different gradients on XTerra RP18.



Figure A.4.11 Gradient screening of AZOX using 3, 5, 7, 10, 12, 15, 18, or 22 different gradients on XTerra RP18.



Figure A.4.12 Gradient screening of BOSC using 3, 5, 7, 10, 12, 15, 18, or 22 different gradients on XTerra RP18.



Figure A.4.13 NOM co-elution average for HPLC purification on XTerra RP18 of two or three compounds (early eluting: CAF, middle eluting: DEA, late eluting: BOSC).



Figure A.4.14 NOM co-elution average for HPLC purification on XTerra RP18 of two or three compounds (early eluting: CAF, middle eluting: SIM, late eluting: BOSC).



Figure A.4.15 Gradient screening for the individual compounds SIM and BOSC and their NOM co-elution average for HPLC purification on XTerra RP18 of both compounds at the same time (SIM+BOSC). The optimal gradient with the lowest NOM co-elution is encircled both for the individual compound purification (SIM, BOSC, gradient_i) and multiple compound purification (SIM+BOSC, gradient_m). The arrows show the difference between the optimal gradient_i and the optimal gradient_m, the number next to the arrows the difference of NOM co-elution in % between gradient_i and gradient_m.

Number of Gradients	CAF	BAM	DIA	DEA
3	8.2	6.8	7.8	7.2
5	8.0	6.4	6.8	7.2
7	8.0	6.4	6.8	7.2
10	8.0	6.4	6.8	7.2
12	8.0	6.4	6.8	7.2
15	8.0	6.4	6.8	7.2
18	8.0	6.4	6.8	7.2
22	8.0	6.4	6.8	7.2

Table A.4.14 Minimal NOM co-elution on XTerra RP18 column dependent on the number of gradients screened (from 3 to 22 gradients). All gradient mixes include convex, concave, and linear gradients. The number of gradients that is sufficient to find the optimal conditions within a precision of 1% is marked bold.

Table A.4.15 Minimal NOM co-elution on XTerra RP18 column dependent on the number of gradients screened (from 3 to 22 gradients). All gradient mixes include convex, concave, and linear gradients. The number of gradients that is sufficient to find the optimal conditions within a precision of 1% is marked bold.

Number of Gradients	SIM	ATZ	AZOX	BOSC
3	6.6	3.2	2.3	3.2
5	6.2	3.2	2.3	2.0
7	6.2	3.2	2.3	2.0
10	5.3	3.2	2.3	2.4
12	5.3	3.2	2.3	2.4
15	5.3	3.2	2.3	2.0
18	5.3	3.2	2.3	2.0
22	5.3	3.2	2.3	2.0

 Table A.4.16 Analyte recovery in % during HPLC purification.

DIA	DEA	ATZ	BOSC
91.4 ± 4.8	86.2±0.1	84.9 ± 3.1	89.2±4.3

Table A.4.17 Higher NOM co-extraction during an optimized multi compound HPLC purification on XTerra RP18 incomparison to the optimized HPLC purification for a single compound is shown as optimization loss in % NOM (loss/ %).%). The different compounds are classified into early, middle, and late eluting.

	compound	1		loss/%	
early	middle	late	early	middle	late
CAF	DEA		0.6	0	
CAF	SIM		0.2	2.0	
BAM	DEA		0.5	0	
BAM	SIM		1.1	2.0	
CAE		۸ Т7	0.2		24
CAF			0.2		2. 4 4 9
CAF		BOSC	0.2		23
BAM		ATZ	1.1		2.5 2.4
BAM		AZOX	24		1.4
BAM		BOSC	2.4		0
	DEA	ATZ		1.4	1.9
	DEA	AZOX		1.7	1.7
	DEA	BOSC		1.7	0.9
	SIM	ATZ		1.3	0
	SIM	AZOX		1.3	0
	SIM	BOSC		1.9	0.4
BAM	DEA	ATZ	0	1.4	4.8
BAM	DEA	ATZ	2.4	2.1	1.8
BAM	DEA	ATZ	2.5	1.5	2.1
BAM	DEA	AZOX	2.4	2.4	1.4
BAM	DEA	AZOX	2.5	1.5	2.9
BAM	DEA	AZOX	0.5	0	5.9
BAM	SIM	ATZ	3.9	1.3	0
BAM	SIM	ATZ	2.4	0.9	1.8
BAM	SIM	ATZ	1.1	2.0	2.4
BAM	SIM	AZOX	3.9	1.3	0
BAM	SIM	AZOX	2.4	1.2	2.4
CAF	DEA	BOSC	3.3	1.5	1.4
CAF	DEA	BOSC	0	1.5	4.7
CAF	DEA	BOSC	3.3	3.1	0
CAF	SIM	BOSC	3.3	1.9	0.4
CAF	SIM	BOSC	0.2	2.0	3.9

	compound	ł		loss/%	
early	middle	late	early	middle	late
CAF	DEA		0	0.1	
CAF	SIM		4.3	0	
BAM	DEA		0	0.1	
BAM	SIM		2.9	0	
CAF		ATZ	1.3		0
CAF		AZOX	1.3		0
CAF		BOSC	1.3		0
BAM		ATZ	1.7		0
BAM		AZOX	1.7		0
BAM		BOSC	1.7		0
	DEA	ATZ		0	0.6
	DEA	AZOX		0	2.1
	DEA	BOSC		0	1.8
	SIM	ATZ		0	0.6
	SIM	AZOX		0	2.1
	SIM	BOSC		0	1.8
BAM	DEA	ATZ	2.9	0	0.6
BAM	DEA	AZOX	2.9	0	2.1
BAM	DEA	AZOX	1.4	0.8	1.9
BAM	SIM	ATZ	2.9	0	0.6
BAM	SIM	AZOX	2.9	0	2.1
CAF	DEA	BOSC	1.5	0.8	1.5
CAF	SIM	BOSC	4.3	0	1.8

Table A.4.18 Higher NOM co-extraction during an optimized multi compound HPLC purification on Orbit 100 C8 in comparison to the optimized HPLC purification for a single compound is shown as optimization loss in % NOM (loss/%). The different compounds are classified into early, middle, and late eluting.

publication	compounds	matrix	column
Schreglmann et al. ⁶⁸	pesticides	water	ODS (30) Ultracarb
Piper et al. ²⁸	steroids	urine	LiChrospher 100 RP18
Melsbach et al. ⁶⁶	pesticides	water	Synergi Hydro-RP
Tripp et al. ⁷⁵	amino acids	bones	Waters Symmetry or Supelco Discovery HS F5
Lalonde et al. ⁷⁶	steroids	urine	Zorbax Eclipse XDB Phenyl column
			and Zorbax Eclipse XDB-C18 columns
Swalethorp et al. ⁷⁷	amino acids	fish	Primesep A
Yun et al. ⁷⁸	pesticides	plants	Zorbax Eclips XDB C18
Cheng et al. ⁷⁹	hexabromocyclododecane	no	Zorbax SB-C18
Shrivastava et al. ⁸⁴²	steroids	urine	LiChroCART
Akamatsu et al. ²⁶²	glucose	sake	VG50-4E
Murata et al. ⁸⁴³	aroma compounds	green tea	CAPCELLPAK ODS
Zhu et al. ⁸⁴⁴	decabrominated diphenyl ether	no	Zorbax Eclipse Plus-C18
Iannella et al. ⁸⁴⁵	prednisolone or prednisone	pharmaceutical formulation	ACE® C18
Saccon et al. ⁸⁴⁶	phenols	air	Supelco Supelcosil TM LC-18
Broek et al. ⁸⁴⁷	amino acids	proteinaceous samples	SiELC Primesep A
Drenzek et al. ⁵²⁴	PCBs	bacteria culture	Chrompack Chromsep Omnipher 5 C18

Table A.4.19 Overview of columns used in the field of CSIA during HPLC purification of compounds present in different sample matrices.

Abbreviations

Г	Bandwidth of the resonance
γ-MAPS	γ -Methacryloxypropyltrimethoxysilane
$\Delta \mathbf{f}$	Resonance frequency change
AIBN	2,2'-Azobis(2-methylpropionitrile
ATZ	Atrazine
AZOX	Azoxystrobin
BAM	2,6-dichlorobenzamide
BOSC	Boscalid
BTEX	Benzene, toluene, ethylbenzene, and xylene
С	Mass sensitivity coefficient
CAD	Charged aerosol detector
CAF	Caffeine
COF	Covalent organic framework
CSIA	Compound-specific isotope analysis
D	Dissipation
DAD	Diode array detector
DCM	Dichloromethane
DEA	Desethylatrazine
D _{hyd}	Hydraulic diameter
DIA	Desisopropylatrazine

EDX	Energy dispersive X-ray mapping
EGDMA	Ethylene glycol dimethacrylate
ELSD	Evaporative light-scattering detector
f ₀	Fundamental frequency
FTIR	Fourier-transform infrared
GC-c-IRMS	Gas chromatography combustion isotope ratio mass spectrometry
НСН	Hexachlorocyclohexane
HPLC	High-performance liquid chromatography
IAC	Immunoaffinity chromatography
IEC	Ion-exchange chromatography
LLE	Liquid-liquid extraction
LOD	Limits of detection
LOQ	Limits of quantification
MAA	Methacrylic acid
ME%	Matrix effect in percent
MeOH	Methanol
MIPs	Molecularly imprinted polymers
MISPE	Molecularly imprinted solid phase extraction
MOF	Metal organic framework
MQL	Method detection limits
NOM	Natural organic matter
NVP	N-vinylpyrrolidone
РАН	Polycyclic aromatic hydrocarbon
РСВ	Polychlorinated biphenyl

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PCDD	Polychlorinated	dibenzodioxins
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- PDMS Polydimethylsiloxane
- **Prop** Propargite
- **PS-DVB** Polystyrene-divinylbenzene
- **P&T** Purge and trap
- PTFE Polytetrafluorethylene
- **QCM** Quartz crystal microbalance
- **QCM-D** QCM with dissipation measurement
- **QCM-R** QCM with resistance measurement
- **RAFT** Reversible addition-fragmentation chain-transfer
- **RP** Reversed-phase
- SEM Scanning electron microscopy imaging
- SIM Simazine
- SPE Solid phase extraction
- TMSD Trimethylsilyl diazomethane
- **TOC** Total organic carbon
- UV/Vis UV-Visible spectrometry
- T. C. Schmidt, L. Zwank, M. Elsner, M. Berg, R. U. Meckenstock, S. B. Haderlein, Compound-specific stable isotope analysis of organic contaminants in natural environments: a critical review of the state of the art, prospects, and future challenges, Analytical and Bioanalytical Chemistry 378 (2004) 283–300.
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