

Understanding the Structural Complexity of Dissolved Organic Matter: isomeric diversity

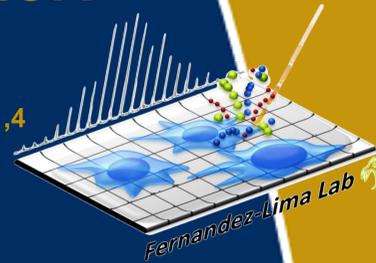
Dennys Leyva^{1,2}, Lilian V. Tose¹, Jacob Porter¹, Jeremy Wolff³, Rudolf Jaffé² and Francisco Fernandez-Lima^{1,4}

¹Department of Chemistry and Biochemistry, Florida International University, Miami, Florida, United States

²Southeast Environmental Research Center, Florida International University, Miami, Florida, United States

³Bruker Daltonics, Inc., Billerica, Massachusetts, United States

⁴Biomolecular Sciences Institute, Florida International University, Miami, Florida, United States



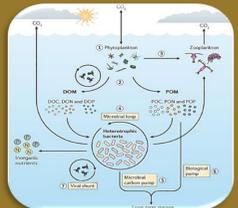
Overview

In the present work, we addressed the isomeric complexity of DOM samples collected from Pantanal (PAN) National Park (Brazil) using TIMS-FT-ICR MS. An average of 3000 chemical assignments were identified in a single infusion experiment. A high isomeric complexity (4-10 isomers per m/z signal) was found at nominal mass. An upper estimate of the number of isomers per chemical formula was provided based on unique neutral loss fragmentation patterns and core fragments resulting from the FT-ICR MS/MS analysis at nominal mass isolation.

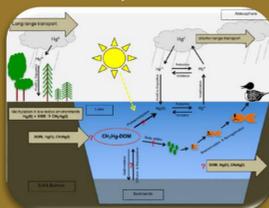
Introduction

Dissolved Organic Matter (DOM): Complex mixture resulting from the degradation of bacteria, algae, and plants.

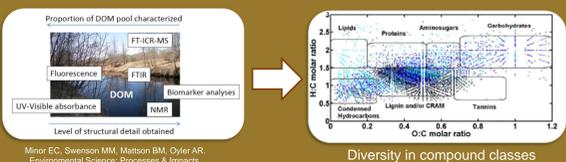
DOM in the global carbon cycle



Bioavailability of trace elements



Bulk vs Molecular level characterization



- Analysis of DOM is challenging due to its high structural heterogeneity and functionalities, isomeric complexity and wide range of molecular weights.
- Trapped Ion Mobility Spectrometry offers a promising alternative toward a more reliable isomeric characterization of DOM when coupling TIMS to FT-ICR MS

References

- M. Zark, J. Christoffers and T. Dittmar, *Marine Chemistry*, 2017, 191, 9-15.
- N. Hertkorn, M. Harir, K. M. Cawley, P. Schmitt-Kopplin and R. Jaffé, 2016.
- M. Zark and T. Dittmar, *Nature Communications*, 2018, 9, 3178.
- L. V. Tose, P. Benigni, D. Leyva, A. Sundberg, C. E. Ramirez, M. E. Ridgeway, M. A. Park, W. Romão, R. Jaffé and F. Fernandez-Lima, *Rapid Communications in Mass Spectrometry*, 2018, 32, 1287-1295.
- D. Leyva, L. Valadares, J. Porter, J. Wolff, R. Jaffé and F. Fernandez-Lima, *Faraday Discussions*, 2019, DOI: 10.1039/C8FD00221E.
- F. A. Fernandez-Lima, C. Becker, A. M. McKenna, R. P. Rodgers, A. G. Marshall and D. H. Russell, *Anal. Chem.*, 2009, 81, 9941-9947.
- P. Benigni, J. Porter, M. E. Ridgeway, M. A. Park and F. Fernandez-Lima, *Analytical Chemistry*, 2018, 90, 2446-2450.
- C. Ruttkies, E. L. Schymanski, S. Wolf, J. Hollender and S. Neumann, *Journal of Cheminformatics*, 2016, 8, 3.
- M. Witt, J. Fuchser and B. P. Koch, *Analytical Chemistry*, 2009, 81, 2688-2694.

Experimental

Sample preparation

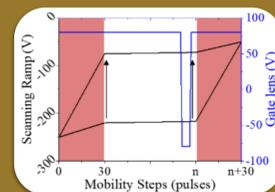
- The PAN samples were collected from the Paraguay River (PAN-L) and a wetland channel in Pantanal National Park, Brazil (PAN-S).
- DOM was dissolved in 50:50 v/v CH₃OH/H₂O (1 ppm).

TIMS-FT-ICR MS

Custom built TIMS-FT-ICRMS 7T Solarix spectrometer equipped with an infinity ICR cell (Bruker Daltonics Inc., MA).



R_{IMS} (up to 400)
R_{MS} >400,000



Non linear TIMS scan

- TIMS cell fill/trap/elute/quench sequence: 9/3/9/3 ms
- 1000 IMS scans per MS spectrum
- Voltage difference across the ΔE gradient: 5.0 V

FT-ICR MS/MS analysis

FT-ICR MS/MS experiments: quadrupole isolation at nominal mass and CID energies of 15-20 eV.

Results TIMS-FT-ICR MS

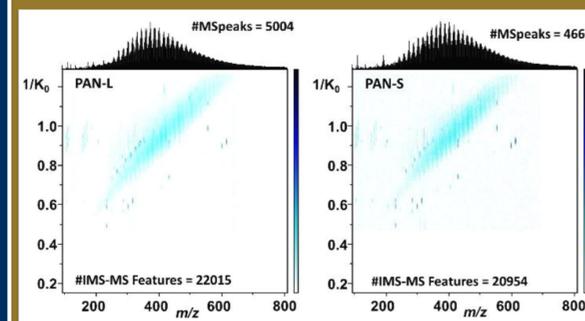


Figure 2. MS and 2D-IMS-MS contour plots of PAN samples

- 3,066 and 2,830 compounds identified in PAN-L and PAN-S samples respectively based on the general formula: C_xH_yN₀₋₃O₀₋₁₉S₀₋₁.
- Around 80% of compounds corresponded to highly conjugated oxygen species (O₁-O₂₀).

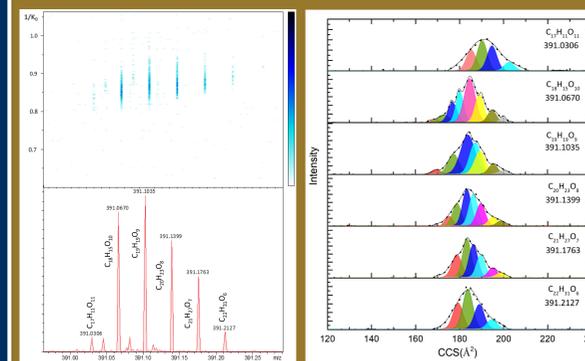
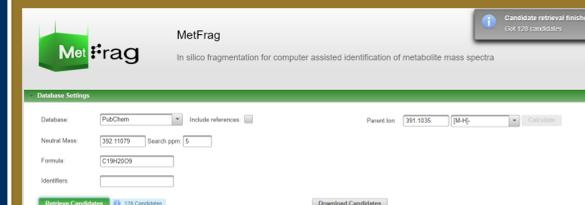


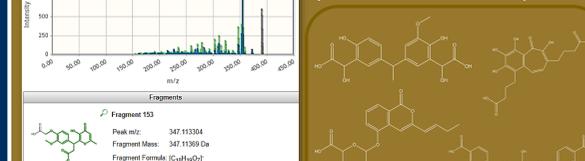
Figure 3. 2D-IMS-MS, MS and IMS projections at nominal mass 391 m/z.

Large isomeric diversity at nominal mass and per chemical formula (average of 6-10 structural and conformational isomers per chemical formula)

In silico fragmentation of m/z 391.1035 (C₁₉H₁₉O₉)



96 candidate structures based on accurate masses of precursor and fragment ions (1mDa mass tolerance).



Results FT-ICR-MS/MS

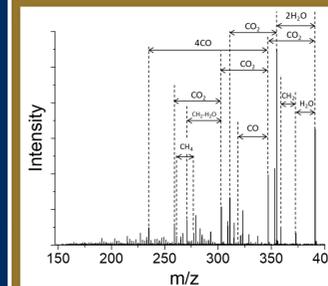
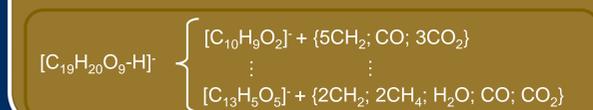


Figure 4. FT-ICR MS/MS spectrum of q-isolated 391 m/z precursor ion and subjected to CID.

Precursor ion m/z	Core Fragment m/z	Structural isomers
	161.0607	13
	C ₁₀ H ₉ O ₂	
	163.0763	7
	C ₁₀ H ₁₁ O ₂	
	165.0192	3
	C ₉ H ₉ O ₄	
	165.056	2
	C ₉ H ₉ O ₃	
	167.0349	1
	C ₉ H ₉ O ₄	
	171.0814	23
	C ₁₂ H ₁₁ O	
	173.0607	23
	C ₁₁ H ₉ O ₂	
	175.0400	15
	C ₁₀ H ₉ O ₃	
391.1035	183.0450	40
	C ₉ H ₉ O ₂	
	183.0814	25
	C ₉ H ₁₁ O	
	185.0607	29
	C ₁₂ H ₉ O ₂	
	187.0400	25
	C ₁₁ H ₉ O ₃	
	201.0192	25
	C ₁₁ H ₉ O ₄	
	202.9984	15
	C ₁₀ H ₉ O ₃	
	205.0140	7
	C ₁₀ H ₉ O ₃	
	241.0140	7
	C ₁₁ H ₉ O ₂	

- Neutral losses can be directly associated with functional groups and the overall structure of the precursor ion.
- The number of pathways could provide an upper estimate of the number of structural isomers.
- 260 structural isomers based on core fragments and unique fragmentation pathways.



Conclusions

- A single infusion TIMS FT-ICR MS experiment permitted the identification of around 3,000 chemical components in PAN samples based on mass accuracy and assuming a total general formula of C_xH_yN₀₋₃O₀₋₁₉S₀₋₁.
- TIMS measurements provided structural and conformational isomeric content per chemical formula (e.g., 4-10 isomers).
- A further estimation of the number of structural isomers was possible based on unique neutral loss fragmentation patterns and core fragments from tandem MS/MS.
- Overall data suggested that multiple structural isomers could share very closely related CCS, which will require the use of ultrahigh resolution TIMS mobility scan functions in tandem with MS/MS.

Acknowledgments

This research was supported by NSF Division of Chemistry, under CAREER award CHE-1654274, co-funding from the Division of Molecular and Cellular Biosciences and the NSF grant HRD-1547798 through FIUs Centers of Research Excellence in Science and Technology (CREST) program.

Analytical workflow

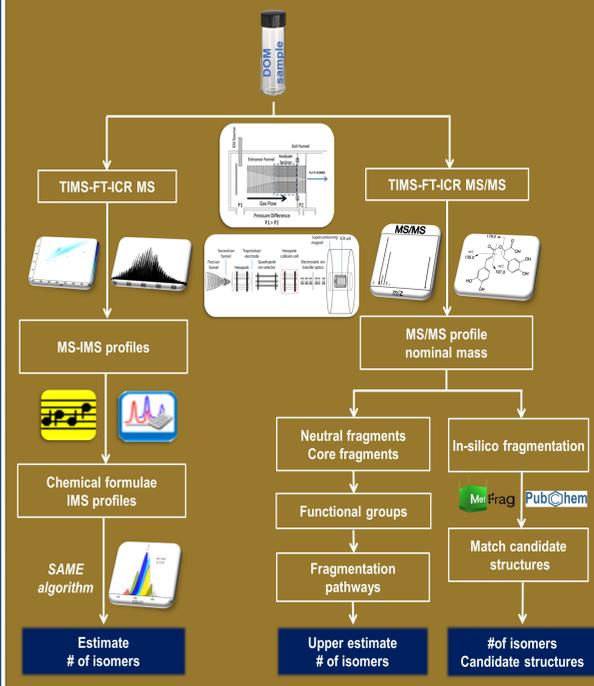


Figure 1. Workflow used to estimate the number of isomers in PAN sample