

IDBac

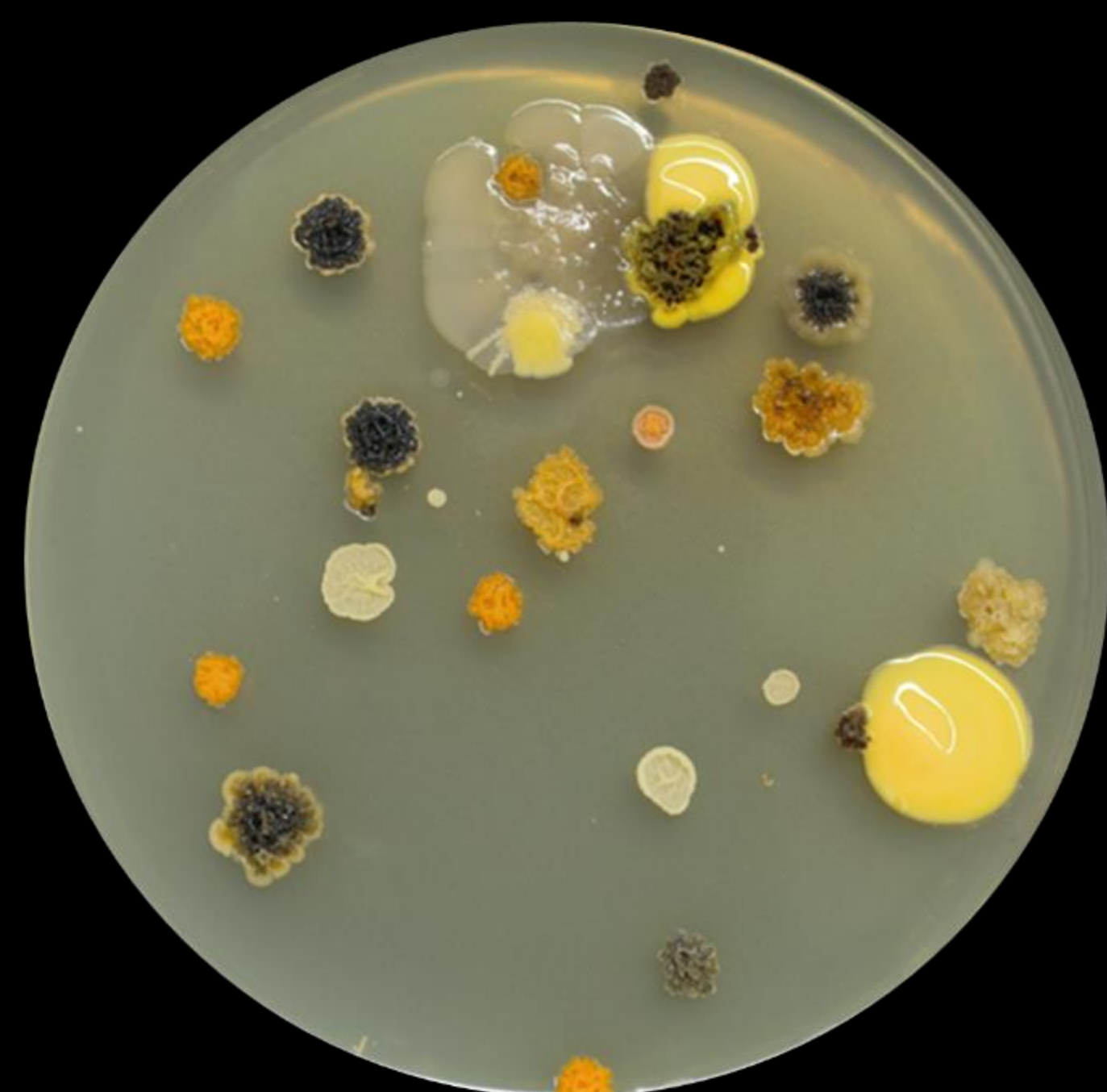
Creating MALDI-TOF MS Software for Microbial Drug Discovery and Culturomics Characterization

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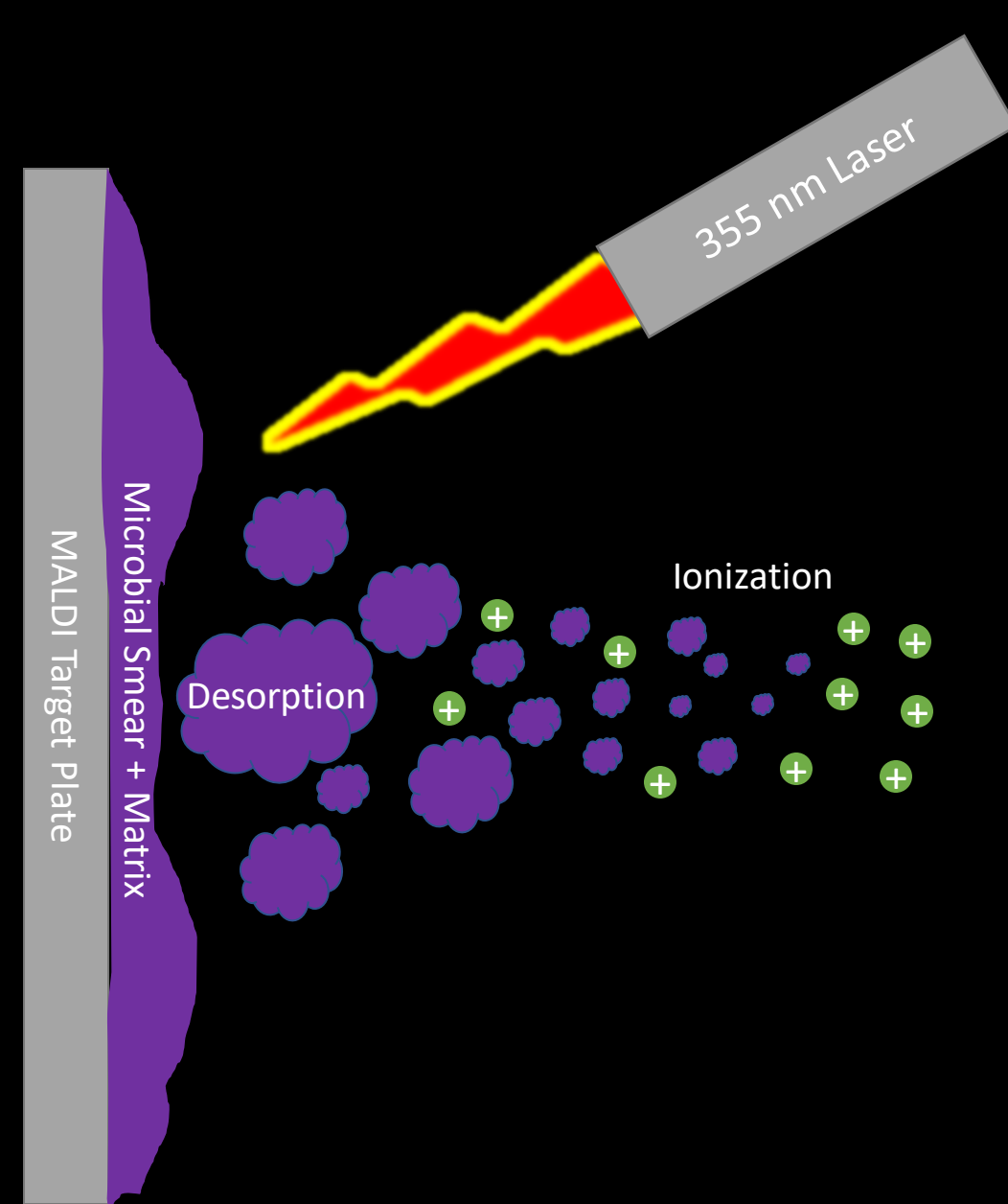
Sample Collection

Finding new microbial natural products begins with sample collection. Our lab has collected sediment and marine organisms from across the globe, including Iceland (shown here), the Great Lakes, and Vietnam.



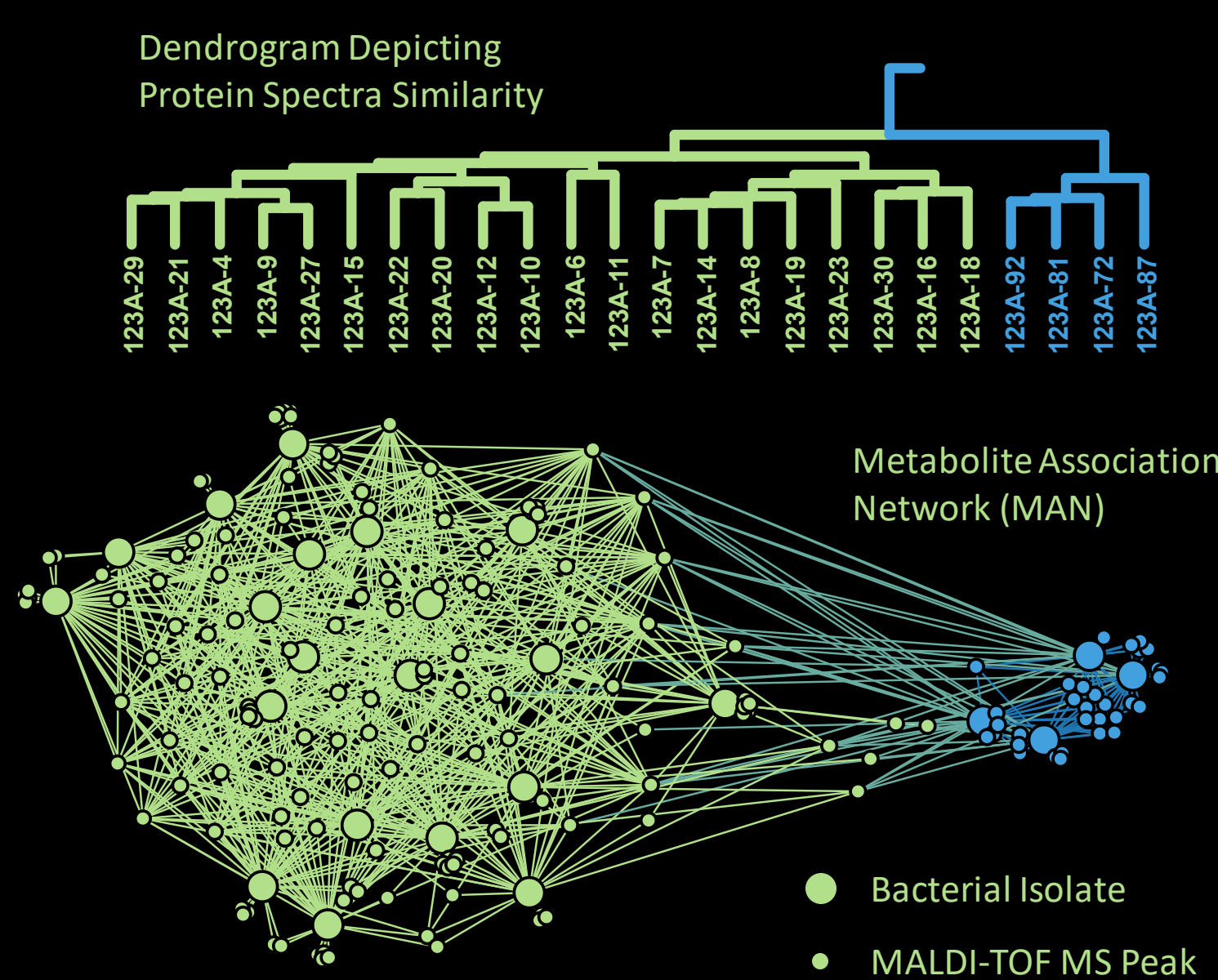
Diversity Plates

Back in lab, sediment, sponges, nudibranchs, etc. are processed and plated onto agar nutrient media promoting the growth and later isolation of microorganisms. A typical expedition generates 100's of plates with 0-100's of colonies.



Matrix Assisted Laser Desorption/Ionization Time of Flight Mass Spectrometry

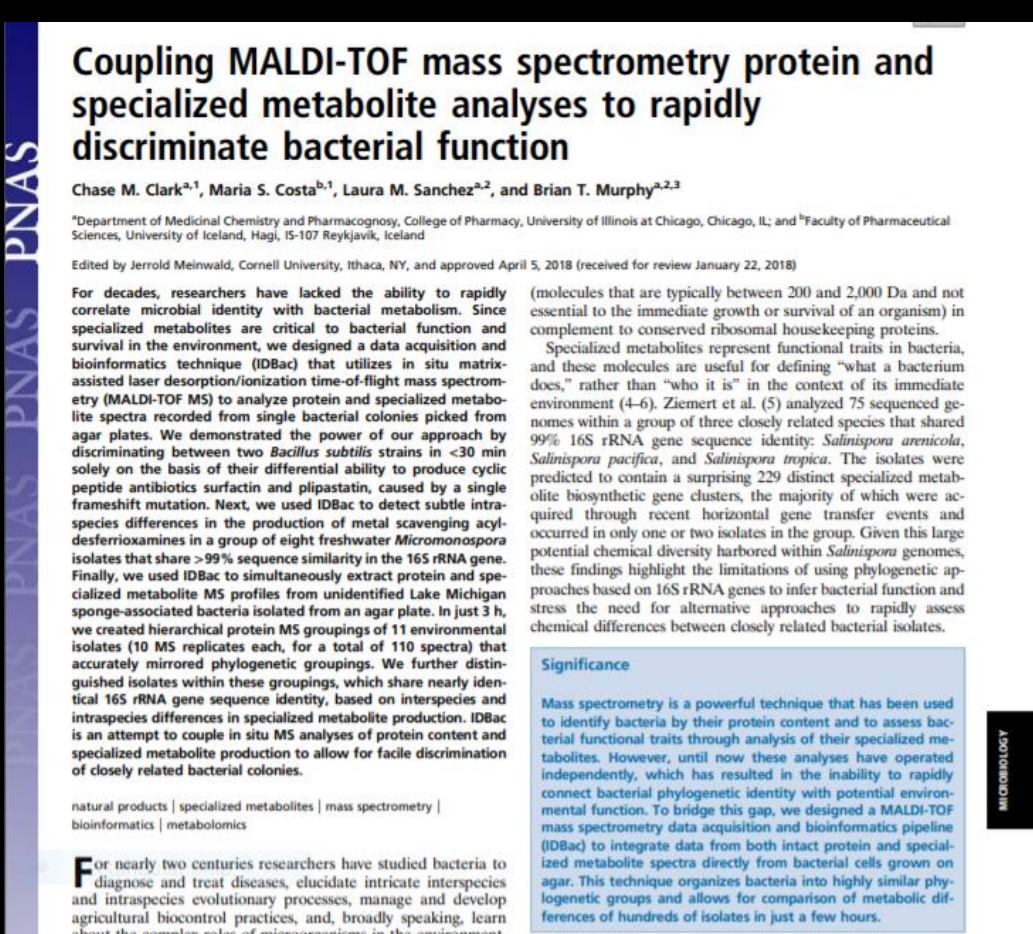
MALDI-TOF MS is a soft ionization technique that, with easy sample preparation, allows us to gather MS data on "protein" (2-20 kDa) and "small molecule" (0.2-2 kDa) mass regions.



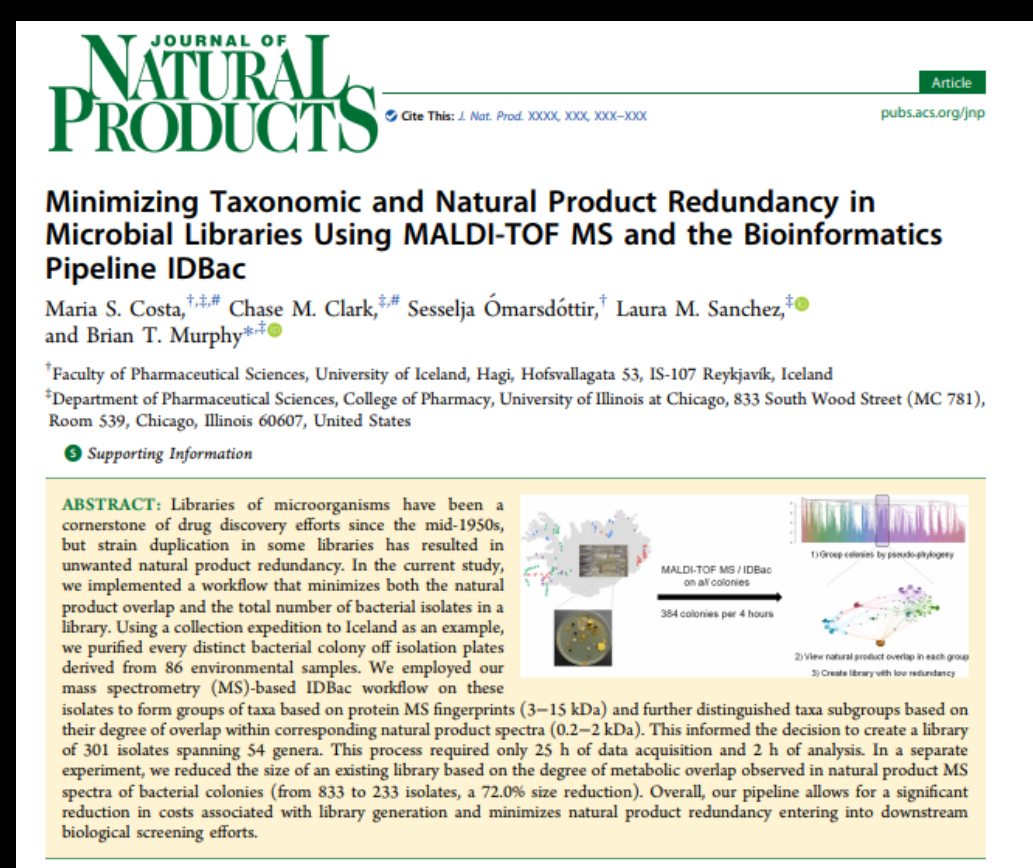
IDBac Software

IDBac was originally developed as a GUI (R/Shiny) to help users analyze typical IDBac MALDI-TOF MS experiments that often generate thousands of protein and small molecule spectra. It is also an R package that was recently redesigned for easier programmatic use. For every IDBac "experiment" a SQLite database is created that contains metadata, mzML files, processed spectra and peaks- all contained within a single, shareable file.

IDBac Publications



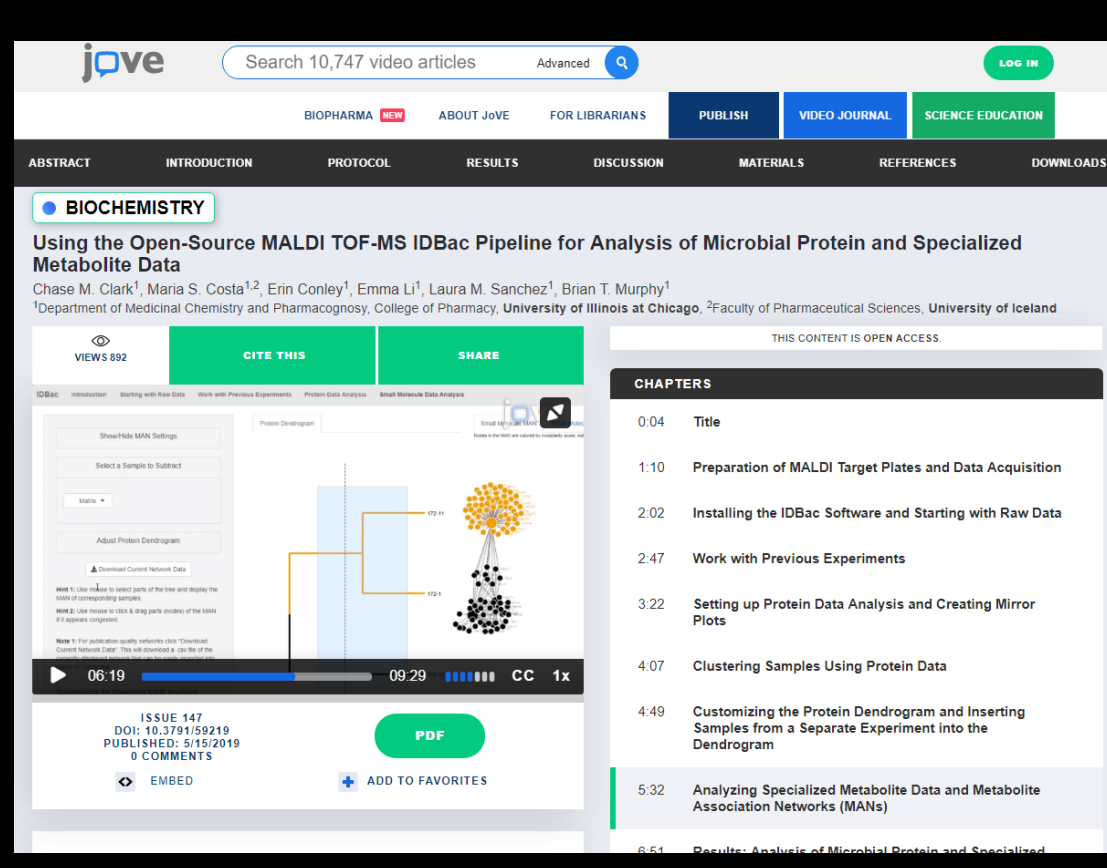
Clark CM, Costa MS, Sanchez LM, Murphy BT. Coupling MALDI-TOF mass spectrometry protein and specialized metabolite analyses to rapidly discriminate bacterial function. *Proc Natl Acad Sci U S A*. 2018 May;115(19):4981-4986. <https://doi.org/10.1073/pnas.1802471115>



Clark CM, Clark CM, Omaroddi S, Sanchez LM, Murphy BT. Minimizing Taxonomic and Natural Product Redundancy in Microbial Libraries Using MALDI-TOF MS and the Bioinformatics Pipeline IDBac. *J Nat Prod Am Chem Soc*. 2019 Aug 23;82(8):2167-2173. <https://doi.org/10.1021/acs.jnatprod.9b00168>



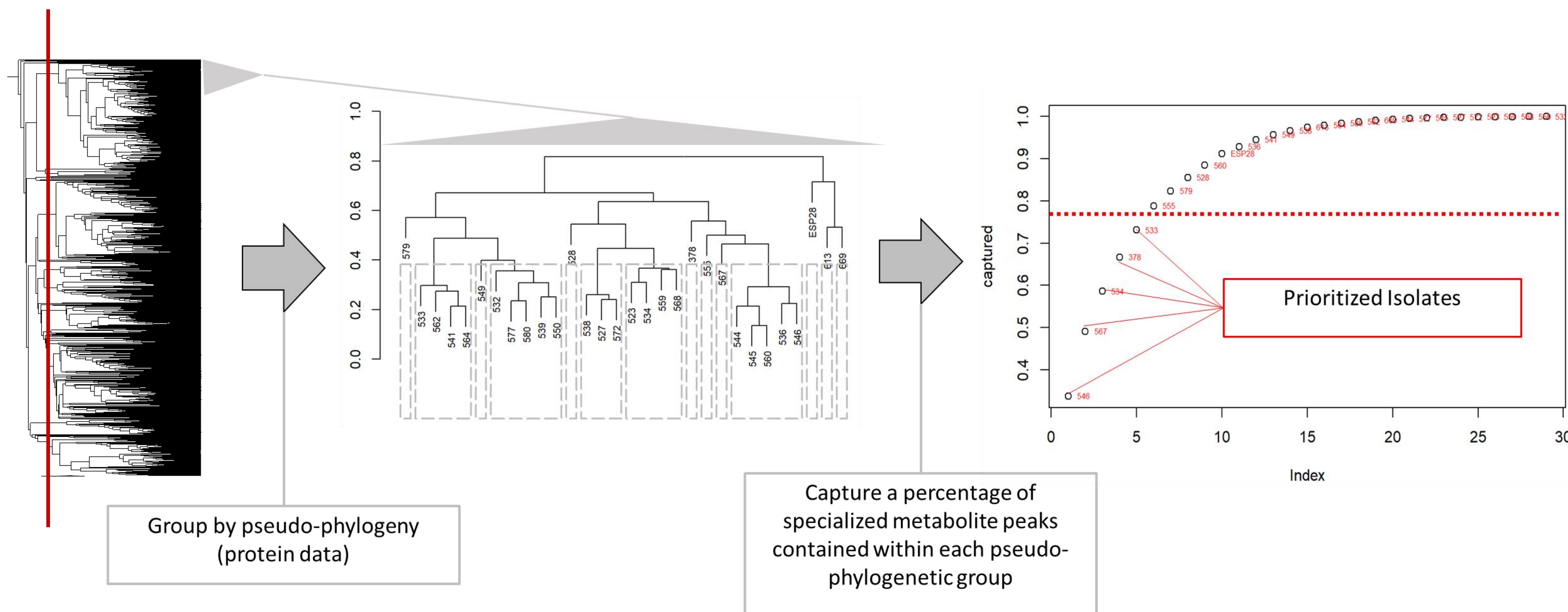
Clark CM, Murphy BT, Sanchez LM. A Call to Action: the Need for Standardization in Developing Open-Source Mass Spectrometry-Based Methods for Microbial Subspecies Discrimination. *mSystems*. 2020;51(1):e00813-19. <https://doi.org/10.1128/mSystems.00813-19>



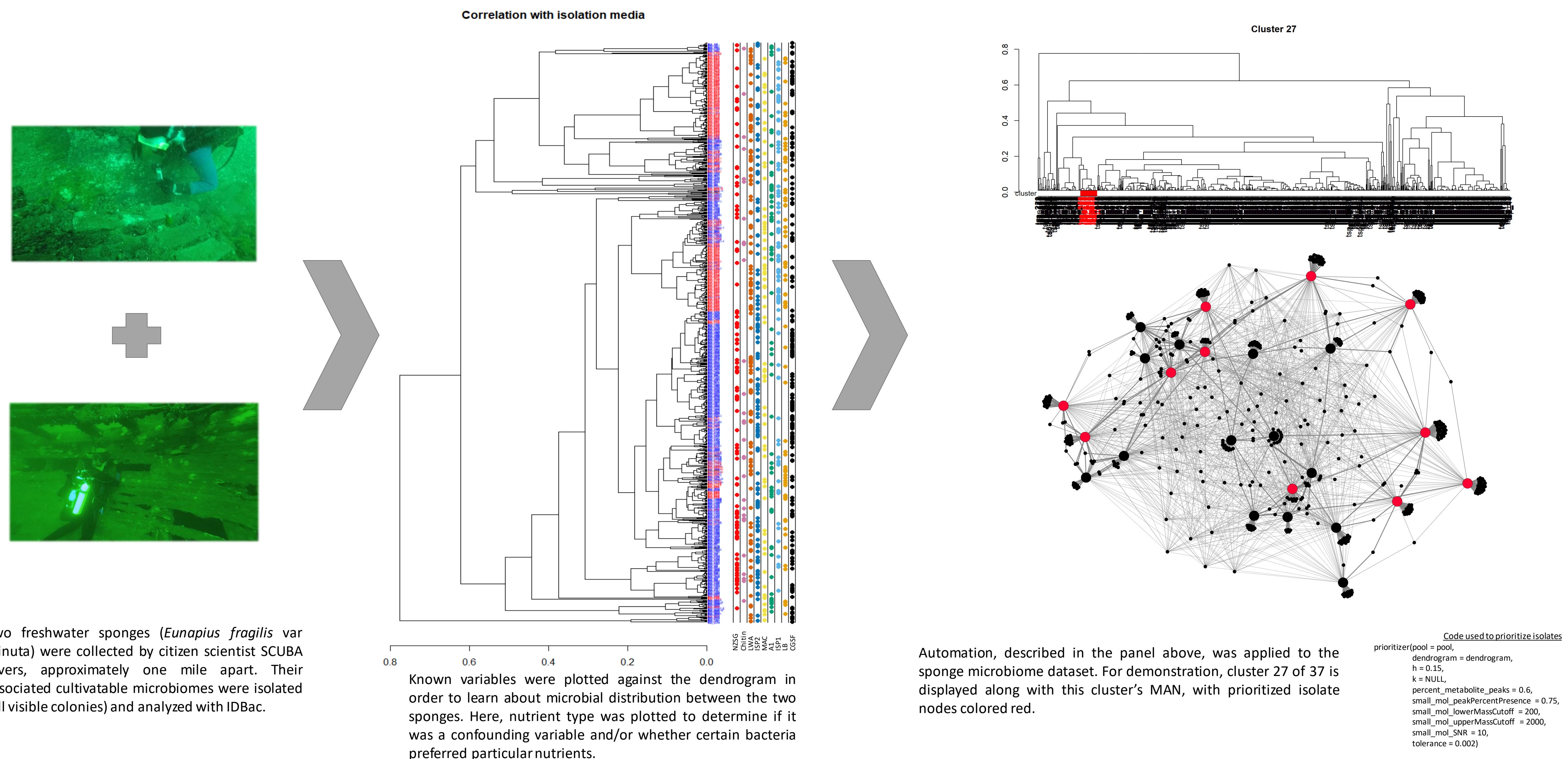
Clark CM, Costa MS, Conley E, Li E, Sanchez LM, Murphy BT. Using the Open-Source MALDI-TOF MS IDBac Pipeline for Analysis of Microbial Protein and Specialized Metabolite Data. *J Vis Exp*. (147), e59219. (2019). <https://doi.org/10.3791/59219>

Automating Microbial Library Prioritization

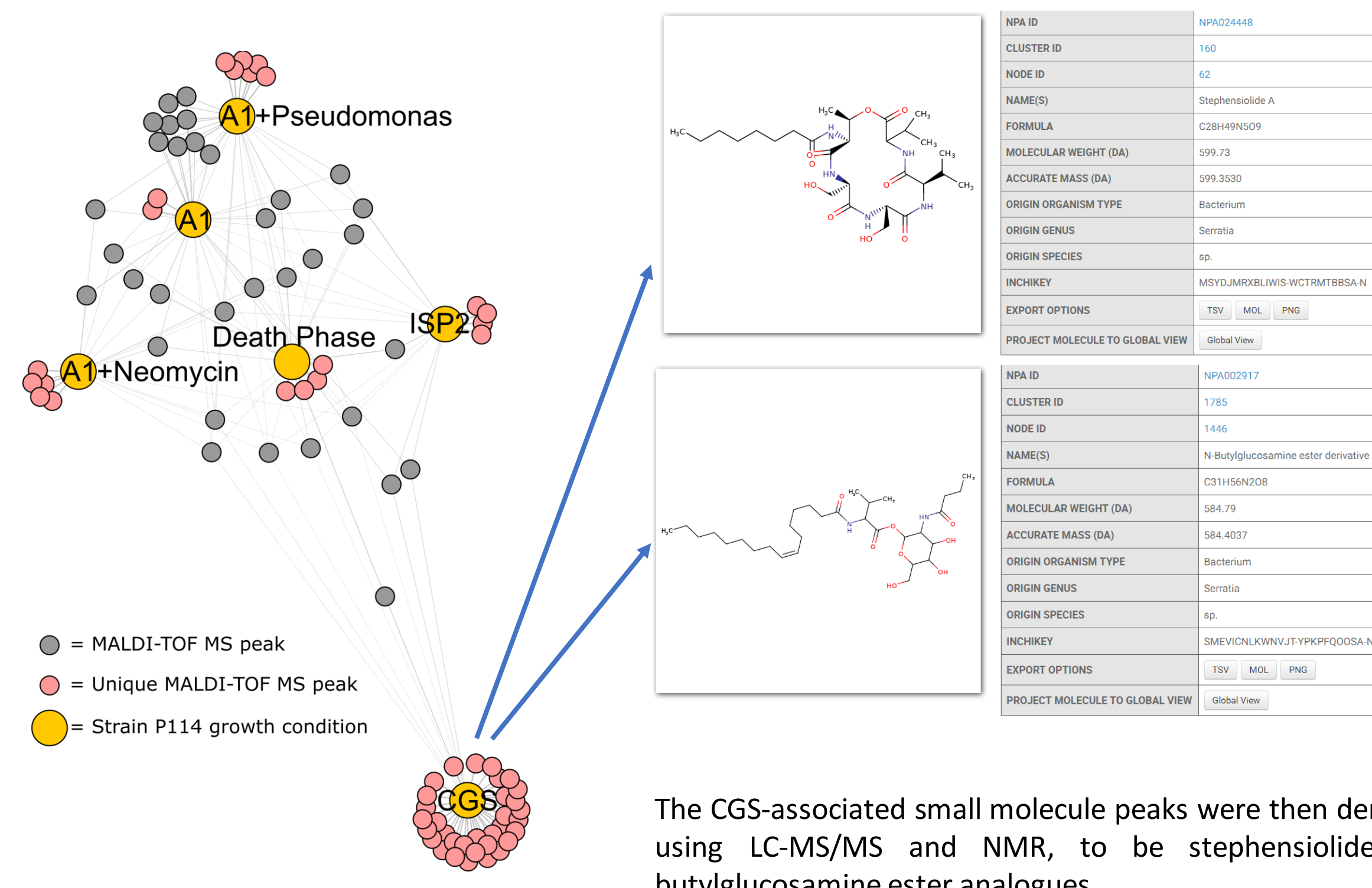
The next version of IDBac will contain automated functions to assist users in quickly parsing through 100's to 1000's of strains to create small but highly-diverse libraries.



Using IDBac to Understand Microbial Natural Product Distribution in Freshwater Sponge Microbiomes

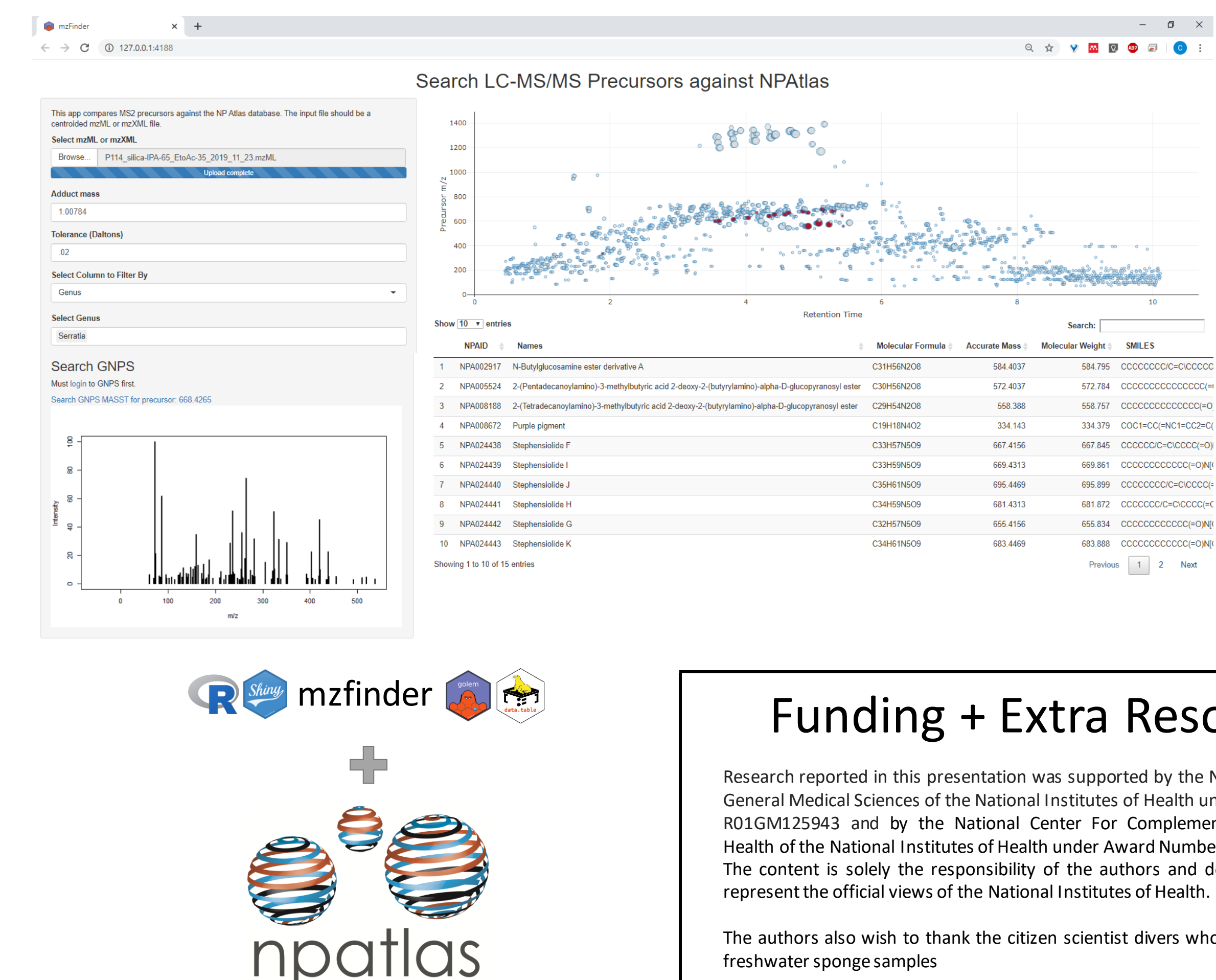


Analyzing the Effect of Culture Conditions on the Production of Antibiotics



The CGS-associated small molecule peaks were then dereplicated, using LC-MS/MS and NMR, to be stephensiolide and N-butylglucosamine ester analogues. Due to the N-butylglucosamine ester derivatives' previously hypothesized activity against *Mycobacterium tuberculosis*¹ we have grown "P114" at 30 L scale and currently have fractions undergoing testing with collaborators at UIC's Institute for Tuberculosis Research.

[1] Dwivedi D, Jansen R, Molinari G, Nimitz M, Johri NB, Wray V. Antimycobacterial Serratomolides and Diacyl Peptidoglycosamine Derivatives from *Serratia* sp. *J Nat Prod*. 2008;71(4):637-641. doi:10.1021/jp7007126



HR-ESI-UPCL-MS/MS afforded no matches from GNPS¹ (other than from culture media). An R package (mzfinder) was written to search all precursor matches against the Natural Products Atlas². This aided dereplication of the N-butylglucosamine ester derivatives.

[1] Wang M, Carver JJ, Phelan V, et al. Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. *Nat Biotechnol*. 2016;34(8):828-837. doi:10.1038/nbt.3597
[2] van Santen JA, Jacob G, Singh AL, et al. The Natural Products Atlas: An Open Access Knowledge Base for Microbial Natural Products Discovery. *ACS Cent Sci*. 2019;5(11):1824-1833. doi:10.1021/acscentsci.9b00806

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