DeltaMS - A Convenient tool to track isotopologues in GC/LC MS data

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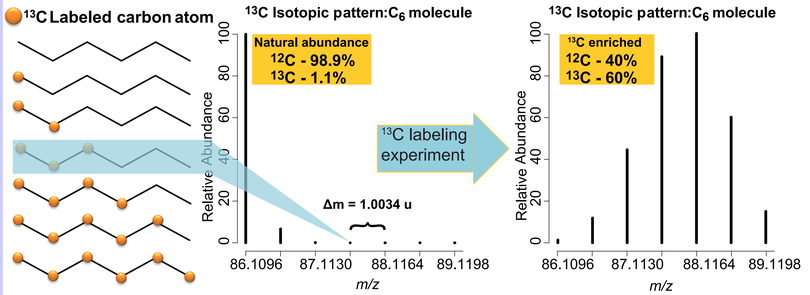
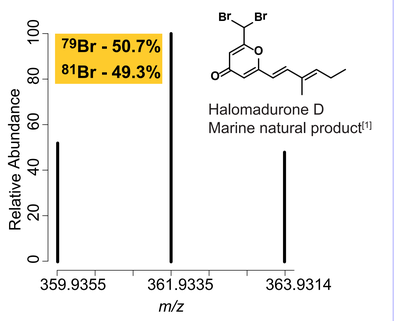
since 1558

Background

Isotopologues: Compounds that differ in their isotopic composition

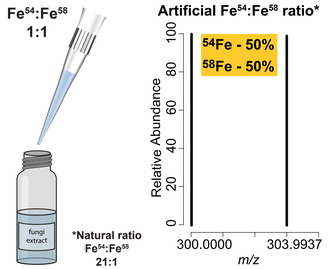


Distinctive isotopologue pattern



Metallophore detection

- Artificial isotope ratio enrichment[2]



Development of isotopologue finder that is..

For detection of: characterstic Δm
distinctive isotope pattern
multilabeled species

Δm and isotope ratio detection

- XCMS[3] for pre-processing of MS data
- X^{13}CMS functions as foundation for Δm detection[4]
- Add isotope ratio detection

Develeopment of user interface

- R package "shiny" for interface development[5]
- App has to be employable offline on local computer

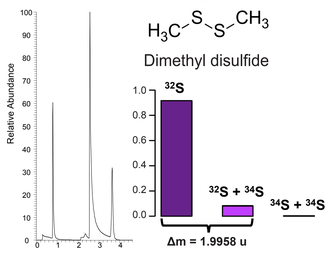
RStudio

DeltaMS Interface

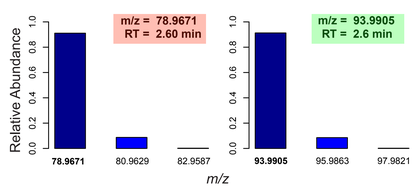
1st Select experiment
2nd Select MS files folder
3rd Select Δm and isotope ratio
4th Pre-processing / report settings
5th Start analysis

DeltaMS output: GC-EI-Orbitrap analysis of DMDS

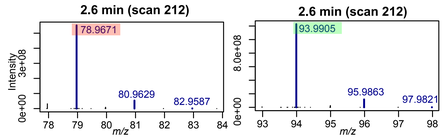
A GC-EI profile of dimethyl disulfide (DMDS) and the expected isotopologue pattern



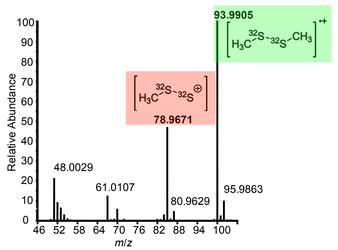
B Identified ions that match Δm and expected isotopologue ratio.



C Mass spectrum of identified ions extracted from raw data file



D Spectrum of raw file. Identified signals in bold and putative structure



Applications

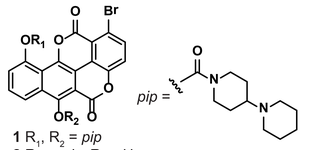
Drug metabolism

Objective
K-562 leukemia cells were treated with **1** for 48 h to identify biotransfornation products.[6]

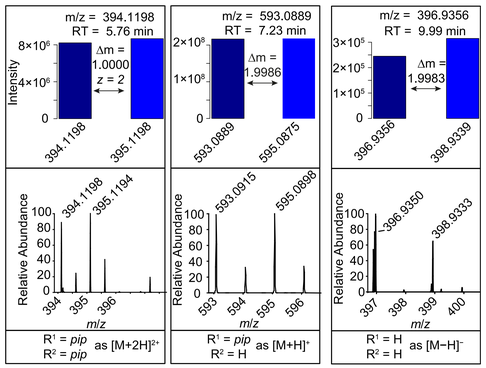
Methods
Metabolomic analysis of methanolic cell extract with HPLC-ESI-Orbitrap (R = 70,000, FWHM)

DeltaMS parameters:
Experiment = 1
Peak detection = matchedFilter *fwhm* = 5
mzdiff = 0.01 *errRatio* = 10% *ppm* = 3
isotope1 = ^{79}Br *isotope2* = ^{81}Br

Results
Compound **1** as well as **2** and **3** as phase one metabolites could be detected.



1 R_1, R_2 = *pip*
2 R_1, = *pip* ,R_2 = H
3 R_1, = H ,R_2 = H



Siderophore detection

Objective
Trace siderophores in a fungal extract using different experimental approaches.

Methods
Analysis of differently spiked methanolic SPE extracts with UHPLC-ESI-Orbitrap (R = 70,000, FWHM)

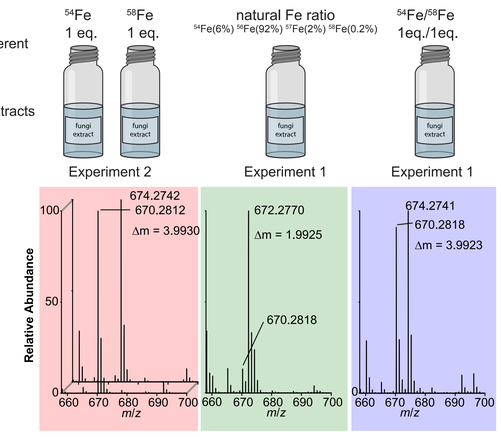
DeltaMS parameter:
Peak detection = „matchedFilter" *fwhm* = 30
mzdiff = 0.1 *errRatio* = 10% *ppm* = 5
RTwindow = 12 s

A *isotope1* = ^{54}Fe *isotope2* = ^{58}Fe
iRatio = 1 to 1

B *isotope1* = ^{58}Fe *isotope2* = ^{54}Fe
iRatio = 15.7 to 1

C *isotope1* = ^{54}Fe *isotope2* = ^{58}Fe
iRatio = 1 to 1

Results
Siderophores were detected in all individual spiked fungi extracts.



Conclusion

We designed a user-friendly app for detection of isotopologues in GC/LC-MS data

- **Reliable isotopologue recognition**
- **User-friendly interface**
- **Open-source R based**

References: [1] J. W. Blunt et al. *Natural Product Reports,* **2015**, *32*, 116-211.
[2] M. Deicke et al. *Analyst,* **2014**, *139*, 6096-6099.
[3] C. A. Smith et al. *Analytical Chemistry,* **2006**, *78*, 779-787.
[4] X. Huang et al. *Analytical Chemistry,* **2014**, *86*, 1632-1639.
[5] *shiny: Web Application Framework for R. R package version 1.0.0*, Chang, W. et al. **2017**.
[6] N. Ueberschaar et al. *Chemical Communications,* **2016**, *52*, 4894-4897.

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